```
=> fil reg ; d que 13
FILE PREGISTRY ENTERED AT 08:54:17 ON 06 JUL 2001
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STRUCTURE FILE UPDATES:
                           5 JUL 2001 HIGHEST RN 344737-88-8
DICTIONARY FILE UPDATES:
                           5 JUL 2001 HIGHEST RN 344737-88-8
TSCA INFORMATION NOW CURRENT THROUGH January 11, 2001
  Please note that search-term pricing does apply when
  conducting SmartSELECT searches.
Structure search limits have been increased. See HELP SLIMIT
for details.
L3
             31 SEA FILE=REGISTRY ABB=ON ^.{0-6}HK[ALIVPFWMSTYNQCG]K.{0-6}^/SO
                SP
=> d rn cn sql kwic nte 13 1-31; fil capl; d que nos 14
     ANSWER 1 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
     344422-23-7 REGISTRY - use Registry # to match sequence to witation
     L-Lysine, L-histidyl-L-lysyl-L-seryl-L-lysyl- (9CI) (CA INDEX NAME)
CN
SQL
         1 HKSKK
SEQ
                                0-12
HITS AT:
           1-5
                                 0,1
L3
     ANSWER 2 OF 31 REGISTRY COPYRIGHT 2001 ACS
     338970-56-2 REGISTRY
RN
CN
     L-Lysine, glycyl-L-histidyl-L-lysyl-L-alanyl-L-lysylglycyl-L-prolyl-L-
     arginyl- (9CI) (CA INDEX NAME)
SQL
     9
SEQ
         1 GHKAKGPRK
HITS AT:
           1-9
L3
     ANSWER 3 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     338970-52-8 REGISTRY
     Glycine, glycyl-L-histidyl-L-lysyl-L-valyl-L-lysyl-L-arginyl-L-prolyl-L-
CN
     lysyl- (9CI) (CA INDEX NAME)
SQL
         1 GHKVKRPKG
SEQ
           _____
HITS AT:
           1-9
     ANSWER 4 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
     334993-69-0 REGISTRY
     L-Lysine, L-.alpha.-glutamyl-L-histidyl-L-lysyl-L-valyl-L-lysyl-L-
CN
     isoleucylglycyl-L-valyl-L-.alpha.-glutamyl-L-glutaminyl- (9CI) (CA INDEX
     NAME)
SQL
     11
SEQ
         1 EHKVKIGVEQ K
```

```
HITS AT:
        1-11
   ANSWER 5 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
   316821-90-6 REGISTRY
   L-Lysine, L-lysyl-L-histidyl-L-lysyl-L-histidyl-L-lysyl-L-histidyl-L-
CN
    lysylglycyl-L-lysyl-L-histidyl-L-lysyl-L-histidyl-L-lysyl-L-histidyl-
    (9CI) (CA INDEX NAME)
   15
SQL
SEQ
       1 КНКНКНКСКН КНКНК
        HITS AT:
        1-15
   ANSWER 6 OF 31 REGISTRY COPYRIGHT 2001 ACS
Т.3
RN
   290374-35-5 REGISTRY
CN
   L-Lysine, N2-acetyl-L-lysyl-L-threonyl-L-.alpha.-glutamyl-L-seryl-L-
   histidyl-L-lysyl-L-alanyl-L-lysylglycyl- (9CI) (CA INDEX NAME)
SQL
   10
       1 KTESHKAKGK
SEQ
        ========
        1-10
HITS AT:
NTE modified
______
            ----- location ----- description
terminal mod. Lys-1 - N-acetyl
ANSWER 7 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
   282712-87-2 REGISTRY
   L-Histidinamide, L-alanyl-L-lysyl-L-arginyl-L-histidyl-L-histidyl-L-lysyl-
CN
   L-tyrosyl-L-lysyl-L-arginyl-L-lysyl-L-phenylalanyl- (9CI) (CA INDEX NAME)
OTHER NAMES:
   22: PN: WO0040965 PAGE: 11 claimed protein
CN
SQL
SEQ
       1 AKRHHKYKRK FH
        _________
HITS AT:
        1-12
NTE modified
----- location ----- description
terminal mod. His-12 -
                                C-terminal amide
   ANSWER 8 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
   278169-06-5 REGISTRY
CN
   L-Serine, L-arginyl-L-histidyl-L-lysyl-L-glutaminyl-L-lysyl-L-isoleucyl-L-
    isoleucyl-L-alanyl-L-prolyl- (9CI) (CA INDEX NAME)
SQL
   10
       1 RHKQKIIAPS
SEQ
        ========
HITS AT:
        1-10
L3
   ANSWER 9 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
   251651-17-9 REGISTRY
CN
   L-Valine, L-methionyl-L-seryl-L-arginyl-L-lysyl-L-histidyl-L-lysyl-L-
```

```
tryptophyl-L-lysyl-L-leucyl-L-serylglycyl- (9CI) (CA INDEX NAME)
SQL
SEO
         1 MSRKHKWKLS GV
          HITS AT:
           1 - 12
L3
    ANSWER 10 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
    225518-96-7 REGISTRY
CN
    L-Threonine, L-histidyl-L-lysylglycyl-L-lysyl-L-lysyl-L-.alpha.-aspartyl-L-
    threonyl-L-seryl-L-isoleucyl- (9CI) (CA INDEX NAME)
SOL
SEO
        1 HKGKKDTSIT
           ==========
HITS AT:
           1-10
    ANSWER 11 OF 31 REGISTRY COPYRIGHT 2001 ACS
1.3
RN
    201799-95-3 REGISTRY
CN
    L-Leucine, L-.alpha.-aspartyl-L-lysyl-L-histidyl-L-lysyl-L-leucyl-L-lysyl-
    L-lysyl-L-seryl-L-.alpha.-glutamyl- (9CI) (CA INDEX NAME)
SQL
    10
SEQ
         1 DKHKLKKSEL
           _____
HITS AT:
           1 - 10
L3
    ANSWER 12 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
    201799-94-2 REGISTRY
    L-Lysine, L-arginyl-L-.alpha.-glutamylglycyl-L-.alpha.-aspartyl-L-lysyl-L-
CN
    histidyl-L-lysyl-L-leucyl-L-lysyl- (9CI) (CA INDEX NAME)
SOL
    10
SEQ
         1 REGDKHKLKK
          _____
HITS AT:
           1-10
    ANSWER 13 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
    187816-25-7 REGISTRY
CN
    L-Alanine, L-.alpha.-glutamyl-L-alanyl-L-prolyl-L-histidyl-L-lysyl-L-
    phenylalanyl-L-lysyl-L-seryl- (9CI) (CA INDEX NAME)
SQL
      🖈 1 EAPHKFKSA
SEQ
           ______
HITS AT:
           1-9
    ANSWER 14 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
    187816-07-5 REGISTRY
RN
CN
    L-Valine, L-.alpha.-glutamyl-L-alanyl-L-prolyl-L-histidyl-L-lysyl-L-
    phenylalanyl-L-lysyl-L-asparaginyl- (9CI) (CA INDEX NAME)
SQL
SEQ
         1 EAPHKFKNV
           =======
HITS AT:
           1-9
    ANSWER 15 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
    186258-89-9 REGISTRY
CN
    L-Histidine, L-alanyl-L-lysyl-L-arginyl-L-histidyl-L-histidyl-L-lysyl-L-
     tyrosyl-L-lysyl-L-arginyl-L-lysyl-L-phenylalanyl- (9CI) (CA INDEX NAME)
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OTHER NAMES:
CN
   15: PN: WO0040965 PAGE: 19 claimed protein
SQL
SEQ
       1 AKRHHKYKRK FH
        HITS AT:
        1-12
   ANSWER 16 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
  176260-60-9 REGISTRY
RN
   histidyl]-L-lysyl]-L-glutaminyl]-L-lysyl]-L-isoleucyl]-L-isoleucyl]-L-
    alanyl]-L-prolyl]-L-alanyl]- (9CI) (CA INDEX NAME)
SQL
   12
SEO
       1 CRHKQKIIAP AK
        *****
HITS AT:
        1 - 12
   ANSWER 17 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
   176260-59-6 REGISTRY
   ĊN
    arginyl]-L-histidyl]-L-lysyl]-L-glutaminyl]-L-lysyl]-L-isoleucyl]-L-
    isoleucyl]-L-alanyl]-L-prolyl]- (9CI) (CA INDEX NAME)
SQL
   12
SEQ
       1 CCRHKQKIIA PA
        ___________
HITS AT:
        1-12
   ANSWER 18 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
   161174-90-9 REGISTRY
RN
   L-Tyrosinamide, L-cysteinyl-L-histidyl-L-lysyl-L-leucyl-L-lysyl-L-alanyl-L-
CN
    alanyl-L-leucyl-L-cysteinyl-, cyclic (1.fwdarw.9)-disulfide (9CI) (CA
    INDEX NAME)
SQL
   10
SEQ
       1 CHKLKAALCY
        =========
HITS AT:
       1-10
NTE modified
----- location ----- description
____________
terminal mod. Tyr-10 - C-terminal amide bridge Cys-1 - Cys-9 disulfide bridge
L3
   ANSWER 19 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
    161174-87-4 REGISTRY
CN
    L-Tyrosinamide, L-cysteinyl-L-histidyl-L-lysyl-L-leucyl-L-lysyl-L-alanyl-L-
    alanyl-L-leucyl-L-cysteinyl- (9CI) (CA INDEX NAME)
SOL
SEQ
       1 CHKLKAALCY
        ______
HITS AT: 1-10
NTE modified
             ----- location ----- description
```

```
Tyr-10
terminal mod.
                                           C-terminal amide
L3
     ANSWER 20 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     157566-35-3 REGISTRY
CN
     L-Glutamic acid, L-arginyl-L-.alpha.-glutamylglycyl-L-.alpha.-aspartyl-L-
     lysyl-L-histidyl-L-lysyl-L-leucyl-L-lysyl-L-lysyl-L-seryl-L.alpha.-
     glutamyl-L-leucyl-L-lysyl- (9CI) (CA INDEX NAME)
SQL
     15
SEO
         1 REGDKHKLKK SELKE
           _______________
HITS AT:
           1-15
L3
     ANSWER 21 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     144776-43-2 REGISTRY
CN
     L-Lysine, N2-[N-[N2-[N-(N2-L-arginyl-L-arginyl)-L-leucyl]-L-histidyl]-L-
     lysyl]-L-leucyl]- (9CI) (CA INDEX NAME)
SQL
SEO
         1 RRLHKLK
           1-7
HITS AT:
     ANSWER 22 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
RN
     144776-41-0 REGISTRY
CN
     L-Lysine, N2-[N-[N2-[N-(N2-L-arginyl-L-arginyl)-L-.alpha.-glutamyl]-L-
     histidyl]-L-lysyl]-L-leucyl]- (9CI) (CA INDEX NAME)
SQL
SEQ
         1 RREHKLK
           ======
HITS AT:
           1 - 7
L3
     ANSWER 23 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     144776-40-9 REGISTRY
CN
     L-Lysine, N2-[N-[N2-[N-[N-(N2-L-arginyl-L-arginyl)-L-seryl]-L-histidyl]-L-
     lysyl]-L-leucyl]- (9CI) (CA INDEX NAME)
SQL
SEO
         1 RRSHKLK
           ======
HITS AT:
           1 - 7
1.3
    ANSWER 24 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     121795-39-9 REGISTRY
CN
    L-Cysteine, L-prolyl-L-threonyl-L-alpha.-glutamyl-L-alanyl-L-arginyl-L-
     histidyl-L-lysyl-L-glutaminyl-L-lysyl-L-isoleucyl-L-valyl-L-alanyl-L-
     prolyl-L-valyl- (9CI) (CA INDEX NAME)
SQL
    15
SEQ
         1 PTEARHKOKI VAPVC
           HITS AT:
           1-15
L3
     ANSWER 25 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
     115154-42-2 REGISTRY
CN
     L-Lysine, N2-[N-[N2-[N-[N-(N-L-.alpha.-aspartyl-L-seryl)-L-
     histidyl]-L-histidyl]-L-lysyl]-L-alanyl]-L-lysyl]-L-alanyl]- (9CI)
     INDEX NAME)
SQL
    9
```

```
SEO
        1 DSHHKAKAK
HITS AT:
          1-9
    ANSWER 26 OF 31 REGISTRY COPYRIGHT 2001 ACS
L3
    115154-41-1 REGISTRY
RN
CN
    L-Lysine, L-seryl-L-histidyl-L-histidyl-L-lysyl-L-alanyl-L-lysylglycyl-
     (9CI)
          (CA INDEX NAME)
OTHER CA INDEX NAMES:
    L-Lysine, N2-[N-[N2-[N-[N2-[N-(N-L-seryl-L-histidyl)-L-histidyl]-L-lysyl]-
    L-alanyl]-L-lysyl]glycyl]-
SQL
SEO
        1 SHHKAKGK
HITS AT:
          1-8
    ANSWER 27 OF 31 REGISTRY COPYRIGHT 2001 ACS
1.3
RN
    112424-93-8 REGISTRY
CN
    D-Alaninamide, N-acetyl-3-(2-naphthalenyl)-D-alanyl-4-chloro-D-
    phenylalanyl-3-(3-pyridinyl)-D-alanyl-L-seryl-L-histidyl-N6-(3-
    pyridinylcarbonyl)-D-lysyl-L-leucyl-N6-(3-pyridinylcarbonyl)-L-lysyl-L-
    prolyl- (9CI) (CA INDEX NAME)
SQL
    10
SEQ
        1 AFASHKLKPA
          ========
          1-10
HITS AT:
NTE modified
                ----- location ----- description
-----
terminal mod. Ala-1
                                         N-acetyl
terminal mod. Ala-10
                                         C-terminal amide
modification Ala-1
                                         2-naphthalenyl<2-Naph>
modification
               Phe-2
                                         chloro<Cl>
modification
               Ala-3
                                         3-pyridinyl<3Py>
             Lys-6
modification
                                         3-pyridinylcarbonyl
                                         3-pyridinylcarbonyl
modification
               Lys-8
L3
    ANSWER 28 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
    97461-89-7 REGISTRY
CN
    L-Lysine, N2-[1-(N2-L-histidyl-L-lysyl)-L-prolyl]- (9CI) (CA INDEX NAME)
SQL
SEO
        1 HKPK
HITS AT:
          1 - 4
L3
    ANSWER 29 OF 31 REGISTRY COPYRIGHT 2001 ACS
RN
    92269-40-4 REGISTRY
    L-Isoleucine, N-[N2-[N2-[N2-(N-L-arginyl-L-histidyl)-L-lysyl]-L-
CN
    glutaminyl]-L-lysyl]- (9CI) (CA INDEX NAME)
SQL
SEO
        1 RHKQKI
HITS AT:
          1-6
```

```
L3 ANSWER 30 OF 31 REGISTRY COPYRIGHT 2001 ACS
```

RN 92269-39-1 REGISTRY

CN L-Lysine, N2-[N2-[N-(N2-L-alanyl-L-arginyl)-L-histidyl]-L-lysyl]-L-glutaminyl]- (9CI) (CA INDEX NAME)

SQL 6

SEQ 1 ARHKQK

HITS AT: 1-6

L3 ANSWER 31 OF 31 REGISTRY COPYRIGHT 2001 ACS

RN 92227-36-6 REGISTRY

CN L-Valine, N-[N-[N2-[N2-(N2-L-histidyl-L-lysyl)-L-glutaminyl]-L-lysyl]-L-isoleucyl]- (9CI) (CA INDEX NAME)

SQL 6

SEQ 1 HKQKIV =====

HITS AT: 1-6

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FILE COVERS 1947 - 6 Jul 2001 VOL 135 ISS 3 FILE LAST UPDATED: 5 Jul 2001 (20010705/ED)

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L3 31 SEA FILE=REGISTRY ABB=ON ^.{0-6}HK[ALIVPFWMSTYNQCG]K.{0-6}^/SQ

L4 25 SEA FILE=CAPLUS ABB=ON L3 Registry file answer set crossed over into CAPLUS to get citations.

=> d ibib abs hitrn 14 1-25; fil hom

ANSWER 1 OF 25 CAPLUS COPYRIGHT 2001 ACS L4

ACCESSION NUMBER:

2001:429545 CAPLUS

TITLE:

Peptides and peptidomimetics with structural

similarity to human p53 that activate p53 function

INVENTOR(S):

Halazonetis, Thanos; Hartwig, Wolfgang

PATENT ASSIGNEE(S):

Bayer Corp., USA; The Wistar Institute

SOURCE:

U.S., 22 pp., Cont.-in-part of U.S. 6,169,073.

CODEN: USXXAM

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

2

PATENT INFORMATION:

PATENT NO.				KIND	DATE	APE	DATE	
	US	6245886		B1	20010612	US	1997-894327	19971204
	US	6169073		B1	20010102	US	1995-392542	19950216
	WO	9625434		A1	19960822	WO	1996-US1535	19960216

W: AU, CA, JP, KR, US

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.:

US 1995-392542 A2 19950216 WO 1996-US1535 W 19960216

The present invention provides peptides and peptidomimetics corresponding AΒ to part or to the entirety of the region encompassed by residues 360-386 of human p53, said peptides and peptidomimetics characterized by the ability to activate DNA binding of wild-type p53 and to select tumor-derived p53 mutants. Pharmaceutical compns. of the compds. of the invention and methods of using these compns. therapeutically are also

344422-23-7 - Use Registry # to match citation to sequence TΤ

RL: PRP (Properties)

(unclaimed sequence; peptides and peptidomimetics with structural similarity to human p53 that activate p53 function)

REFERENCE COUNT:

34

REFERENCE(S):

- (1) Anon; EP 0518650 1992 CAPLUS (2) Anon; WO 94/08241 1994 CAPLUS
- (3) Anon; WO 94/10306 1994 CAPLUS
- (4) Anon; WO 94/12202 1994 CAPLUS (5) Anon; WO 95/17213 1995 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

CAPLUS COPYRIGHT 2001 ACS ANSWER 2 OF 25

ACCESSION NUMBER:

2001:284116 CAPLUS

DOCUMENT NUMBER:

134:306975

TITLE:

Recombinant factor C and factor C fragments for endotoxin detection or removal and for use as

anti-microbials

INVENTOR(S): PATENT ASSIGNEE(S): Ding, Jeak Ling; Ho, Bow; Tan, Nguan Soon National University of Singapore, Singapore

SOURCE:

PCT Int. Appl., 123 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.

KIND DATE

APPLICATION NO. DATE

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20001013
     WO 2001027289
                     A2
                            20010419
                                          WO 2000-SG162
            RW: GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZW, AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE, BF, BJ,
             CF, CG, CI, CM, GA, GN, GW, ML, MR, NE, SN, TD, TG
                                        US 1999-159569 P 19991015
US 2000-626795 A 20000726
PRIORITY APPLN. INFO.:
     Recombinant fragments of Factor C are disclosed. These proteins and
     peptides show great potency in recognizing, binding to, neutralizing, and
     removing endotoxin. These mols. can thus be used for anti-microbial,
     anti-endotoxin, and anti-sepsis therapy. SSCrFCES is a 38 kDa protein
     representing the LPS-binding domain of Factor C. The ability of SSCrFCES
     to bind lipid A was analyzed using an ELISA-based assay as well as surface
     plasmon resonance. Surface plasmon resonance similarly carried out for
     SSCrFC-sushi-1,2,3-GFP, SSCrFC-sushi-1-GFP, and SSCrFC-sushi-3-GFP
     confirmed their superior affinity for endotoxin. The 50 \mbox{\%}
     endotoxin-neutralizing concn. of SSCrFCES against 200 EU of endotoxin is
     0.069 .mu.M, suggesting that SSCrFCES is an effective inhibitor of Limulus
     amoebocyte lysis coagulation cascade. Although partially attenuated by
     human serum, as low as 1 .mu.M of SSCrFCES inhibits the LPS-induced
     secretion of hTNF-.alpha. and hIL-8 THP-1 and human peripheral blood
     mononuclear cells with a potency more superior than polymyxin B. SSCrFCES
     is non-cytotoxic, with a clearance rate of 4.7 mL/min. The LD90 of
     SSCrFCES for LPS lethality in mice is achieved at 2 .mu.M. These results
     demonstrate the endotoxin-neutralizing capability of SSCrFCES in vitro and
     in vivo, as well as its potential for use in the treatment of
     endotoxin-induced septic shock. Also embodied in this application is the
     use of the sushi peptides and their mutant derivs. as potent
     antimicrobials. Further embodied in this application is the use of sushi
     peptides or sushi recombinant proteins to remove endotoxin from liqs.
ΙT
     334993-69-0P
     RL: ARG (Analytical reagent use); BAC (Biological activity or effector,
     except adverse); BPN (Biosynthetic preparation); PRP (Properties); THU
     (Therapeutic use); ANST (Analytical study); BIOL (Biological study); PREP
     (Preparation); USES (Uses)
        (Sushi 3 peptide; recombinant factor C and factor C fragments for
        endotoxin detection or removal and for use as anti-microbials)
     ANSWER 3 OF 25 CAPLUS COPYRIGHT 2001 ACS
L4
ACCESSION NUMBER:
                         2001:211598 CAPLUS
DOCUMENT NUMBER:
                         134:351765
TITLE:
                         Recombinant human adenovirus: targeting to the human
                         transferrin receptor improves gene transfer to brain
                         microcapillary endothelium
AUTHOR(S):
                         Xia, Haibin; Anderson, Brian; Mao, Qinwen; Davidson,
                         Beverly L.
CORPORATE SOURCE:
                         Program in Gene Therapy, Departments of Internal
                         Medicine, University of Iowa College of Medicine, Iowa
                         City, IA, 52242, USA
SOURCE:
                         J. Virol. (2000), 74(23), 11359-11366
                         CODEN: JOVIAM; ISSN: 0022-538X
PUBLISHER:
                         American Society for Microbiology
DOCUMENT TYPE:
                         Journal
LANGUAGE:
                         English
AΒ
     Some inborn errors of metab. due to deficiencies of sol. lysosomal enzymes
```

cause global neurodegenerative disease. Representative examples include the infantile and late infantile forms of the ceroid lipofuscinoses (CLN1 or CLN2 deficiency, resp.) and mucopolysaccharidoses type VII (MPS VII), a deficiency of .beta.-glucuronidase. Treatment of the central nervous system component of these disorders will require widespread protein or enzyme replacement, either through dissemination of the protein or through dissemination of a gene encoding it. We hypothesize that transduction of brain microcapillary endothelium (BME) with recombinant viral vectors, with secretion of enzyme product basolaterally, could allow for widespread enzyme dissemination. To achieve this, viruses should be modified to target the BME. This requires (i) identification of a BME-resident target receptor, (ii) identification of motifs targeted to that mol., (iii) the construction of modified viruses to allow for binding to the target receptor, and (iv) demonstrated transduction of receptor-expressing cells. In proof of principal expts., we chose the human transferrin receptor (hTfR), a mol. found at high d. on human BME. A nonamer phage display library was panned for motifs which could bind hTfR. Forty-three clones were sequenced, most of which contained an AKxxK/R, KxKxPK/R, or KxK motif. Ten peptides representative of the three motifs were cloned into the HI loop of adenovirus type 5 fiber. All motifs tested retained their ability to trimerize and bind transferrin receptor, and seven allowed for recombinant adenovirus prodn. Importantly, the fiber-modified viruses facilitated increased gene transfer (2- to 34-fold) to hTfR expressing cell lines and human brain microcapillary endothelia expressing high levels of endogenous receptor. Our data indicate that adenoviruses can be modified in the HI loop for expanded tropism to the hTfR.

ፐጥ 338970-52-8P 338970-56-2P

> RL: BPR (Biological process); SPN (Synthetic preparation); BIOL (Biological study); PREP (Preparation); PROC (Process)

(recombinant human adenovirus: targeting to the human transferrin receptor improves gene transfer to brain microcapillary endothelium)

REFERENCE COUNT:

36

REFERENCE(S):

(1) Anderson, R; Gene Ther 2000, V7, P1034 CAPLUS

- (2) Bosch, A; Hum Gene Ther 2000, V11, P1139 CAPLUS
- (4) Broadwell, R; Exp Neurol 1996, V142, P47 CAPLUS
- (6) Chartier, C; J Virol 1996, V70, P4805 CAPLUS
- (8) Douglas, J; Nat Biotechnol 1996, V14, P1574 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

CAPLUS COPYRIGHT 2001 ACS L4 ANSWER 4 OF 25

ACCESSION NUMBER:

CORPORATE SOURCE:

2000:728698 CAPLUS

DOCUMENT NUMBER:

134:91012

TITLE:

Co-polymer of histidine and lysine markedly enhances

transfection efficiency of liposomes

AUTHOR(S):

Chen, Q-R.; Zhang, L.; Stass, S. A.; Mixson, A. J. Department of Pathology and Greenebaum Cancer Center,

University of Maryland Baltimore, Baltimore, MD,

21201, USA

SOURCE:

Gene Ther. (2000), 7(19), 1698-1705

CODEN: GETHEC; ISSN: 0969-7128

PUBLISHER:

Nature Publishing Group

DOCUMENT TYPE:

LANGUAGE:

Journal English

Development of nonviral delivery systems is progressing toward a transfection efficiency sufficient to affect metabolic and neoplastic diseases in humans. Nevertheless, inadequate transfection efficiency of target cells with current nonviral systems still limits the utility of this therapy. In the current study, we have detd. that a co-polymer of histidine and lysine (H-K) enhances the transfection efficiency of liposomes, a leading nonviral system. We found that in the absence of serum, the addn. of this polymer increased transfection as much as 10-fold

in comparison with the liposome: DNA complex alone. More impressively, the co-polymer in the presence of serum increased transfection efficiency up to 100-fold. Furthermore, in vivo expression of luciferase in a tumor increased 15-fold with the addn. of H-K polymer to the liposome:plasmid DNA complexes. Without liposomes, the H-K polymer had little to no effect on transfection efficiency. We anticipate that further modifications of this co-polymer will yield mols. with both increased complexity and transfection efficiency.

ΙT 316821-90-6P

RL: BPR (Biological process); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); PROC (Process); USES (Uses)

(co-polymer of histidine and lysine enhances transfection efficiency of liposomes)

REFERENCE COUNT:

REFERENCE(S):

- (1) Behr, J; Proc Natl Acad Sci USA 1989, V86, P6982 CAPLUS
- (2) Boussif, O; Proc Natl Acad Sci USA 1995, V92, P7297 CAPLUS
- (3) Budker, V; Nat Biotechnol 1996, V14, P760 CAPLUS
- (4) Cayot, P; Anal Biochem 1997, V249, P184 CAPLUS
- (5) Chen, Q; Cancer Res 1999, V59, P3308 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 5 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

2000:475506 CAPLUS

DOCUMENT NUMBER:

133:115150

TITLE:

Methods using a histatin, histatin fragment, or related peptide for treating cystic fibrosis Spacciapoli, Peter; Rothstein, David M.; Friden, Phillip M.

PATENT ASSIGNEE(S):

INVENTOR(S):

Periodontix, Inc., USA PCT Int. Appl., 27 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent English

LANGUAGE:

SOURCE:

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
WO 2000040204	A2	20000713	WO 2000-US480	20000107

W: AU, CA, NZ

RW: AT, BE, CH, CY, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

PRIORITY APPLN. INFO.:

US 1999-226666 A 19990108

OTHER SOURCE(S):

MARPAT 133:115150

Methods are disclosed for treating cystic fibrosis in a mammal that include administering an effective amt. of a histatin, a histatin. fragment, or a histatin-related peptide.

186258-89-9 282712-87-2 ΙT

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (histatin, histatin fragment, or related peptide for treating cystic fibrosis)

ANSWER 6 OF 25 CAPLUS COPYRIGHT 2001 ACS L4ACCESSION NUMBER:

2000:386830 CAPLUS

DOCUMENT NUMBER:

133:218720

TITLE:

Ni(II) Specifically Cleaves the C-Terminal Tail of the Major Variant of Histone H2A and Forms an Oxidative

Damage-Mediating Complex with the Cleaved-Off

Octapeptide

AUTHOR(S):

Bal, Wojciech; Liang, Rongti; Lukszo, Jan; Lee, Sang-Han; Dizdaroglu, Miral; Kasprzak, Kazimierz S. Laboratory of Comparative Carcinogenesis, National

CORPORATE SOURCE: Cancer Institute, Frederick, MD, 21702, USA SOURCE: Chem. Res. Toxicol. (2000), 13(7), 616-624

CODEN: CRTOEC; ISSN: 0893-228X

American Chemical Society

PUBLISHER:

Journal English

DOCUMENT TYPE: LANGUAGE:

AB The acetyl-TESHHK-amide peptide, modeling a part of the C-terminal "tail" of histone H2A, was found previously by us to undergo at pH 7.4 a Ni(II)-assisted hydrolysis of the E-S peptide bond with formation of a stronger Ni(II) complex with the SHHK-amide product (1998). To further characterize the hydrolysis and test the resulting Ni(II) complex for redox activity, bovine histone H2A and three peptides were investigated: acetyl-LLGKVTIAQGGVLPNIQAVLLPKKTESHHKAKGK (H2A34), modeling the entire "C-tail" of H2A; SHHKAKGK (H2A8), modeling the cutoff product of hydrolysis; and acetyl-KTESHKAKGK (H2A10), modeling a putative Ni(II) binding site in a minor variant H2A.4 of human histone H2A. Ni(II)-assisted hydrolysis of H2A and H2A34 was found to proceed approx. 7-fold faster than that of the Ni(II)-acetyl-TESHHK-amide complex under comparable conditions. In both cases, the Ni(II) complex with H2A8 was the smaller product of the hydrolysis, indicating a high site specificity of the reaction. Of three other metals tested with H2A34, only Cu(II) cleaved the E-S bond, although much less efficiently than Ni(II); Co(II) and Zn(II) had no effect whatsoever. The H2A10 peptide appeared to be fully resistant to hydrolytic cleavage and did not exhibit any redox activity vs. H2O2 in the presence of Ni(II) at pH 7.4. Likewise, redox-inactive was the Ni(II)-H2A34 complex. In contrast, the Ni(II)-H2A8 complex promoted oxidative damage of pUC19 DNA by H2O2, evidenced by a significant increase in the no. of single strand breaks and nucleobase modifications typical for a hydroxyl radical-like species attack on DNA. Interestingly, instead of 8-oxopurines, the corresponding formamidopyrimidines were the major products of the damage. difference in redox activity between the Ni(II)-H2A34 and Ni(II)-H2A8 complexes is most likely assocd. With their different geometries: octahedral and square planar, resp. Incubation of the Ni(II)-H2A8 complex with H2O2 also resulted in degrdn. of the peptide ligand, esp. at its Ser and His residues. Thus, binding of Ni(II) to the ESHHK motif of the histone H2A C-tail is damaging to the histone C-terminal tail and to histone-assocd. DNA. The results support a dual mechanism of Ni(II)-induced carcinogenesis, including both genotoxic and epigenetic effects.

115154-41-1 290374-35-5 ΙT

RL: BSU (Biological study, unclassified); RCT (Reactant); BIOL (Biological

(Ni(II) specifically cleaves C-terminal tail of major variant of histone H2A and forms oxidative damage-mediating complex with cleaved-off octapeptide)

REFERENCE COUNT:

REFERENCE(S):

54

- (1) Arents, G; Proc Natl Acad Sci USA 1991, V88, P10148 CAPLUS
- (2) Arents, G; Proc Natl Acad Sci USA 1995, V92, P11170 CAPLUS
- (3) Bal, W; Arch Biochem Biophys 1999, V364, P161 CAPLUS
- (4) Bal, W; Chem Res Toxicol 1995, V8, P683 CAPLUS
- (5) Bal, W; Chem Res Toxicol 1997, V10, P915 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 7 OF 25 CAPLUS COPYRIGHT 2001 ACS ACCESSION NUMBER: 2000:295355 CAPLUS

DOCUMENT NUMBER:

133:103515

TITLE:

Analysis of foreign epitope inserts in HBcAq.

approaches to solving the problem of core particle

self-assembly

AUTHOR(S):

Karpenko, L. I.; Ivanisenko, V. A.; Pika, I. S.; Chikaev, N. A.; Eroshkin, A. M.; Melamed, N. V.;

Veremeiko, T. A.; Il'ichev, A. A.

CORPORATE SOURCE:

Institute of Biotechnology, State Research Center

VECTOR, Novosibirsk, 633159, Russia Mol. Biol. (2000), 34(2), 194-199 CODEN: MOLBBJ; ISSN: 0026-8933

PUBLISHER:

SOURCE:

MAIK Nauka/Interperiodica Publishing

DOCUMENT TYPE:

Journal. LANGUAGE: English

The hepatitis B virus core antigen (HBcAg) is a promising protein carrier for exposing the epitopes of various human and animal pathogens. HBcAq-based chimeric proteins can be used in creating highly efficient vaccines; however, not all chimeric HBcAg with foreign epitope inserts are capable of assembly into virus-like particles. Using computer programs ProAnalyst, SALIX, and QSARPro, the authors examd. the relation between the self-assembly capability of chimeric HBcAg and the physicochem. properties of the inserts. The self-assembly was impaired when the inserted peptides contained highly hydrophobic and bulky residues tending to form .beta.-structures; this esp. concerned the C-proximal residues in the insert. Recommendations were elaborated for constructing foreign epitopes that would ensure correct self-assembly of chimeric HBcAq particles.

278169-06-5D, fusion products with hepatitis B core antigen ITRL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)

(self-assembly core antigen particles expressing foreign epitopes in hepatitis B core antigen)

REFERENCE COUNT:

26

REFERENCE(S):

(1) Argos, P; EMBO J 1988, V7, P819 CAPLUS

- (2) Bogardt, R; J Mol Evol 1980, V15, P197 CAPLUS (3) Borisova, G; J Virology 1993, V67, P3696 CAPLUS
- (4) Boulter, N; Vaccine 1995, V13, P1152 CAPLUS (6) Clarke, B; Nature 1987, V330, P381 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 8 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:479138 CAPLUS

DOCUMENT NUMBER:

132:11552

TITLE:

T cell response pattern to glutamic acid decarboxylase 65 (GAD65) peptides of newly diagnosed type 1 diabetic

patients sharing susceptible HLA haplotypes

Rharbaoui, F.; Mayer, A.; Granier, C.; Bouanani, M.; Thivolet, C.; Pau, B.; Orgiazzi, J.; Madec, A.-M.

CORPORATE SOURCE:

Faculte de Pharmacie, Montpellier, Fr. Clin. Exp. Immunol. (1999), 117(1), 30-37

CODEN: CEXIAL; ISSN: 0009-9104

PUBLISHER:

AUTHOR(S):

SOURCE:

Blackwell Science Ltd.

DOCUMENT TYPE:

Journal

LANGUAGE:

English

Autoantibodies and autoreactive T lymphocytes directed against several pancreatic .beta. cell proteins such as GAD65 have been identified in the circulation before and at the onset of clin. type 1 (insulin-dependent) diabetes. Using GAD65 synthetic peptides, the authors studied the

proliferative response of peripheral blood mononuclear cells (PBMC) either from recently diagnosed type 1 diabetic patients, of whom the majority share the disease-assocd. HLA class II haplotype (DR4-DQB1*0201 or DR3-DQB1*0302), or from HLA-matched control subjects. The authors found that 67% (14/21) of the type 1 diabetic patients and 39% (9/23) of the control subjects exhibited a pos. proliferative response. Compared with control subjects, however, PBMC from diabetic patients proliferated more frequently in the presence of peptide pools from the C-terminal region of GAD65 (amino acids 379-585). Diabetic patients with the same HLA-DQ or HLA-DR alleles showed partially identical T cell reactivity, but no clear correlation could be made between MHC class II specificity and T cell epitopes because of multiple combinations of class II alleles. by flow cytometry, the authors studied the direct binding of GAD65 peptides to MHC class II mols. of Epstein-Barr virus (EBV)-transformed B (EBV-B) cells obtained from a diabetic patient. They found that 11 GAD peptides were able to bind to the highly susceptible haplotype DRB1*0301/0401-DQA1*0301/0501-DQB1*0302/0201 on the surface of EBV-B cells in partial correlation with the results obtained in the proliferation assays.

IT 251651-17-9

RL: PRP (Properties)

(T cell response pattern to glutamic acid decarboxylase 65 (GAD65) peptides of newly diagnosed type 1 diabetic patients sharing susceptible HLA haplotypes)

REFERENCE COUNT:

32

REFERENCE(S):

- (2) Atkinson, M; J Clin Invest 1994, V94, P2125 CAPLUS
- (4) Baekkeskov, S; Nature 1990, V347, P151 CAPLUS
- (7) Brooks-Worrell, B; J Immunol 1996, V157, P5668 CAPLUS
- (9) Calvo-Calle, J; J Immunol 1997, V159, P1362 CAPLUS
- (10) Durinovic-Bello, I; Diabetes 1996, V45, P795 CAPLUS

ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 9 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1999:393960 CAPLUS 131:39718

DOCUMENT NUMBER:

TITLE: INVENTOR(S):

SOURCE:

Antifungal and antibacterial histatin-based peptides Oppenheim, Frank G.; Xu, Tao; Roberts, F. Donald;

Spacciapoli, Peter; Friden, Phillip M.

PATENT ASSIGNEE(S):

Periodontix, Inc., USA; Trustees of Boston University

U.S., 35 pp., Cont.-in-part of U.S. 5,631,228.

CODEN: USXXAM

Patent

DOCUMENT TYPE:

LANGUAGE: English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PATENT NO.	KIND	DATE	A	PPLICATION	ON NO.	DATE					
US 5912230 US 5486503	A A	19990615 19960123	•	S 1998-9		19980311 19940809					
US 5631228	A	19970520	บ	S 1995-48	31888	19950607					
WO 9640768 WO 9640768	A2 A3	19961219 19970306	•	O 1996-US	59374	19960607					
		U, AZ, BB,		BY, CA,	CH, CN,	CZ, DE,	DK, EE,				
•		E, HU, IL,				•					
LT, SE,		ID, MG, MK,	MN, MW,	MX, NO,	NZ, PL,	PT, RO,	RU, SD,				
RW: KE,	LS, MW, S	SD, SZ, UG, MC, NL, PT,					GB, GR,				

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US 1991-786571
PRIORITY APPLN. INFO.:
                                                       B1 19911101
                                       US 1993-145030
                                                       B1 19931028
                                       US 1994-287717
                                                       A2 19940809
                                       US 1995-481888
                                                       A2 19950607
                                       WO 1996-US9374
                                                        W 19960607
     Histatin-based peptides representing defined portions of the amino acid
     sequences of naturally occurring human histatins, and methods for
     treatment of fungal or bacterial infection, are described. The
     histatin-based peptides represent the active anti-fungal and
     anti-bacterial region of naturally occurring human histatins.
ΙT
     186258-89-9 186258-89-9D, derivs.
     RL: BAC (Biological activity or effector, except adverse); THU
     (Therapeutic use); BIOL (Biological study); USES (Uses)
        (histatin-based peptides for antifungal and antibacterial agents)
REFERENCE COUNT:
                         41
                         (1) Anon; JP 03261747 1994 CAPLUS
REFERENCE(S):
                         (2) Anon; JP 06234653 1994 CAPLUS
                         (3) Anon; JP 06287146 1994 CAPLUS
                         (4) Anon; WO 9421672 1994 CAPLUS
                         (5) Chang, C; Peptides 1990 1991, P843 CAPLUS
                        ALL CITATIONS AVAILABLE IN THE RE FORMAT
     ANSWER 10 OF 25 CAPLUS COPYRIGHT 2001 ACS
T.4
ACCESSION NUMBER:
                        1999:208580 CAPLUS
DOCUMENT NUMBER:
                        130:232464
TITLE:
                        Antifungal and antibacterial D-amino acid
                        histatin-based peptides
                        Oppenheim, Frank G.; Xu, Tao; Roberts, F. Donald;
INVENTOR(S):
                        Spacciapoli, Peter; Friden, Phillip M.
                        Periodontix, Inc., USA; Trustees of Boston University
PATENT ASSIGNEE(S):
                        U.S., 34 pp., Cont.-in-part of U.S. 5,631,228.
SOURCE:
                        CODEN: USXXAM
DOCUMENT TYPE:
                        Patent
                        English
LANGUAGE:
FAMILY ACC. NUM. COUNT:
                        7
PATENT INFORMATION:
     PATENT NO.
                     KIND DATE
                                          APPLICATION NO.
                                                          DATE
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                                                          -----
                    A
     US 5885965
                           19990323
                                         US 1998-973563
                                                          19980312
                     Α
     US 5486503
                           19960123
                                         US 1994-287717
                                                           19940809
                     A
                           19970708
     US 5646119
                                         US 1995-485273
                                                          19950607
    WO 9640770
                    A2
                           19961219
                                         WO 1996-US9962
                                                         19960607
                     A3
     WO 9640770
                          19970206
        W: AL, AM, AT, AU, AZ, BB, BG, BR, BY, CA, CH, CN, CZ, DE, DK, EE,
             ES, FI, GB, GE, HU, IL, IS, JP, KE, KG, KP, KR, KZ, LK, LR, LS,
             LT, LU, LV, MD, MG, MK, MN, MW, MX, NO, NZ, PL, PT, RO, RU, SD,
             SE, SG
         RW: KE, LS, MW, SD, SZ, UG, AT, BE, CH, DE, DK, ES, FI, FR, GB, GR,
             IE, IT, LU, MC, NL, PT, SE, BF, BJ, CF, CG, CI, CM, GA
PRIORITY APPLN. INFO.:
                                       US 1991-786571
                                                        B1 19911101
                                       US 1993-145030
                                                        B1 19931028
                                       US 1994-287717
                                                        A2 19940809
                                       US 1995-485273
                                                        A2 19950607
                                       WO 1996-US9962
                                                       W 19960607
AB
     D-Amino acid histatins and histatin-based peptides and methods for
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AB D-Amino acid histatins and histatin-based peptides and methods for treatment of fungal or bacterial infection are described. These D-amino acid histatins and histatin-based peptides are longer-acting antifungal or antibacterial agents than their L-enantiomeric analogs.

IT 186258-89-9D, D-amino acid-contg.

RL: BAC (Biological activity or effector, except adverse); PRP

(Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (antifungal and antibacterial D-amino acid histatin-based peptides)
REFERENCE COUNT: 32
REFERENCE(S): (1) Anon; JP 03261747 1994 CAPLUS

(2) Anon; JP 06234653 1994 CAPLUS (3) Anon; JP 06287146 1994 CAPLUS (4) Anon; WO 9421672 1994 CAPLUS (5) Barkovitz: US 5459237 1995 CAP

(5) Berkowitz; US 5459237 1995 CAPLUS ALL CITATIONS AVAILABLE IN THE RE FORMAT

L4 ANSWER 11 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1999:169524 CAPLUS

DOCUMENT NUMBER: 131:1843

TITLE: A 7-amino-acid insert in the heavy chain nucleotide

binding loop alters the kinetics of smooth muscle

myosin in the laser trap

AUTHOR(S): Lauzon, Anne-Marie; Tyska, Matthew J.; Rovner, Arthur

S.; Freyzon, Yelena; Warshaw, David M.; Trybus,

Kathleen M.

CORPORATE SOURCE: Department of Molecular Physiology and Biophysics,

University of Vermont, Burlington, VT, 05405, USA J. Muscle Res. Cell Motil. (1998), 19(8), 825-837

CODEN: JMRMD3; ISSN: 0142-4319

PUBLISHER: Kluwer Academic Publishers

DOCUMENT TYPE: Journal LANGUAGE: English

SOURCE:

Two smooth muscle myosin heavy chain isoforms differ by a 7-amino-acid AB insert in a flexible surface loop located near the nucleotide binding site. The non-inserted isoform is predominantly found in tonic muscle, while the inserted isoform is mainly found in phasic muscle. The inserted isoform has twice the actin-activated ATPase activity and actin filament velocity in the in vitro motility assay as the non-inserted isoform. We used the laser trap to characterize the mol. mechanics and kinetics of the inserted isoform ((+)insert) and of a mutant lacking the insert ((-)insert), analogous to the isoform found in tonic muscle. The constructs were expressed as heavy meromyosin using the baculovirus/insect cell system. Unitary displacement (d) was similar for both constructs (.apprx. 10 nm) but the attachment time ton for the (-)insert was twice as long as for the (+)insert regardless of the [MgATP]. Both the relative av. isometric force (Favg(-insert)/Favg(+insert)) = 1.1.+-.0.2 (mean .+-. SE) using the in vitro motility mixt. assay, and the unitary force (F .apprx. 1 pN) using the laser trap, showed no difference between the two constructs. However, as under unloaded conditions, ton under loaded conditions was longer for the (-)insert compared with the (+)insert construct at limiting [MgATP]. These data suggest that the insert in this surface loop does not affect the mechanics but rather the kinetics of the cross-bridge cycle. Through comparisons of ton from d measurements at various [MgATP], we conclude that the insert affects two specific steps in the cross-bridge cycle, i.e., MgADP release and MgATP binding.

IT **225518-96-7**

RL: BSU (Biological study, unclassified); BIOL (Biological study) (7-amino-acid insert in heavy chain nucleotide binding loop alters kinetics of smooth muscle myosin in laser trap)

REFERENCE COUNT:

44

REFERENCE(S):

- (1) Babij, P; Nucleic Acid Res 1993, V21, P1467 CAPLUS
- (2) Bobkov, A; Proc Natl Acad Sci USA 1996, V93, P2285 CAPLUS
- (3) Cooke, R; Physiol Rev 1997, V77, P671 CAPLUS
- (4) Cremo, C; Biochem 1998, V37, P1969 CAPLUS
- (5) Cuda, G; Biophys J 1997, V72, P1767 CAPLUS
- ALL CITATIONS AVAILABLE IN THE RE FORMAT

ANSWER 12 OF 25 CAPLUS COPYRIGHT 2001 ACS L4ACCESSION NUMBER: 1998:65926 CAPLUS DOCUMENT NUMBER: 128:127089 TITLE:

Methods for determining the presence of brain protein

S-100

INVENTOR(S): Brundell, Jan; Nyberg, Lena

PATENT ASSIGNEE(S):

AB Sangtec Medical, Swed.; Brundell, Jan; Nyberg, Lena

SOURCE: PCT Int. Appl., 29 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT: 1

PATENT INFORMATION:

F	PATENT NO.		KIN	D DATE		APPLI	CATION	DATE						
-														
M.	0 9801471		A1	19980115		WO 19	97-SE1	164	19970	0627				
	W: AU	J, BR,	CA, I	FI, HU, IL,	JP,	NO, NZ,	US							
	RW: AT	, BE,	CH, I	DE, DK, ES,	FΙ,	FR, GB,	GR, I	E, IT,	LU,	MC,	NL,	PT,	SE	
C	A 2259413	}	AA	19980115		CA 19	97-225	9413	19970	0627				
P	U 9735633	}	A1	19980202		AU 19	97-356	33	19970	0627				
P	U 715797		B2	20000210										
E	P 931094		A1	19990728		EP 19	19970627							
	R: AT	, BE,	CH, I	DE, DK, ES,	FR,	GB, GR,	IT, L	I, LU,	NL,	SE,	MC,	PT,		
	IE	, FI												
E	R 9710175)	A	20000111		BR 19	97-101	75	19970	0627				
J	JP 2000515854			20001128		JP 19	98-505	124	19970	0627				
N	0 9806218	}	А	19981230		NO 19	98-621	8	19983	1230				
PRIORI	TY APPLN.	INFO	.:			SE 1996-	2677	А	19960	0705				
						WO 1997-	SE1164	W	19970	0627				

Assay methods for detq. the presence of the brain protein S-100 in a clin. AB sample which use antibodies directed to epitopes in the region from Serl . to Asn38 and from Thr82 to Glu93 of the amino acid sequence of the .beta. subunit of human S100B is provided. The methods developed include luminescent immunoassay, ELISA, and IRMA, and is used for detecting cerebral dysfunction, melanoma cancer, and for evaluating the influence of extracorporal circulation equipment on injured brain.

201799-94-2 201799-95-3

RL: BSU (Biological study, unclassified); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (monoclonal antibodies to human brain protein S-100 epitopes for diagnosis of cerebral dysfunction and melanoma)

ANSWER 13 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1998:62220 CAPLUS

DOCUMENT NUMBER:

128:136508

TITLE:

Peptide inhibitors of selectin binding, preparation,

and therapeutic and diagnostic use

INVENTOR(S):

Heavner, George A.; Kruszynski, Marian

PATENT ASSIGNEE(S):

Centocor, Inc., USA

SOURCE:

U.S., 29 pp. Cont.-in-part of U.S. Ser. No. 997,771,

abandoned. CODEN: USXXAM

DOCUMENT TYPE: Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT: 2

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE

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US 5710123
                     Α
                           19980120
                                          US 1995-454207
                                                          19950609
     WO 9414836 A
W: CA, JP, US
                                          WO 1993-US12110 19931213
                           19940707
                     A1
         RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
PRIORITY APPLN. INFO.:
                                       US 1992-997771
                                                           19921218
                                       WO 1993-US12110
                                                           19931213
OTHER SOURCE(S):
                        MARPAT 128:136508
AB
     The present invention provides novel peptides having as their core region
     portions of the 109-118 amino acid sequence of P-selectin, E-selectin or
     L-selectin. The invention also provides pharmaceutical compns. comprising
     the peptides of the invention, and diagnostic and therapeutic methods
     utilizing the peptides and pharmaceutical compns. of the invention.
ΙT
     161174-87-4P 161174-90-9P
     RL: BAC (Biological activity or effector, except adverse); PRP
     (Properties); SPN (Synthetic preparation); THU (Therapeutic use); BIOL
     (Biological study); PREP (Preparation); USES (Uses)
        (peptide inhibitors of selectin binding, prepn., and therapeutic and
        diagnostic use)
     ANSWER 14 OF 25 CAPLUS COPYRIGHT 2001 ACS
ACCESSION NUMBER:
                        1997:244274 CAPLUS
DOCUMENT NUMBER:
                        126:224281
TITLE:
                        cDNAs for the plant panallergen co-factor-independent
                        phosphoglycerate mutase and identification of
                        diagnostic and therapeutically useful epitopes
                        Ferreira, Fatima; Richter, Klaus; Engel, Edwin; Ebner,
INVENTOR(S):
                        Christof; Jilek, Alexander; Rheinberger, Hans-Joerg;
                        Kraft, Dietrich; Breitenbach, Michael
                        Biomay Produktions- Und Handelsgesellschaft Mbh,
PATENT ASSIGNEE(S):
                        Austria; Ferreira, Fatima; Richter, Klaus; Engel,
                        Edwin; Ebner, Christof; Jilek, Alexander; Rheinberger,
                        Hans-Joerg; Kraft, Dietrich; Breitenbach, Michael
SOURCE:
                        PCT Int. Appl., 159 pp.
                        CODEN: PIXXD2
DOCUMENT TYPE:
                        Patent
LANGUAGE:
                        German
FAMILY ACC. NUM. COUNT:
PATENT INFORMATION:
     PATENT NO.
                    KIND DATE
                                          APPLICATION NO. DATE
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                                          _____
                                                          -----
                           19970213
     WO 9705258
                                          WO 1996-AT141
                    A2
                                                           19960802
     WO 9705258
                     A3 19970327
         W: AU, CA, JP, NO, US
         RW: AT, BE, CH, DE, DK, ES, FI, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE
     AT 9501320
                           19961015
                                          AT 1995-1320
                     Α
                                                           19950802
     AT 402505
                      В
                           19970625
     AU 9666059
                      A1 19970226
                                          AU 1996-66059
                                                           19960802
PRIORITY APPLN. INFO.:
                                       AT .1995-1320
                                                           19950802
                                       WO 1996-AT141
                                                          19960802
AΒ
     CDNAs for the pollen panallergen co-factor-independent phosphoglycerate
     mutase (E.C. 5.4.2.1.) of birch, mugwort and timothy grass pollen are
     cloned and characterized. This sequence of the allergen is highly
     conserved in all plants, but not in animals. The amino acid sequence and
     the most important B and T cell epitopes of the mol. are derived and
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mutase (E.C. 5.4.2.1.) of birch, mugwort and timothy grass pollen are cloned and characterized. This sequence of the allergen is highly conserved in all plants, but not in animals. The amino acid sequence and the most important B and T cell epitopes of the mol. are derived and demonstrated. The allergen was manufd. in E. coli and bound the IgE serum of patients who are allergic to tree, grass and weed pollens and various foodstuffs. A monoclonal antibody (BIP 3) specifically binds to this protein from all plants tested. The significance of the co-factor-independent phosphoglycerate mutase (E.C. 5.4.2.1.) derives from the fact that it results in the cross-sensitization of patients. The

protein and peptide fragments can be used in diagnostic and therapeutic methods based, for example, on antigen -antibody interaction, mediator release or T-cell reactivity.

IT 187816-25-7

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)

(B-cell epitope of mugwort pollen phosphoglycerate mutase isoenzyme Art17; cDNAs for plant panallergen co-factor-independent phosphoglycerate mutase and identification of diagnostic and therapeutically useful epitopes)

IT 187816-07-5

RL: ADV (Adverse effect, including toxicity); BPR (Biological process); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); PROC (Process); USES (Uses)

(B-cell epitope of mugwort pollen phosphoglycerate mutase isoenzyme Art6; cDNAs for plant panallergen co-factor-independent phosphoglycerate mutase and identification of diagnostic and therapeutically useful epitopes)

L4 ANSWER 15 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1997:116549 CAPLUS

DOCUMENT NUMBER:

126:113162

TITLE:

Anti-fungal and anti-bacterial histatin-based peptides

INVENTOR(S): Oppenheim, Frank G.; Xu, Tao; Roberts, F. Donald;

Spacciapoli, Peter; Friden, Phillip M.

PATENT ASSIGNEE(S):

Periodontix, Inc., USA; Trustees of Boston University;

Oppenheim, Frank G.; Xu, Tao; Roberts, F. Donald;

Spacciapoli, Peter; Friden, Phillip M.

SOURCE:

PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

LANGUAGE:

Patent English

FAMILY ACC. NUM. COUNT: 7

PATENT INFORMATION:

PA	TENT	NO.		KI	ND	DATE			I	APPLI	CATI	ON NO	0.	DATE			
	9640768 9640768								WO 1996-US9374					19960607			
	W: AL, AM, ES, FI, LT, LU, SE, SG		AM, FI, LU,	AT, GB,	AU, GE,	AZ, HU,	BB, IL,	IS,	JP,	KE,	KG,	KP,	KR,	ΚZ,	LK,	LR,	LS,
	RW:	KE,	LS,			SZ, NL,										GB,	GR,
AU	US 5631228 AU 9661585				A 19970520 A1 19961230 B2 19990826												
EP				A	2	19980401		EP 1996-919182 19960607									
		ΙE,	FΙ			DK,										MC,	PT,
AT US	AT 196475					2000 1999		JP 1996-501707 19960 AT 1996-919182 19960 US 1998-973559 19980 US 1995-481888 A 19950 US 1991-786571 B1 19911 US 1993-145030 B1 19931 US 1994-287717 A2 19940 WO 1996-US9374 W 19960					0607 0311 0607 1101 1028 0809				

OTHER SOURCE(S): MARPAT 126:113162

AB Histatin-based peptides representing defined portions of the amino acid sequences of naturally occurring human histatins and methods for treatment of fungal or bacterial infection are described. These histatin-based peptides represent the active anti-fungal and anti-bacterial region of naturally occurring human histatins.

IT 186258-89-9

RL: BAC (Biological activity or effector, except adverse); PRP (Properties); THU (Therapeutic use); BIOL (Biological study); USES (Uses) (anti-fungal and anti-bacterial histatin-based peptides)

L4 ANSWER 16 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1996:260618 CAPLUS

DOCUMENT NUMBER: 124:314670

TITLE: A protective anti-peptide antibody against the

immunodominant site of the A24 Cruzeiro strain of foot-and-mouth disease virus and its reactivity with other subtype viruses containing the same minimum

binding sequence

AUTHOR(S): Barnett, P. V.; Pullen, L.; Staple, R. F.; Lee, L. J.;

Butcher, R.; Parkinson, D.; Doel, T. R.

CORPORATE SOURCE: Inst. Animal Health, Pirbright Lab., Pirbright,

Woking, Surrey, GU24 ONF, UK

SOURCE: J. Gen. Virol. (1996), 77(5), 1011-18

CODEN: JGVIAY; ISSN: 0022-1317

DOCUMENT TYPE: Journal LANGUAGE: English

AB A synthetic peptide vaccine of the general sequence Cys-Cys-(200-213)-Pro-Pro-Ser-(141-158)-Pro-Cys-Gly(peptide A40), where the numbered residues refer to the VP1 sequence of foot-and-mouth disease virus (FMDV) strain A24 Cruzeiro, has previously been shown to elicit neutralizing and protective antibodies in guinea-pigs and cattle. To examine this immunogenic tract in more detail monoclonal antibodies (MAbs) were raised to this peptide. One such MAb, C1.1, which recognized the homologous peptide, bound to native virus, neutralized infectivity in vitro and passively protected mice from challenge. Using overlapping dodecameric peptides the min. binding 'footprint' of this MAb incorporated residues 149-154 which were resp. Gly-Ser-Leu-Ala-Ala-Arg. Since this 'footprint' occurs in several other A subtype strains of FMDV, the extent to which MAb C1.1 could cross-react was also examd. Using a liq.-phase competition ELISA, only viruses with a sequence that encompassed the same min. binding 'footprint', namely A27 Cundinamarca Colombia/76, A Argentina/79, and A Venceslau Brazil/76 reacted with similar affinity against MAb C1.1. However, further serol. examn. of Cl.1 with these viruses by indirect ELISA, in vitro neutralization and passive protection showed clear functional disparity. In contrast to the lig.-phase ELISA, the ability of C1.1 to react with electrostatically bound virus varied significantly depending on the subtype examd. Moreover, the capacity of this MAb to neutralize these subtypes showed wide divergence which was mirrored by the protection data.

IT 176260-59-6 176260-60-9

RL: BPR (Biological process); PRP (Properties); BIOL (Biological study); PROC (Process)

(epitope mapping and neutralizing activity of anti-VP1 monoclonal antibody against peptide of foot-and-mouth disease virus A24 Cruzeiro)

L4 ANSWER 17 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1995:380112 CAPLUS

DOCUMENT NUMBER: 122:161381

TITLE: Preparation of peptide inhibitors of selectin binding.

INVENTOR(S): Heavner, George A.; Kruszynski, Marian

PATENT ASSIGNEE(S):

Centocor, Inc., USA

SOURCE:

PCT Int. Appl., 52 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE
WO 9414836 A1 19940707 WO 1993-US12110 19931213

W: CA, JP, US

RW: AT, BE, CH, DE, DK, ES, FR, GB, GR, IE, IT, LU, MC, NL, PT, SE

US 5710123 A 19980120 US 1995-454207 19950609 PRIORITY APPLN. INFO.: US 1992-997771 19921218 WO 1993-US12110 19931213

OTHER SOURCE(S): MARPAT 122:161381

R1X1A1B1C1D1E1F1G1H1H1J1X2R2, R1X1-cyclo-(A2B1C1D1E1F1G1H1I2)-J1X2R2 (X1 = N-terminal sequence of 0-10 amino acids; R1 = H, alkyl, aryl, CHO, alkanoyl, aroyl, alkoxycarbonyl, aryloxycarbonyl; X2 = C-terminal sequence of 0-10 amino acids; R2 = OH, OR3, NR5R6; R3 = alkyl, aryl; R5, R6 = H, alkyl, aryl, cycloalkyl; A1 = null, D- or L-Cys; A2 = D- or L-Cys; B1 = Dor L-His, -Ser, -Leu, -Phe, -Asn, -Pro, -Glu; C1 = D- or L-Lys, -His, -Arg, -Ser; D1 = D- or L-Lys, -Leu, -Ala, -Phe, -His, -Arg, -Ser; E1 = Dor L-Lys, -Phe, -Gln, -Arg; F1 = D- or L-His, -Leu, -Ala, -Ile, -Thr, -Arg; G1 = D- or L-Ala, -Phe, -His, -Gln; H1 = D- or L-Leu, -Phe, -Ile, -Pro, -Ala; I1 = D- or L-Cys, -Phe, -Ile, -His, -Leu, -Val, -Thr, -Ser; I2 = D- or L-Cys; J1 = D- or L-Tyr, -Phe, -Ile, -Val), were prepd. The peptides have as their core region portions of the 109-118 amino acid sequence of P-selectin, E-selectin or L-selectin. Diagnostic and therapeutic methods are given utilizing the peptides and pharmaceutical compns. thereof. Thus, Cys-Leu-Lys-Lys-Lys-His-Ala-Leu-Cys-Tyr-NH2 was prepd. using BOC-protected amino acids on methylbenzhydrylamine resin. Title compds. inhibited binding of human neutrophils to P-selectin with IC50 = 0.003-1.013 mM.

IT 161174-87-4P 161174-90-9P

RL: BAC (Biological activity or effector, except adverse); BUU (Biological use, unclassified); SPN (Synthetic preparation); THU (Therapeutic use); BIOL (Biological study); PREP (Preparation); USES (Uses) (prepn. of peptide inhibitors of selectin binding)

L4 ANSWER 18 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1994:555572 CAPLUS

DOCUMENT NUMBER:

121:155572

TITLE:

Experimental autoimmune panencephalitis and uveoretinitis transferred to the Lewis rat by T lymphocytes specific for the S100.beta. molecule, a

calcium binding protein of astroglia

AUTHOR(S):

Kojima, Kimikazu; Berger, Thomas; Lassmann, Hans; Hinze-Selch, Dunja; Zhang, Yiping; Gehrmann, Jochen;

Reske, Konrad; Wekerle, Hartmut; Linington,

Christopher

CORPORATE SOURCE:

Dep. Neuroimmunol., Max-Planck Inst. Psychiatr.,

Martinsried, 82152, Germany

SOURCE:

J. Exp. Med. (1994), 180(3), 817-29

CODEN: JEMEAV; ISSN: 0022-1007

DOCUMENT TYPE:

Journal

LANGUAGE: English

AB The pathogenic potential of autoimmune T cell responses to nonmyelin autoantigens was investigated in the Lewis rat using the astrocyte-derived calcium binding protein S100.beta., as a model nonmyelin autoantigen. The

Robinson 09/437912

Lewis rat mounts a vigorous RT1B (major histocompatibility complex class II) restricted autoimmune response to an immunodominant S100.beta. epitope (amino acid residues 76-91). The adoptive transfer of S100.beta.-specific T cell lines induced a severe inflammatory response in the nervous system, but only minimal neurol. dysfunction in naive syngeneic recipients. The inability of S100.beta.-specific T cell transfer to induce severe disease was assocd. with a decreased recruitment of ED1+ macrophages into the central nervous system (CNS) in comparison with that seen in severe exptl. autoimmune encephalomyelitis (EAE) induced by the adoptive transfer of myelin basic protein (MBP)-specific T line cells. Moreover, unlike encephalitogenic MBP-specific T lines, S100.beta.-specific T cell lines exhibited no cytotoxic activity in vitro. Histopathol. anal. also revealed striking differences in the distribution of inflammatory lesions in MBP- and S100.beta.-specific T cell-mediated disease. In contrast to the MBP paradigm, S100.beta.-specific T cell transfer induces intense inflammation not only in the spinal cord, but throughout the entire CNS and also in the uvea and retina of the eye. In view of the distribution of lesions throughout the gray and white matter of the CNS the authors propose to term this new model exptl. autoimmune panencephalomyelitis (EAP) to differentiate at from EAE. These expts. demonstrate for the first time that nonmyelin CNS autoantigens can initiate a pathogenic autoimmune T cell response, although the nature of the target autoantigen profoundly influences the clin. and histopathol. characteristics of the resulting autoimmune disease. This is not simply a consequence of the distribution of the autoantigen, as both MBP and S100.beta. are coexpressed in many areas of the CNS, but reflects differences in the capacity of different regions of the CNS to process and present autoantigens. This new model of T cell-mediated autoimmune CNS disease exhibits a no. of similarities to multiple sclerosis (MS), such as its mild clin. course and the involvement of areas of the brain and eye, which are absent in myelin-mediated models of EAE. Nonmyelin autoantigens may therefore play an unexpectedly important role in the immunopathogenesis of inflammatory diseases of the CNS.

ΙT 157566-35-3

RL: BIOL (Biological study)

(in epitope mapping for nonmyelin autoantigen S100.beta., autoimmune panencephalitis and uveoretinitis in relation to)

L4ANSWER 19 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1992:658207 CAPLUS

DOCUMENT NUMBER:

117:258207

TITLE: INVENTOR(S): Antiasthmatic compositions containing peptides Nishimoto, Ikuo; Okamoto, Taku; Okuni, Yoshihiro

PATENT ASSIGNEE(S):

SOURCE:

Jpn. Kokai Tokkyo Koho, 5 pp.

CODEN: JKXXAF

DOCUMENT TYPE:

Patent

LANGUAGE:

Japanese

FAMILY ACC. NUM. COUNT:

PATENT INFORMATION:

PATENT NO.	KIND	DATE	APPLICATION NO.	DATE
~				
JP 04164036	. A2	19920609	JP 1990-285748	19901025

AΒ Antiasthmatic compns. contain peptides having basic amino acids (arginine, lysine, and histidine) at the N-terminal 1st and 2nd positions and the C-terminal last position and the 3rd or 4th positions therefrom. example, 9 peptides are presented, but no pharmacol. data given.

IT 144776-40-9 144776-41-0 144776-43-2

RL: BIOL (Biological study)

(as antiasthmatic)

ANSWER 20 OF 25 CAPLUS COPYRIGHT 2001 ACS ACCESSION NUMBER:

DOCUMENT NUMBER:

1989:534755 CAPLUS

111:134755

TITLE:

Preparation of decapeptides as LHRH antagonists having high antiovulatory activity and negligible histamine

releasing activity

INVENTOR(S):

Folkers, Karl; Bowers, Cyril Y.; Ljungquist, Anders; Tang, Pui Fun Louisa; Kobota, Minoru; Feng, Dong Mei

University of Texas System, USA

PATENT ASSIGNEE(S): SOURCE:

PCT Int. Appl., 70 pp.

CODEN: PIXXD2

DOCUMENT TYPE:

Patent

LANGUAGE:

English

FAMILY ACC. NUM. COUNT:

2

PATENT INFORMATION:

PATENT NO. KIND DATE APPLICATION NO. DATE WO 8901944 A1 19890309 WO 1988-US2922 19880824 W: AT, AU, BB, BG, BR, CH, DE, DK, FI, GB, HU, JP, KP, KR, LK, LU, MC, MG, MW, NL, NO, RO, SD, SE, SU, US RW: AT, BE, BJ, CF, CG, CH, CM, DE, FR, GA, GB, IT, LU, ML, MR, NL, SE, SN, TD, TG US 4935491 19900619 US 1987-88431 19870824 Α AU 8825294 A1 19890331 AU 1988-25294 19880824 AU 619221 В2 19920123 EP 377665 **A**1 19900718 EP 1988-908786 19880824 EP 377665 19950712 В1 R: AT, BE, CH, DE, FR, GB, IT, LI, LU, NL, SE

JP 03501969 T2 19910509 JP 1988-507982 19880824 HU 59940 A2 19920728 HU 1988-5868 19880824 HU 213098 В 19970228 A1 CA 1339659 19980203 CA 1988-587364 19881230 A DK 9000486 19900419 DK 1990-486 19900223 A NO 9000888 19900423 NO 1990-888 19900223 NO 9402179 A 19900423 NO 1994-2179 19940610 PRIORITY APPLN. INFO.: US 1987-88431 19870824 WO 1988-US2922 19880824 NO 1990-888 19900223

AB Decapeptide analogs of LHRH, e.g. [N-Ac-D-2-Nall, D-pClPhe2, D-3-Pal3, NicLys5, D-NicLys6, Ilys8, D-Ala10]-LHRH [2-Nal = 3-(2-naphthyl)alanine, pClPhe = 3-(4-chloro)phenylalanine, 3-Pal = 3-(3-pyridyl)alanine, NicLys = N.epsilon.-nisotinoyllysine, Ilys = N.epsilon.-isopropyllysine] (I) (Antide) having high ovulation inhibition activity and very low histamine release activity, were prepd. I and other decapeptides were synthesized by the solid phase method using a Beckman Model 990 peptide synthesizer, new lysine, ornithine, alanine, glutamic acid and arginine derivs., and benzhydrylamine hydrochloride resin as a solid support. I showed antiovulatory activity (AOA) of 100% at 1 .mu.g and 36% at 0.5 .mu.g in rats and an ED50 of .gtoreq.300 .mu.g/mL for histamine release in a rat mast cell assay.

IT 112424-93-8P

RL: SPN (Synthetic preparation); PREP (Preparation) (prepn. of, as LHRH antagonist)

ANSWER 21 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER:

1989:455372 CAPLUS

DOCUMENT NUMBER:

111:55372

TITLE:

Neutralizing epitopes of type O foot-and-mouth disease virus. II. Mapping three conformational sites with

synthetic peptide reagents

Parry, N. R.; Barnett, P. V.; Ouldridge, E. J.; Rowlands, D. J.; Brown, F. AUTHOR(S):

Dep. Virol., Wellcome Biotechnol. Ltd., CORPORATE SOURCE:

Beckenham/Kent, BR3 3BS, UK J. Gen. Virol. (1989), 70(6), 1493-503

CODEN: JGVIAY; ISSN: 0022-1317

DOCUMENT TYPE: Journal LANGUAGE: English

Four neutralizing monoclonal antibodies (MAbs), recognizing 3 functionally independent, conformational sites on type O foot-and-mouth disease virus (FMDV) failed to react with immobilized structural proteins or synthetic peptides but bound to the isolated capsid protein VP1 and peptides in soln. Inhibition ELISA techniques were, therefore, applied using peptide antigens and anti-peptide sera to block MAb binding to virus particles, permitting the identification of those portions of the VP1 protein contributing to the epitopes. The binding site of one MAb, which neutralized a range of type O FMDV isolates, was shown to have components within regions 146-150 and 200-213 of VP1 with a crit. involvement of the amino acids at positions 146 and 206 or 207. The determinants recognized by 2 other MAbs which were directed at similar, but not identical, epitopes from a second site included components from the 200 to 213 and 143 to 146 regions with amino acids 143 and 144, resp., being crit. for the inhibition of the virus binding of the 2 antibodies. Thus, the 2 previously identified immunogenic tracts of VP1 are brought into proximity in the quaternary structure of the virion to form an antigenic domain contg. several conformational epitopes, some of which are functionally independent. A fourth, strain-specific MAb was effectively blocked from reacting with virus by peptides corresponding to residues 161-180 and 200-213.

121795-39-9 ΙT

SOURCE:

RL: PROC (Process)

(monoclonal antibody recognition of, of foot-and-mouth disease virus VP1 protein)

ANSWER 22 OF 25 CAPLUS COPYRIGHT 2001 ACS L4

ACCESSION NUMBER: 1988:433575 CAPLUS

DOCUMENT NUMBER: 109:33575

TITLE: Comparison of benzo[a]pyrene-diol-epoxide binding to

histone H2A with different carboxy-terminal regions

AUTHOR(S): Kurokawa, Masahiko; MacLeod, Michael C.

CORPORATE SOURCE: Syst. Cancer Cent., Univ. Texas, Smithville, TX, USA

SOURCE: Carcinogenesis (London) (1988), 9(3), 419-25

CODEN: CRNGDP; ISSN: 0143-3334

DOCUMENT TYPE: Journal

English LANGUAGE:

(.+-.)-7r,8t-Dihydroxy-9t,10t-oxy-7,8,9,10-tetrahydrobenzo[a]pyrene (DPBE-I) binding was compared in 3 vertebrate histones H2A with different C-terminal regions. HPLC analyses of core histones prepd. from nuclei exposed to [3H]BPDE-I showed that rat liver and chicken erythrocyte histones H2A were heavily labeled by [3H]BPDE-I, but Xenopus laevis liver histone H2A was not. This result was confirmed by HPLC analyses of V8-protease digests of BPDE-I bound to histone H2A purified from the 3 different nuclei. There are significant amino acid sequence differences only in the C-terminal regions of the different histones H2A, where rat liver and chicken erythrocyte histones H2A contain 2 and 1 histidine residues, resp., while the amino acid sequence of Xenopus histone H2A contains no histidine. Pre-treatment of the in situ BPDE-I-modified H2A.2 from rat liver with carboxypeptidase B, which should remove the C-terminal lysine from the protein, resulted in increased retention times on reverse-phase HPLC for the adduct-contg. peptides upon subsequent

V8-protease digestion. This suggested that the site(s) of BPDE-I modification are located primarily in the C-terminal octapeptide of rat H2A.2. To confirm this, C-terminal V8-peptides of the different histones H2A were isolated and reacted with BPDE-I at physiol. pH in vitro. The HPLC analyses of the reaction mixts. indicated that the C-terminal peptide of rat liver and chicken erythrocyte histones H2A was a target site for BPDE-I binding in nuclei. Thus, the nucleophilic target amino acid for BPDE-I binding in histone H2A may be a histidine located close to the C terminus.

IT 115154-41-1 115154-42-2

RL: BIOL (Biological study)

(of C-terminal of histone H2A, benzopyrene diol epoxide binding in relation to, species differences in)

L4 ANSWER 23 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1988:49436 CAPLUS

DOCUMENT NUMBER: 108:49436

TITLE: Design, synthesis and bioassays of antagonists of

LH-RH which have high antiovulatory activity and

release negligible histamine

AUTHOR(S): Ljungqvist, Anders; Feng, Dong Mei; Tang, Pui Fun

Louisa; Kubota, Minoru; Okamoto, Tadashi; Zhang, Yawen; Bowers, Cyril Y.; Hook, William A.; Folkers,

Karl

CORPORATE SOURCE: Inst. Biomed. Res., Univ. Texas, Austin, TX, 78712,

USA

SOURCE: Biochem. Biophys. Res. Commun. (1987), 148(2), 849-56

CODEN: BBRCA9; ISSN: 0006-291X

DOCUMENT TYPE: Journal

LANGUAGE: English

AB Potent antagonists of LH-RH were achieved which release negligible histamine. [N-Ac-D-2-Nall, D-pClPhe2, D-3-Pal3, NicLys5, D-NicLys6, ILys8, D-Ala10]-LHRH (2-Nal = 3-(2-naphthylalanine; 3-Pal = 3-(3-pyridylalanine); NicLys = N.epsilon.-nicotinoyllysine; ILys = N.epsilon.-isopropyllysine) showed 100% antiovulatory activity (AOA)/1 .mu.g and 36% AOA/0.5 .mu.g; the ED50 for histamine release was >300 .mu.g/mL. [N-Ac-D-2-Nall, D-pClPhe2, D-3-Pal3, PicLys5, D-PicLys6, ILys8, D-Ala10]-LHRH (PicLys = N.epsilon.-picoloyllysine) showed 100% AOA/0.5 .mu.g, 40% AOA/0.25 .mu.g, and an ED50 for histamine release of 93 .mu.g/mL; it was the most potent of 52 new peptides. These antagonists feature designs with weakly basic acylated D-Lys6 (D-NicLys6 and D-PicLys6), alkylated Lys8 or Orn8 (ILys8 and IOrn8 (N.delta.-isopropylornithine)), NicLys5, and PicLys5. Concepts included balanced overall basicity, superiority of ILys8 and IOrn8 which are sequence dependent, and sensitivity of positions 5 and 6 for potency.

IT 112424-93-8

RL: BIOL (Biological study)
 (ovulation inhibition by, with negligible histamine release, mol.
 structure in relation to)

L4 ANSWER 24 OF 25 CAPLUS COPYRIGHT 2001 ACS

ACCESSION NUMBER: 1985:465120 CAPLUS

DOCUMENT NUMBER: 103:65120

TITLE: Products from catabolism of proteins as analogs of

peptide bioregulators (structural factors of the

physiological activity)

AUTHOR(S): Leonova, V. I.; Tseitlin, V. M.; Galaktionov, S. G.;

Nikolaichik, V. V.

CORPORATE SOURCE: Opornyi Punkt, VNII Genet. Sel. Prom. Mikroorg.,

Minsk, USSR

SOURCE: Konform. Funkts. Biol. Mol. (1984), 73-81. Editor(s):

Chipens, G. I. Zinatne: Riga, USSR.

CODEN: 53VVAG

DOCUMENT TYPE: LANGUAGE:

Conference Russian

AB The presence of sequences of peptide bioregulators fragments in blood proteins and their potential release following degrdn. of the proteins by enzymes present in circulating blood were discussed. E.g., the tuftsin analog His, Lys, Pro [97461-89-7] was found in fragment 535-538 of serum albumin and could be released by plasmin. The enkephalin analog Tyr-Gly-Phe-Tyr [97461-90-0] could be released from the .beta.-chain of fibrinogen by plasmin, esterase, and exopeptidase. The angiotensin analogs Glu-Glys-Ile-Tyr-Ile-His-Pro-Arg [97474-91-4] and Glu-Lys-Ile-Tyr-Ile-His-Pro-Arg-Tyr [97461-88-6] were released from fragments 405-412 and 405-413 of prothrombin [9001-26-7]. stabilities of the conformational analogs of these bioregulator peptides were given and related to potential bioacty.

ΙT 97461-89-7

RL: BIOL (Biological study)

(release from serum albumin and stability of)

ANSWER 25 OF 25 CAPLUS COPYRIGHT 2001 ACS L4

1985:94015 CAPLUS ACCESSION NUMBER:

DOCUMENT NUMBER: 102:94015

TITLE: Use of peptide synthesis to probe viral antigens for

epitopes to a resolution of a single amino acid

AUTHOR(S): Geysen, H. Mario; Meloen, Rob H.; Barteling, Simon J.

Commonw. Serum Lab., Parkville, 3052, Australia

CORPORATE SOURCE: SOURCE: Proc. Natl. Acad. Sci. U. S. A. (1984), 81(13),

3998-4002

CODEN: PNASA6; ISSN: 0027-8424

DOCUMENT TYPE: Journal LANGUAGE: English

AB A procedure is described for rapid concurrent synthesis on solid supports of hundreds of peptides, of sufficient purity to react in an ELISA. Interaction of synthesized peptides with antibodies is then easily detected without removing them from the support. In this manner, an immunogenic epitope of the immunol. important coat protein of foot-and-mouth disease virus (type O1) was located with a resoln. of 7 amino acids, corresponding to amino acids 146-152 of that protein. Then, a complete replacement set of peptides in which all 20 amino acids were substituted in turn at every position within the epitope was synthesized, and the particular amino acids conferring specificity for the reaction with antibody were detd. The leucine residues at positions 148 and 151 were essential for reaction with antisera raised against intact virus. lesser contribution was derived from the glutamine and alanine residues at positions 149 and 152, resp. Aside from the practical significance for locating and examg. epitopes at high resoln., these findings may lead to better understanding of the basis of antigen-antibody interaction and antibody specificity.

ΙT 92227-36-6DP, polymer-bound 92269-39-1DP, polymer-bound 92269-40-4DP, polymer-bound

RL: BAC (Biological activity or effector, except adverse); BIOL

(Biological study); PREP (Preparation)

(prepn. and antigenicity of)

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                                                                                                                                                                                                                                                                                                                                               clones.";
DNA Res. 7:131-135(2000).
EMBL; AB022215; BAB17274.1
STOTIENCE 333 AA; 37450
  Q9W4C1;
Q9W4C1;
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouercus robur (English oak).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
Fagales; Fagaceae; Quercus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-COLUMBIA;
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                                                                                                                                                                                                                                                        Local Similarity hes 8; Conserv
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8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                              ral analysis of of the regions
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(TrEMBLrel. 16,
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    (TrEMBLrel.
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                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PubMed=10819329;
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EMBL/GenBank/DDBJ databases.
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Pred. No.
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Pred. No.
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8E45CABF40F00B6F CRC64;
                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                 86C21350D8DB3089 CRC64;
                                                                                                                                                                                                                                                           Mismatches
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1.9;
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Q9VHR3
ID Q0
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DT 00
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RA Adams D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S. Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chenen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Fefankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Clodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N., Moyu M., Murphy B., Murphy L., Mussy D.H., Nelson D.L.,
RA Mcunt S.M., Moyu M., Murphy B., Murphy L., Musny D.M., Nelson D.L.,
RA Mcinctt K., Remington K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mcinctt K., Remington K., Sungeton M., Sungki M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Schepter E., Wang A.H., Wang X.,
Wang S., Yao Q.A.,
Wang S., Wang S., Yao Q.A.,
Wang S
                                                                                                                                                                                                                                                        Query Match
Best Local
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   01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                        Q9VHR3;
                                                                          Q9VHR3
                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0029766; CG15784.
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Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Diptera; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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9; Conser
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   (TrEMBLrel. (TrEMBLrel. (TrEMBLrel.
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                                                                           PRELIMINARY;
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52.9%;
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Pred. No. 3.7;
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Best Local Similarity
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Best Local
                                                           Q9VYJ9;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                      1790
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=99417957; PubMed=10488333; Tsai C.-C., Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.; Tsai C.-C., Kao H.-Y., Yao T.-P., McKeown M., Evans R.M.; "SMRTER, a Drosophila nuclear receptor coregulator, reveals that EcR-mediated repression is critical for development."; mediated repression is critical for development."; Mol. Cell 4:175-186(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ye J. Yeh R.-F. Zaveri J.S. Zhan M. Zhang G., Zheng X.H., Zhong F.N. Zhong W., Zhou X., Zhu S., Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(200).
EMBL; AE003454; AAF46744.1; -
ETJBBase; FBgn0034645; CG10320.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                          Q9VYJ9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                           Pfam; Pf00249; myb_DNA-binding; 1.
PRINTS; PR00308; ANTIFREEZEI.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1.
SMART; SM00395; SANT; 1.
SMART; SM00395; SANT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SANT DOMAIN PROTEIN SMRTER.
SMR OR SMRTER OR CG4013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9U4I2;
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01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                           InterPro;
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                                                PROTEIN
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                                       CG4013
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8; Conser
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                                                                                                          PRELIMINARY;
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80.0%;
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66.7%;
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                                                                                                                                                                                                                                         Length 3469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                  Indels
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Smith
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                                                                                                                                                                                                                  Gaps
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RESULT
Q9M435
ID Q9
AC Q9
DT 01
DT 01
DT 01
DT 9H
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                    Q9M435;
Q9M435;
01-OCT-2000
01-OCT-2000
01-OCT-2000
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Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cadieu E., Center A., Chandra I.,
Cherry J.M., Cayley S., Daller H., Cayley S., Candra I.,
Cherry J.M., Cayley S., Daller H., Cayley S., Candra I.,
Cherry J.M., Cayley S., Daller H., Cayley S., Candra I.,
Cherry J.M., Cayley S., Cayley S., Cayley S.,
Cherry J.M., Cayley S., Cayley S., Cayley S., Cayley S.,
Cherry J.M., Cayley S., Cayley S., Cayley S., Cayley S., Cayley S.,
Cherry J.M., Cayley S., Cayley S., Cayley S., Cayley S., Cayley S.,
Cherry J.M., Cayley S., Cayley S., Cayley S., Cayley S., Cayley S., Cayley S.,
Cherry J. Cayley S., Cayley S., Cayley S., Cayley S., Cayley S., Cayley S.,
Cherry J., Cayle
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PRINTS; PR00308; ANTIFREEZEI.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SMART; SM00395;
SEQUENCE 3502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0024308; Smr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; AE003490; AAF48196.1; -.
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                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                        PRELIMINARY;
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Pred.
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(TrEMBLrel. 15, (TrEMBLrel. 15,

Last sequence update)
Last annotation update)

FlyBase; FBgn0003053; peb.

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RESULT OPWAJII OPWAJII
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Loude A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Krafte C., Kravitz S., Kulp D., Lai Z.,
Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLood M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLood M.P., McPherson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., McPherson D.L.,
RA Merkulov G., Milshina N.V., McDarry C., Morris J., McPherson D.L.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Wilskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Millams, S.M., Wodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
RA Milshina M., Sheng G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SQ DR DR DR
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00096; zf-C2H2; 12.
PRINTS; PR00048; ZINCFINGER.
PROSITE; PS00028; ZINCFINGER_C2H2; 11.
SMART; SM00355; ZnE_C2H2; 1.
DNA-binding; Metal-binding; Nuclear protein; Zinc-finger SEQUENCE 1891 AA; 205368 MW; 9E882364C36BB9BF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001
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nes 8; Conser
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OR EG:66A1.1 OR CG12212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  55.1%;
66.7%;
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16,
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Last annotation updat
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Pred.
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5;
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RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., preiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Beeson K.Y., Benos P. V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bellew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gabart W.M., Glasser K.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kinmel B.E., Kodira C.D., Kraft C.I., Xie Z., Kanja D.J., Ketchum K.A.,
RA Melson D.R., Malshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K.A., Samoders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Ranger Z.-Y.; Wassasman D.A., Weinstock G.M., Weinssenbah J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
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FlyBase; FBgn000822; -.

InterPro; IPR000822; -.

Pfam; PF00096; zf-C2H2; 12.

PROSITE; PS00028; zINC_FINGER_C2H2; 11

SMART; SM00355; ZnF_C2H2; 1.

DNA-binding; Metal-binding; Zinc-finge SEQUENCE 1893 AA; 205673 MW; 1B223
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O9W2E8;

O1-MAY-2000 (TIEMBLITE1. 1

O1-MAY-2000 (TIEMBLITE1. 1

O1-MAY-2000 (TIEMBLITE1. 1
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Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;

Pterygota; Neoptera; Endopterygota; Diptera; Brachyce

Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
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1893 AA;
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Last annotation update)
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Pred. No.
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Best Local
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01-NOV-1996
01-NOV-1996
01-NOV-1998
                                                                                                                                                                                                                                                     O9P6BO;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation updat
HYPOTHETICAL 13.3 KDA PROTEIN.
                                                                                                      German Neurospora genome project;
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ
EMBL; AL355927; CAB91259.1; -
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EMBL; U13892; AAA83555.1; -.
SEQUENCE 450 AA; 47185 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Baron B., Buttin G., Paco-Larson M.L.;

"Molecular characterization of an 18 kb

Bradysia hygida (Diptera, sciaridae).";

Chromosoma 103:715-724(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
TISSUE=SALIVARY GLAND;
MEDLINE=95393845; PubMed=7664619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PC4-1
                                                                                     Hypothetical protein. SEQUENCE 125 AA; 1
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SEQUENCE FROM N.A.
Aign V.,
                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota;
Sordariales; Sordariaceae; Neu
NCBI_TaxID=5141;
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Pterygota; Neoptera;
Sciaridae; Bradysia.
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                                                                                                                                     SEQUENCE FROM N.A.
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Nyakatura G., Mewes
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74
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nes 8; Conservative
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                                      Conservative
                                                                                                                                                                                                                                                                                                       PRELIMINARY;
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                                              55.6%;
73.3%;
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53.3%;
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Neurospora.
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Last annotation update)
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                                              Score 54.5;
Pred. No. 0
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                                     Gaps
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Q9U229;
01-MAY-2000 (TrEMBLrel. 1
01-MAY-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                      PEB OR EG:66A1.1 OR CG12212.

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc.

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         077275
077275;
                        -!- SUBCELLULAR LOCATION: NUCLE
-!- SIMILARITY: BELONGS TO THE
EMBL; AL031227; CAA20227.1; -.
                                                                                                                                                                                            SEQUENCE FROM N.A.

Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;

Fegraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;

"Sequencing the distal X chromosome of Drosophila melanogaster.";

Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EG:66A1.1 PROTEIN
PEB OR EG:66A1.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00070; pyr_redox; 1.
PRINTS; PR00368; FADPNR.
PRINTS; PR00411; PNDRDTASEI.
FAD; Flavoprotein; Oxidoreductase; Redox-active center FAD; Flavoprotein; Oxidoreductase; Redox-active CRC64; SEQUENCE 643 AA; 71257 MW; EAC5A54980A5F75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 investigating biology,";
Science 282:2012-2018 (1998).
-!- COFACTOR: FAD (BY SIMILARITY).
-!- SIMILARITY: TO PYRIDINE NUCLEOTIDE-DISULPHIDE OXIDOREDUCTASES
                                                                                              Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR001327; Pfam; PF00070; pyr_r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL132860; CAB60511.1; InterPro; IPR001100; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. MEDLINE=99069613; PubMed=9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        none;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                         Benos P.;
                                                                                                                                               SEQUENCE FROM N.A.
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8; Conserv
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                                                                                              (OCT-1998)
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72.7%;
                                                                          to the EMBL/GenBank/DDBJ databases
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Pred.
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                                                   NUCLEAR
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red. No. 1.8;
Mismatches
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                                                   HORMONE RECEPTORS FAMILY
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RA Beson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Weil M.-H., Ibegwam C.,

RA Hostin D., Lei Y., Levitsky A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D. L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Wang Z.-Y., Wassarman D. A., Weinscheber F., Shen H.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Yirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassarman D. A., Weinscheber G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhou X., Zhang G., Zhao Q., Zheng L.,

RA Zheng S., Zhao Q., Zheng L.,

RA Zheng S., Zhao Q., Zheng L.,

RA Zheng S., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng S., Zhong W., Zhou X., Zhu X., Smith H.O.,

RA Zheng S., Zhong S., Zho
                                                                                                                                                                                                                                                                                                                                                                       Matches
      Q9VWS0;
Q9VWS0;
01-MAY-2000
01-MAY-2000
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01-MAY-2000
01-MAY-2000
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AE003638; AAF53230.1; -. FlyBase; FBgn0032462; CG16800. SEQUENCE 255 AA; 29296 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Bandrews-Pfannkoch C., Baldwin D.,
The Market Property of the Property 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                  KKGHKHGEHSEKGEK
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9; Conserv
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0 (TrEMBLrel.
      (TrEMBLrel.
                                                                                              PRELIMINARY;
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13,
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13,
Created)
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                                                                                                                                                                                                                                                                                                                                                                    Score 56; DB Pred. No. 0.36
2; Mismatches
                                                                                              PRT;
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                                                                                              686 AA
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0.36;
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                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR00334; KININGEN.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SMART; SM00249; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000104; -.
InterPro; IPR000169; -.
InterPro; IPR001965; -.
InterPro; IPR002395; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00628; PHD; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FlyBase; FBgn0030945; CG6632.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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ALIGNMENTS

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RESULT 1

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OE K-KININOGEN
OE RATTUS norveg
OC ENKATYOTA; ME
OC MAMMAILA; ENT
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                                                                                                                                    Query Match 66...
Best Local Similarity 60.0
Matches 12; Conservative
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Mammalia; Eutheria; R
NCBI_TaxID=10116;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                       kininogen genes allow mapping Mamm. Genome 8:791-792(1997).
                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97468288; PubMed=9321484;
Harris E.L., Grigor M.R., Innes B.A., Harrap S.B., Koike
                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-DONRYU;
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                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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126 AA; 14092 MW;
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Best Local S
Matches
           Loeffen J., Smeets R., van den Heuvel L., Ruitenbeek W., Trijbels F., Smeitink J.;
"Human Bl2 subunit of NADH:ubiquinone oxidoreductase: cD chromosomal localization, tissue distribution, mutation chromosomal localization, tissue distribution, mutation
                                                                                                                                                                                  Ton C., Hwang D.M., Dempsey A.A., Liew C.-C.; "Identification and primary structure of five human oxidoreductase subunits.";
                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                      15-JUL-1999 (Rel. 38, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
NADH-UBIQUINONE OXIDOREDUCTASE B12 SUBUNIT (E
                                                                                                                                                                                                                                                                                                                                                                                                                 043676;
15-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for non-entities requires a license second
    <del>:</del>
                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                       Biochem.
                                                                                                                                                                                                                             MEDLINE=98086396; PubMed=9425316;
                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
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                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
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9; Conserv
                                                                                                                                                                      Biophys.
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 ACTIVITY: NADH +
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                                                                                                                                                                       Res.
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Primates;
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Pred. No. 5.6;
1; Mismatches
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N-LINKED (GLCNAC. . .) (POTENTIAL).
; 9F9770017C2455FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POTENTIAL.
CYTOPLASMIC (POTENTIAL)
6 X 2 AA APPROXIMATE RF
                                                                                                                                                                                                                                                                                                 Craniata; Vertebrata; I
Catarrhini; Hominidae;
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UBIQUINONE = NAD(+) + UBIQUINOI
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                                                                                                                                                                                               NADH-ubiquinone
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                                                                                               cDNA cloning,
                                                                                 detection,
                                                                                                                           Sengers
                            IS BELIEVED
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RESULT 15
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Best Local S
Matches 7
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Q9PUB8;
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
01-OCT-2000 (Rel. 4
                                                                                        Transmembrane;
TRANSMEM 128
TRANSMEM 128
TRANSMEM 161
CARBOHYD
NON_TER
SEQUENCE
                                                                 TRANSMEM TRANSMEM
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MUTTAY B.W., Sueltmann H., Klein J.;

"Identification of a homolog of the human HKE4 gene in zebrafis
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.

-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).

-!- SUMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
                                        DOMAIN
DOMAIN
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                           Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                           EMBL; AF196345;
                                                                                                                                                                      or send an
                                                                                                                                                                                                                                                                                                                                                                                                                                HKE4
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                                                                                                                                                                                  entities
                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7955;
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INIT_MET 0
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603839; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          7; Conserv
                                                                                                                                                                  requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                              Glycoprotein.
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40, Last sequence update)
40, Last annotation updat
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0 BY SIMILARITY.
1 ACETYLATION (BY SIMILARITY).
1271 MW; 851709573DD5E586 CRC64;
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70.0%;
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HIS-RICH.
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Pred. No.
                            N-LINKED
  C8C8C60F6D2BA8A6 CRC64;
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                          (GLCNAC.
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                         .) (POTENTIAL).
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SQUETTTT WWR. REPORT OF THE CORRESPONDENT OF THE CO

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Query Match
Best Local Similarity
Matches 7; Conserv
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SEQUENCE
                                                                                                                                                          Palmiter R.D., Findley S.D.;
"Cloning and functional characterization of a mammalian zinc transporter that confers resistance to zinc.";
EMBO J. 14:639-649(1995).
-i- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.
LETHALITY OF KNCCKOUT EARLY IN GESTATION SUGGESTS A ROLE OF PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.
-i- SUBUNIT: MULTIMER (PROBABLE).
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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DOMAIN
                                 the
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         modified and this statement is not removed. entities requires a license agreement (See
                                                     between
                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SLC30A1 OR ZNT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZNT1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute.
                                                                    This SWISS-PROT entry is copyright. It is produced through a
                                                                                                                                                                                                                                                                                                                    MEDLINE-95188868; PubMed-7882967;
                                                                                                                                                                                                                                                                                                                                            FISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Pfam; PF00512; signal; 1.
Hypothetical protein; Sensory transduction; Transferase;
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                                  European Bioinformatics Institute.
                                                                                                      TISSUE SPECIFICITY: WIDELY EXPRESSED. SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: TO OTHER PROKARYOTIC SENSORY TRANSDUCTION HISTIDINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                           LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AY 2000 (Rel. 39, Created)
AY 2000 (Rel. 39, Last sequence update)
CT 2000 (Rel. 40, Last annotation update)
TRANSPORTER 1 (ZNT-1).
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                                                     the Swiss
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208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ROT entry is copyright. It is produced through Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB40768.1;
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                                                 Institute of Bioinformatics
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Rodentia;
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institutions as long tement is not removed
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Pred. No.
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PHOSPHORYLATION (AUTO-) (BY SIMILARITY)
B3D78C0810241519 CRC64;
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            There are no restrictions ng as its content is in
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"Cloning and functional characterization of a transporter that confers resistance to zinc.";
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Mammalia; Eutheria;
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01-OCT-2000
                                                                                                       TISSUE-Intestine;
MEDLINE-98226729; PubMed-9560190;
                                                                                                                                                                                                                                 Rattus norvegicus (Rat).
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Rodentia;
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PT DRX XX PX XX XX XX Human; high molecular weight kininogen; HK; two-chain high molecular weight kininogen; HKa; anglogenesis inhibhtion; tumour; cancer; ocular disorder; rheumatoid arthritis; endothelial cell apoptosis. (UTEM) UNIV TEMPLE. (MCCR/) MCCRAE R K. WPI; 2000-376483/32. 10-NOV-1998; 05-NOV-1999; WO200027866-A1 Homo sapiens. Human high molecular weight kininogen domain 5 fragment #3 16-OCT-2000 (first entry) 18-MAY-2000-98US-0107833 99WO-US26419

A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis

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RESULT
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                                                                                            A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                  McCrae
                                                                                                                                                                                                                                                                 05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                             two-chain high molecular weight kininogen; HKa; angiogenesis inhibition; tumour; cancer; ocular disorder; rheumatoid arthritis; endothelial cell apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 СНКНКНСНСНСК 12
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                                                                                                                                      2000-376483/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ghkhkhghghgk 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12;
                                                                                                                                                                                            UNIV TEMPLE MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; ilarity 100.0%; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sequence is derived from human high molecular weight HK) domain 5. HK is a 120 kD glycoprotein which binds with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA;
                                                                                                                                                                                                                                     98US-0107833
                                                                                                                                                                                                                                                                 99WO-US26419
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        52pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 21;
2.1e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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0

The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain

Claim 13; Page 29; 52pp; English.

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AAY93345
ID AAY9
XX
     CCCCCCCCXXPTXXRTXRTPXXRXXEXXXEXXC
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
The present sequence represents a fragment of the light chain of huma high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant pentides.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                               Claim 3;
                                                                                                                                                                                             Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                             WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                           Colman WR, Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000
                                                                                                                                                                                                                                                                                                                                        (UTEM ) UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain of human high molecular weight kininogen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93345 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             methods
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                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                سر
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ghkhkhghghgk 12
                                                                                                                                                                                                                                                                                                        ) DUPONT PHARM CO.
) COLMAN W R.
) MOUSA A S.
                                                                                                                                                           Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              natural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            synthesised,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AA;
                                                                                                                                                                                                                                                                                                                                                                                          98US-0107844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptides, or synthetic peptides. They may also sised, using, for example, solid phase synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 79;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21;
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Best Local Similarity Matches 12; Conserv

Conservative

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Pred. No. 1.2e-05;); Mismatches 0;

Indels

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Gaps

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100.0%;

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RESULT
AAY93348
ID AAY9
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Best Local S
Matches 12
                                  The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                                                                                                                                                                                      WPI;
Sequence
                                                                                                                                                                                                                Claim 6;
                                                                                                                                                                                                                                         Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                 Colman WR, Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93348 standard; peptide; 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                            inhibit migration
                                                                                                                                                                                                                                                                                                                                             (Nous/)
                                                                                                                                                                                                                                                                                                                                                                        (UTEM ) UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GHKHKHGHGHGK 12
||||||||||
21 ghkhkhghghgk 32
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                                                                                                                                                                                                                                                                                      2000-376306/32
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                                                                                                                                                                                                                                                                                                                                             MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                         DUPONT PHARM CO. COLMAN W R.
                                                                                                                                                                                                               Page
62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of human high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
AA;
                                                                                                                                                                                                             37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                     98US-0107844.
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                            of.
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                            endothelial
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Pred. No. 9.2e-06;
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                          cells
                          to vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitronectin.
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Query Match

100.0%;

Score 79;

DΒ 21;

Length 62;

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RESULT
AAR75186
AAY93347
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SO
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                                                                                                                                                                                                                                                   Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 12; Conservative
         Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                    ARR75186 is a partial peptide corresponding to human kininogen fragment 1, amino acids 458-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                           Light chain
                                                                                    04-SEP-2000
                                                                                                             AAY93347;
                                                                                                                                    AAY93347 standard; peptide;
                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                           on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARH ) HOECHST JAPAN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial peptide of human HMW kininogen
                                                                                                                                                                                                    37
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                                                                                                                                                                                                                            1 GИКНКИGHGHGK 12
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                                                                                                                                                                                            ghkhkhghghgk 48
                                                                                                                                                                                                                                                                                                                                                                                                                                Page 8; 8pp;
                                                                                                                                                                                                                                                                                                                   63
                                                           of human
                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                   <u>Α</u>,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93ЛР-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12
                                                           high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                 Japanese.
                                                                                                                                      83
                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                   Score 79; DB 16;
Pred. No. 1.3e-05;
                                                                                                                                      Ā
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment
                                                                                                                                                                                                                                                                                                                                                    nent. The fragments are growth promotion activity
                                                                                                                                                                                                                                                                            Length 63;
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RESULT
AAY93351
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting
                                                                                                               Synthetic
                                                                                                                                     Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                 Light chain
                                                                                                                                                                                                                           04-SEP-2000
                                                                                                                                                                                                                                                        AAY93351;
                                                                                                                                                                                                                                                                                 AAY93351 standard; peptide; 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 5; Page 37; 41pp; English.
           09-NOV-1999;
                                        18-MAY-2000
                                                                    WO200027415-A2
                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colman WR, Mousa AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                     57 ghkhkhghghgk 68
                                                                                                                                                                                                                                                                                                                                                                                  1 СНКНКНСНСНСК 12
                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            od for inhibiting endothelial cell proliferation, using compound inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83
                                                                                                                                                                                               of human high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A,
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           99WO-US26377.
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                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                           Score 79; DB 21;
Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                  AA
                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                               0;
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                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                 analogue
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RESULT
AAR75181
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting endothelial cell proliferation.
                                     A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains.
                                                                               WPI; 1995-158909/21
                                                                                                                                    17-SEP-1993; ·
                                                                                                                                                               17-SEP-1993;
                                                                                                                                                                                            28-MAR-1995
                                                                                                                                                                                                                     JP07082172-A
                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                       high molecular weight; kininogen; wound treating agent; human; growt
                                                                                                                                                                                                                                                                                                               Partial peptide of human HMW kininogen fragment 1.2.
                                                                                                                                                                                                                                                                                                                                            05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                              AAR75181 standard; peptide; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\color{black} \cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colman WR, Mousa AS
                                                                                                         (FARH ) HOECHST JAPAN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an analogue of the light chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
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COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                         growth
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Pred. No. 1.9e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                         fragment; 1.2; 1; 2; partial;
th promotion; fibroblast.
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Claim 7; Page 7; 8pp; Japanese

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Best Local
                                          The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit of angiogenesis. The compounds can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragment 1.2, a maino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activion of fibroblasts.
                                                                                                                                                                                                                                                      Claim 11; Page 40-41; 41pp; English.
                                                                                                                                                                                                                                                                                   Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                          Colman WR, Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain of human high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        04-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75181 is a partial peptide corresponding fragment 1.2, amino acids 390-520. Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                 inhibit migration
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                                                                                                                                                                                                                                                                                                                                                                                                                             COLM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MATCH 100.0%; Local Similarity 100.0%; es 12; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      131 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0107844.
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                                 o f
                                 endothelial cells to vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
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. 2.7e-05;
ches 0;
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Sequence

179

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1 GHKHKHGHGHGK 12 ghkhkhghghgk

Best Loc Matches Query Match

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100.0%; ilarity 100.0%; Conservative 0

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Mismatches

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4e-05; DΒ 21;

Length 186;

Score 79; Pred. No.

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RESULT 1
AAY93349
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Best Local Similarity
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                                                     The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can base be inhibiting endothelial cell proliferation. The compounds can also be
                                                                                                                                                                                                                                                                                                                                                                                 (UTEM )
(DUPO )
(COLM/)
Sequence
                                                                                                                                                                                                                              Claim
                                                                                                                                                                                                                                                         Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                       Colman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; high molecular weight kininogen; glycoprotein;
plasma kallikrein; heavy chain; light chain; analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93349 standard; peptide; 186 AA
                            used for inhibiting angiogenesis. The compounds can also inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                        WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                              10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                                                                                       WR,
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COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                   MOUSA A S.
                                                                                                                                                                                                                            Page
186 AA;
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                                                                                                                                                                                                                                                                                                                                       Mousa AS
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                                                                                                                                                                                                                           38; 41pp;
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Pred. No. 3.8e-05;
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0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis;
                                            can also be
be used to
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RESULT 1
AAR75180
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AC AAR7
XC AAR7
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DT 05-C
XX
DE Part
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AAY93342
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Partial peptide of HMW kininogen fragment 2
                              05-DEC-1995
                                                           AAR75180;
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for inhibiting endothelial cell proliferation, using that inhibit endothelial cell migration \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
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                                                                                     AAR75180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman WR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
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(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
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                                                                                                                                                                                                                                                                                            255 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 3; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mousa AS;
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                              (first entry)
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                                                                                     peptide;
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                                                                                                                                                                                                                                   Score 79; [Pred. No. 5.
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                                                                                                                                                                                                                     Mismatches
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5.5e-05;
                                                                                                                                                                                                                                               Length 255;
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XX
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                                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 11; Conserv
                                           JP07082172-A.
                                                                             Misc-difference
                                                                                                    Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns, and act as the active component. The fragments are
17-SEP-1993;
                                                                                                                           Misc-difference
                                                                                                                                                              Bos taurus
                                                                                                                                                                                high molecular weight; kininogen; wound treating agent; bovine; grow
                                                                                                                                                                                                                    Partial peptide of HMW kininogen fragment 1.2.
                                                                                                                                                                                                                                            05-DEC-1995
                                                                                                                                                                                                                                                                   AAR75178;
                                                                                                                                                                                                                                                                                         AAR75178 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            useful in wound on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6; Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high molecular weight; wound treating agent; !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      JP07082172-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-158909/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                     41
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AA;
 93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         93ЛР-0230616
                                                                             69
                                                                                                                           Location/Qualifiers
                                                                  /label= Lys or Arg
                                                                                         label= Val or Leu
                                                                                                              label=
                                                                                                                                                                                                                                                                                                                                                                                                          91.18;
91.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; kininogen; fragment; 1.2; 1; 2; partial; bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                         110 AA
                                                                                                                                                                                                                                                                                                                                                                                                         Score 72;
Pred. No.
                                                                                                                                                                                  growth
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                               fragment; 1.2;
                                                                                                                                                                                  promotion;
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                                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
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les 1;
                                                                                                                                                                                   ; 1; 2; partial; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                  Length 41;
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17-SEP-1993;

93JP-0230616

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В
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Best Local
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The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a mathematical contraction of the method of the invention.
                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                        Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment 1.2, amino acids 387.496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compons. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      have
                                                                                        Claim 10;
                                                                                                             Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                               Colman WR,
                                                                                                                                                                                                                   (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                            09-NOV-1999;
                                                                                                                                                                                                                                                                                                                     18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                              WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                     Homo
                                                                                                                                                                                                                                                                                                                                                                                 Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Light chain of human high molecular weight kininogen analogue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93352 standard; peptide; 11 AA.
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                                                                                                                                                                                                                                                                    10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblasts.
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ghghkhghghgk
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                                                                                                                                                                                                                                                                                                                                                                    sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and treating agent contg. a partial peptide of kininogen
growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                        MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       is a partial peptide corresponding 1.2, amino acids 387-496. Partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page
                                                                                      Page 40; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 110 AA;
                                                                                                                                                                               Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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91.78;
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                                                                                        English.
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Pred. No. 0.00027;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to bovine kininogen
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Matches
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Best Local
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04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
                            11-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
19-MAY-1999;
                                                                                                                                                                                                                                                                            25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                29-MAR-1999;
01-APR-1999;
06-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can esd for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
          20-MAY-1999;
21-MAY-1999;
                                                                                                                                                                          23-APR-1999;
28-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                               06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein identification; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAG06065;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                   19-APR-1
                                                                                                                                                                                                                             16-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                            termination
                                                                                                                                                                                                                                                                                                                                                                                                                                   hybridisation assay; genetic mapping; gene expression control;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                            990S-0134256.
990S-0134218.
990S-0134219.
990S-0134221.
990S-0134221.
990S-01342768.
990S-0134768.
          99US-0135124
99US-0135353
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99US-0132407
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99US-0130510.
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100.0%;
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9.3e-05;
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promoter;
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			9908-01389 9908-01388 9908-01388 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139 9908-0139	s-01 s-01 s-01
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### ALIGNMENTS

RESULT AAY81999 ID AAY8

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AAY81999 standard; peptide;

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A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                       Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                     WPI; 2000-376483/32.
                                                             McCrae
                                                                                                                      10-NOV-1998;
                                                                                                                                             05-NOV-1999;
                                                                                                                                                                                                                                                                                                   Human two-chain high molecular weight kininogen domain 5 fragment #8.
                                                                                                                                                                                            WO200027866-A1.
                                                                                                                                                                                                                  Homo sapiens.
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                                                                                 (UTEM ) UNIV TEMPLE.
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RESULT
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Best Local S
Matches 16
                           Claim 3;
                                                                      Cell adhesion inhibitor - co
The present peptide, and its claimed fragments,
                                                                                                            WPI; 1996-421988/42.
                                                                                                                                                                                                                                                                                                                                                                                                               Human; high polymer; quininogen; L-chain; cell adhesion; cancer metastasis; platelet aggregation; inhibition; wound; inflammatory disease; arteriosclerosis; glomerular nephriti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting anglogenesis. Anglogenesis occurs in a number of disease states, such as tumour formation and composition for inhibiting anglogenesis.
                                                     polymer quininogen L chain
                                                                                                                                       (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                apoptosis. Peptides used in the compostion may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis methods.
                                                                                                                                                                                                28-SEP-1995;
                                                                                                                                                                                                                            13-AUG-1996
                                                                                                                                                                                                                                              JP08208692-A.
                                                                                                                                                                                                                                                                                                  Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymer quininogen L-chain derived peptide
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                                                                   on inhibiting peptide(s), used comprises partial amino acid s
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1.6e-07;
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RESULT
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                     high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                                                                                                                                                    A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       residues 402-498 of the human high polymer quininogen L-chain. They are useful in cell adhesion, cancer metastasis or platelet aggregation inhibitors, and in wound, inflammatory disease, arteriosclerosis or glomerular nephritis treating agents. The present peptide was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                                                                                                                                                    The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with
                                                                                                                                                                                                   high affinity to endothelial cells, where it is cleaved to two-chain
                                                                                                                                                                                                                                                                   Claim 13; Page 29; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                       WPI; 2000-376483/32
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                                                                                                                        The present sequence represents a fragment of the light chain of human high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to the thirt fraction of pagingers in the compounds can also be used to the thirt fraction of pagingers.
                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                    Colman WR, Mousa AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain of human high molecular weight kininogen fragment
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                                                                                                                inhibit migration
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(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
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COLMAN W R.
MOUSA A S.
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                                                                                                                                                                                                                                                                                            Page 36; 41pp; English
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                          Conservative
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                                                                                                                 of endothelial cells
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:.8e-07;
s 0;
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RESULT
AAR75186
ID AAR7
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AAY93348
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Matches 16
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AAR75186;
                        AAR75186 standard; peptide;
                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 6; Page 37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\hspace{1pt}\cdot\hspace{1pt}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colman WR,
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(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
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                                                                                                                                                 Local Similarity
nes 16; Conserv
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                                                                                                                                                Score 98; DE
Pred. No. 6.3
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6.3e-07;
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cell migration; vitronectin.
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Best Local
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                                                                                                                                                                                                                           WO200027415-A2.
                                                                                                                                                                                                                                                                                                                                                                        Human; high molecular weight kininogen;
plasma kallikrein; heavy chain; light cl
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(UTEM ) UNIV TEMPLE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
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                                                                                                                                                                                                                                                                                                                                                    endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                     of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                               ikrein; heavy chain;
cell proliferation;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                               ninogen; glycoprotein; endothelial cell;
light chain; analogue; angiogenesis;
endothelial cell migration; vitronectin
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Method for inhibiting endothelial cell proliferation, that inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                            Colman
                                                                                                                                                                                                                           (UTEM ) UNIV TEMPLE. (DUPO ) DUPONT PHARM CO. (COLM/) COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic.
Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY93351 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 5; Page 37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Method for inhibiting endothelial cell proliferation, using compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          that inhibit endothelial cell migration
                                                                                                                                                                                                    (NOUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (COLM/) COLMAN W R. (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KHGHGHGKHKNKGKKN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
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                                                                                                                                               WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                 MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       83 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mousa AS
                                                                                                                                            Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                             98US-0107844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                        99WO-US26377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21;
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                          compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vitronectin.
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RESULT
AAR75181
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Query Match
Best Local Similarity
Matches 16; Conserv
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Best Local :
                                                                                                                        AAR75181 is a partial peptide corresponding to human kininogen fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, I and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity.
                                                                                                                                                                                                                                                           \boldsymbol{A} wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibition analogues.
                                                                               Sequence
                                                                                                                                                                                                                            Claim 7;
                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                           (FARH ) HOECHST JAPAN
                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Partial peptide of human HMW kininogen fragment 1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                           28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibit migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibiting endothelial cell proliferation. The compounds can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KHGHGHGKHKNKGKKN 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8
                                                                                                                                                                                                                           Page 7; 8pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Page 39; 41pp; English
                                                                               131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        94
 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          weight; kininogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; 131 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
               100.0%;
                                                                                                                                                                                                                            Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       76
 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ogen; fragment; 1.2; 1; 2; partial;
growth promotion; fibroblast.
Score 98; DB 16;
Pred. No. 1.3e-06;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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. 9.5e-07;
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                            Length 131;
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Indels
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0,
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Gaps
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RESULT 1
AAY93349
ID AAY9

AAY93349 standard; peptide; 186 AA

В Š

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khghghgkhknkgkkn

1 KHGHGHGKHKNKGKKN 16

Gaps

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RESULT :
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                   Query Match
Best Local
 Matches
                                                                                                                                 The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to used for inhibiting angiognesis. The compounds can also be used to
                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                          Claim 11; Page 40-41; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                            Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \dot{\phantom{a}}
                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93353;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain of human high molecular weight kininogen analogue
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                                                                                                                     inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1998;
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 Local Similarity
mes 16; Conserv
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                                                                                     179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mousa AS
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0107844
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              100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124
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Score 98; DB 21;
Pred. No. 1.8e-06;
Mismatches 0;
                              Length 179;
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RESULT
AAY93342
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Best Local
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  plasma
                  Human;
                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be
                                      Light chain of human high molecular weight kininogen
                                                                     04-SEP-2000
                                                                                                                        AAY93342 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 9; Page 38; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (DUPO )
                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Method for inhibiting endothelial cell prollferation, using that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Colman WR, Mousa AS
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                                                                                                                                                                                                                                                                                                                                       inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DUPO ) DUPONT PHARM CO (COLM/) COLMAN W R. (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                         40
                                                                                                                                                                                                                 1 KHGHGHGKHKNKGKKN 16
                                                                                                                                                                                     for inhibiting angiogenesis. The compounds can also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sapiens
                                                                                                                                                                                                                                           16;
high molecular weight kininogen; glycoprotein; endothelial cell; kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  high molecular weight kininogen; glycoprotein; endothelial cell; kallikrein; heavy chain; light chain; analogue; angiogenesis; elial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                                                                                                             186
                                                                                                                                                                                                                                           Conservative
                                                                     (first entry)
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                                                                                                                       protein;
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                                                                                                                                                                                                                                                      Score 98;
Pred. No.
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thes 0;
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be used to
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM (COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence represents the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
 17-SEP-1993;
                        17-SEP-1993;
                                                                                                                                                           Partial peptide of
                                                                                                                                                                                     05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                28-MAR-1995
                                                                                                                        wound
                                                                                                                                    high molecular weight; kininogen;
                                                                                                                                                                                                            AAR75180;
                                                                                                                                                                                                                                   AAR75180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibit migration of endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18-MAY-2000
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                                                                                                                                                                                                                                                                                                                       1 KHGHGHGKHKNKGKKN 16
                                                                                                                                                                                                                                                                                                khghghgkhknkgkkn 124
                                                                                                                       treating
                                                                                                                                                                                                                                                                                                                                                16;
                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 3;
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mousa AS
                                                                                                                                                                                  (first entry)
                        93JP-0230616
                                                                                                                       agent;
93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0107844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US26377.
                                                                                                                                                           HMW kininogen
                                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                       bovine; growth promotion;
                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                            Score 98; Pred. No.
                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                          fragment
                                                                                                                                    fragment; 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                     to vitronectin.
                                                                                                                                                                                                                                                                                                                                                            2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                          fibroblast.
                                                                                                                                                                                                                                                                                                                                                                      Length 255;
                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         high molecular
                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                               Gaps
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RESULT 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                             Misc-difference
AAR75178 is a partial peptide corresponding fragment 1.2, amino acids 387-496. Partial human kininogen fragments 1.2, I and 2, are agent compsns. and act as the active compone
                                                                                                        WPI; 1995-158909/21.
                                                                                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR75178 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                 17-SEP-1993;
                                                                                                                                                                                                               JP07082172-A
                                                                                                                                                                                                                                                                                       Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                              05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                            (FARH
                                                                                                                                                                     17-SEP-1993;
                                                                                                                                                                                          28-MAR-1995
                                                                                                                                                                                                                                                                                                                                         wound treating
                                                                                                                                                                                                                                                                                                                                                                        Partial peptide of HMW kininogen fragment 1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (FARH ) HOECHST JAPAN
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                                                                         wound treating agent contg. a ave growth promotion activity c
                                                                                                                                                                                                                                                                                                                                                                                                                                                          14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ۳
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         fibroblasts.
                                                                                                                                                                                                                                                                                                                      taurus
                                                                                                                                                                                                                                                                                                                                                   molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KHGHGHGKHKNKGKKN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-158909/21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             is a partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Page 7; 8pp; Japanese
                                                     Page 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                93JP-0230616
                                                                                                                                                                      93JP-0230616
                                                                                                                                                                                                                                                                                                                                          agent; bovine;
                                                                                                                                                                                                                                                                                                                                                   weight; kininogen;
                                                                                                                                                                                                                                             69
                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                    8pp;
                                                                                                                                                                                                                                  /label=
                                                                                                                                                                                                                                                       /label= Val or Leu
                                                                                                                                                                                                                                                                            /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
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                                                                                                                                                                                                                                                                            Pro,
                                                                                                                                                                                                                                 Lys or Arg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                s the active component. The fragments are because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                       110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                         growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             corresponding
                                                                         partial peptide of kininogen
of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                         fragment; 1.2; 1; 2; partial;
wth promotion; fibroblast.
 2, are use component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16;
2e-06;
 to bovine kininogen peptides of bovine and used in wound treating ent. The fragments are
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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RESULT 15
AAY71879
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Best Local (
                                                                                                                                        The patent discloses a method for preventing or treating a disorder resulting from the release of bradykinin in a mammal which produces a heparin-binding protein (HBP) that binds to a HBP antagonist. This method involves administration of a mammalian HBP antagonist (especially aprotinin) and/or monoclonal antibodies that bind to prekallikrein-H kininogen complexes in the HBP, to decrease the release of bradykinin in the mammal. The antagonists of HBP (e.g. aprotinin) decrease the permeability of the endothelial cells and are used to prevent or treat disorders resulting from the release of bradykinin such as systemic inflammatory response syndrome, ischaemia reperfusion, anaphylaxis and/or allograft rejection. They are also used to treat adult
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-APR-1999;
06-MAY-1999;
01-OCT-1999;
and/or arregions.

and/or arregi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treating systemic inflammatory response syndrome, anaphylaxis and allograft rejection by modulating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         immunosuppressive; vasotropic; prevention; treatment; bradykinin;
aprotinin; H-kininogen; HK; systemic inflammatory response syndrome;
pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in wound treating because they have growth promotion activity on fibroblasts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human HKH20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAY71879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71879 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-APR-2000; 2000WO-DK00213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 KHGHGHGKHKNKGKKN 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         respiratory distress syndrome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 39;
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99DK-0000613.
99DK-0001402.
99US-0157384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lindbom
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                75pp; English.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             domain 5 of H-Kininogen (479-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HKH20
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5.4e-06;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ischaemia reperfusion, release of bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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So Sequence 19 AA;

Obey Matches 14; Conservative 0; St. Pris No. 0.008; 1; Indels 1; Gaps 1;

Oy 1 KHGHGHKKKKKKK 16

Db 2 khijshhx-knykkn 16

Search completed: July 6, 2001, 09:09:19

Job time: 125 sec
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq
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2: /SIDS8/gcgdata/geneseq/geneseqp/Aa1981.DAT:*

3: /SIDS8/gcgdata/geneseq/geneseqp/Aa1982.DAT:*

4: /SIDS8/gcgdata/geneseqy/geneseqp/Aa1983.DAT:*

5: /SIDS8/gcgdata/geneseqy/geneseqp/Aa1985.DAT:*

6: /SIDS8/gcgdata/geneseq/geneseqp/Aa1985.DAT:*

7: /SIDS8/gcgdata/geneseq/geneseqp/Aa1987.DAT:*

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/SIDSB/gcgdata/geneseq/yeneseqp/AA198b.DAT:*

/SIDSB/gcgdata/geneseq/yeneseqp/AA199.DAT:*

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98
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8.533 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

11	10	9	80	7	6	υ	4	ω	2	1	Result No.
93	93	93	93	93	86	86	98	98	98	98	Score
94.9	94.9	94.9	94.9	94.9	100.0	100.0	100.0	100.0	100.0	100.0	Query Match I
131	83	63	62	47	255	186	179	94	28	16	Length DB
16	21	16	21	21	21	21	21	21	21	21	. DB
AAR75181	AAY93347	AAR75186	AAY93348	AAY93345	AAY93342	AAY93349	AAY93353	AAY93351	AAY81997	AAB06337	ID
Partial peptide of	Light chain of hum	Partial peptide of	Light chain of hum	Human high molecul	Human two-chain hi	Description					

A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis

45	44	43	42	41	40	39	38	37	36	35	34	ω ω	32	<b>ω</b> μ	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	12	
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AAG31066	AAG50819	AAG07242	AAG31067	AAG50820	AAG07243	AAG31068	AAG50821	AAG07244	AAP81567	AAR04053	AAB65673	AAB71957	AAG05327	AAG40040	AAG05328	AAG38074	AAG40041	AAG05329	AAG38075	AAG40042	AAG38076	AAG30500	AAG30501	AAG30502	AAB18184	AAG42127	AAG42128	AAY81999	AAY71879	AAW07625	AAR75178	518	AAY81995	
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#### ALIGNMENTS

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RESULT 1
AAB06337
                                                                                                                                                                                                    two-chain high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                    WPI; 2000-376483/32.
                                                                                                                                                                                                                                                        Human two-chain high molecular weight kininogen domain 5 fragment #9
                                                                                                                                                                                                                                                                             16-OCT-2000 (first entry)
                                        McCrae RK;
                                                            (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                             10-NOV-1998;
                                                                                                                 05-NOV-1999;
                                                                                                                                                          WO200027866-A1:
                                                                                                                                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                  AAB06337;
                                                                                                                                                                                                                                                                                                                       AAB06337 standard; Protein;
                                                                                                                                      18-MAY-2000.
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               The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain
                                                                                                                                                                  A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                           Claim 13;
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Matches 16
The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain occular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                              Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                             Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
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                                                                                                                                                                                                                                                                                                               Colman WR,
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(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Page 40-41; 41pp; English.
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ilarity 100.0%;
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                                             Score 98; DB 21;
Pred. No. 2.4e-07;
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Pred. No.
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RESULT AAY93342 ID AAY9

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             Query Match
Best Local
                                                                                                               The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can also be used for inhibiting endothelial cell proliferation. The compounds can also be used to used for inhibiting angiogenesis. The compounds can also be used to
                                                                        Sequence
                                                                                                                                                                                                                                                                                                   Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                               Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                        Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999;
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                                                                                                    inhibit migration
                                                                                                                                                                                                                                                                                                                                              Method for inhibiting
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain
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l Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                 Page 38; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                      Mousa As
                                                                          186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of human high molecular weight kininogen analogue
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                                                                                                      of endothelial cells
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               100.0%;
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                                                                                                                                                                                                                                                                                                 English.
               Score 98;
Pred. No.
                                                                                                      to vitronectin.
             DB 21;
2.5e-07;
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RESULT
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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                      Light chain of human high molecular weight kininogen fragment
                                                                                          04-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (UTEM )
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasma kallikrein;
endothelial cell pr
                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Colman WR, Mousa AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      high molecular weight kininogen; glycoprotein; endothelial cell; kallikrein; heavy chain; light chain; analogue; angiogenesis; kallikrein; heavy chain; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DUPONT PHARM CO COLMAN W R. MOUSA A S.
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                                                                                         entry)
                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                    47
                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                    Score 98;
Pred. No.
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                               DB 21;
3.4e-07;
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                Length 255;
                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                         can also be
be used to
                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                      0
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RESULT
AAY93348
                                                                                                                                                                                                                                                                                                                                                                                 QY
                                                                                                                                                                                                                                                                         DЬ
                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents a fragment of the light chain of human high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                             AAY93348 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \, \cdot \,
                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (DUPO )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (NOUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UTEM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                         \omega_{\omega}
                                                                                                                                                                                                                                                                                            1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                    8
                                                                                                                                                                                                                                                                       hknkgkkngkhngwk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; Page 36; 41pp;
                                                                                                                                                                                                                                                                                                                      15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ) UNIV TEMPLE.
) DUPONT PHARM (
) COLMAN W R.
) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                 47 AA;
                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0107844.
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                                                                                                                                                                                                             peptide; 62
                                                                                                                                                                                                                                                                                                                                 94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                 Score 93;
Pred. No.
                                                                                                                                                                                                             AA
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                 DB 21;
3.4e-07;
                                                                                                                                                                                                                                                                                                                    ·o
                                                                                                                                                                                                                                                                                                                                            Length 47
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                    0,:
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                    0;
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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin

04-SEP-2000

(first entry) human

Light

of,

high molecular weight kininogen

analogue

Homo

sapiens.

Synthetic

WO200027415-A2

0,

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RESULT
AAR75186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting anglogenesis. The compounds can also be used for inhibiting anglogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6;
         A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                   17-SEP-1993;
                                                                                                                                                                                                                                                                                                                   AAR75186;
                                                                                                                                                                                                                                                                                                                                           AAR75186 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTEM )
(DUPO )
(COLM/)
                                                  WPI; 1995-158909/21
                                                                                                                         17-SEP-1993;
                                                                                                                                                                                                                                                                Partial peptide of human HMW kininogen fragment 2.
                                                                                                                                                                                                                                                                                          05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Colman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
                                                                        (FARH ) HOECHST JAPAN
                                                                                                                                                28-MAR-1995.
                                                                                                                                                                             JP07082172-A
                                                                                                                                                                                                    Homo sapiens
                                                                                                                                                                                                                              wound treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (NOUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                         48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                        hknkgkkngkhngwk 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WR, Mousa AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DUPONT PHARM CO-
COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Page 37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          62
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                   93JP-0230616
                                                                                                                          93JP-0230616
                                                                                                                                                                                                                              agent; bovine;
                                                                                                                                                                                                                                         weight;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98US-0107844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US26377.
                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      94.9%;
                                                                          ĸ
                                                                                                                                                                                                                                       kininogen;
                                                                                                                                                                                                                                                                                                                                           63 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 93;
Pred. No.
                                                                                                                                                                                                                           gen; fragment; 1.2; 1; 2; partial;
growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 21; 1
4.5e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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AAY93347
PA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                      Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                              The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains.
                                                                                                                                                                                                           Claim 5; Page 37; 41pp;
                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fragment 1, amino acids 458-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                     Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                 Colman
                                                                                                                                                                                                                                                                                                                                                             (COLM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 8; Page 8; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                          (UTEM ) UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY93347 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR75186 is a partial peptide
                                                                                                                                                                                                                                                                                                                                             (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49 hknkgkkngkhngwk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15;
                                                                                                                                                                                                                                                                                                                WR,
                                                                                                                                                                                                                                                                                                                                                            DUPONT PHARM CO
COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 AA;
                                                                                                                                                                                                                                                                                                                Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                       98US-0107844
                                                                                                                                                                                                                                                                                                                                                                                                                                                  99WO-US26377
            of endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63
                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 93; DB; Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              corresponding to human kininogen
            ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 16; 1
4.5e-07;
            vitronectin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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SS

Sequence

83

B

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AAY81995
ID AAY8
XX AAY8
AC AAY8
XX The control of 
                                                                                                                                                                                                                                                                                                                                  QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75181
ID AAR
                                                                                                                                                                                                                                                                                      B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
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                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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Best Local :
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                   Human high molecular weight kininogen domain 5
                                                                                                                                                            AAY81995 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75181 is a partial peptide corresponding to human kininogen fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compons. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                     AAY81995;
                                                                      16-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (FARH ) HOECHST JAPAN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                wound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         high molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial peptide of human HMW kininogen fragment 1.2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75181 standard; peptide; 131 AA.
                                                                                                                                                                                                                                                                                      117
                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                  1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                                                                   hknkgkkngkhngwk 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7; Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              treating
                                                                                                                                                                                                                                                                                                                                                                                   15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   131
                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    weight; kininogen;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                      94.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94.9%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; growth promotion; fibroblast.
                                                                                                                                                              12 AA
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                      Score 93;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                    DB 16;
9.6e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 21;
6e-07;
                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                     fragment #4.
                                                                                                                                                                                                                                                                                                                                                                                                                       Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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AAR75180
ID AAR7
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                                                                                                                                                                                                                                                                          В
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with C high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising part or all of the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour C formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell proliferation or by recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 12
                                                                                                          Partial peptide of HMW kininogen fragment 2.
                                                                                                                                          05-DEC-1995
                                                                                                                                                                        AAR75180;
                                                                                                                                                                                                   AAR75180 standard;
                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                   wound
                                                                               high molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 10; Page 29; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376483/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      McCrae RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                  Local Similarity
les 12; Conser
                                                                                                                                                                                                                                                                          سا
                                                                                                                                                                                                                                                                                                   5 GKKNGKHNGWKT 16
                                                                                                                                                                                                                                                                        treating
                                                                                                                                                                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                       AA;
                                                             weight; kininogen; fragment; 1.2; 1; 2; partial;
agent; bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0107833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US26419
                                                                                                                                                                                                  peptide; 41
                                                                                                                                                                                                                                                                                                                                              75.5%;
                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                            Score 74;
Pred. No.
                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                            DB 21; 1
5.5e-05;
                                                                                                                                                                                                                                                                                                                                                           Length 12;
                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                0,
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JP07082172-A Bos taurus

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RESULT 1
AAR75178
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
Claim 4; Page 6; 8pp; Japanese
                   A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                Misc-difference
                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compones, and act as the active component. The fragments are
                                                                                                            17-SEP-1993;
                                                                                                                                                     JP07082172-A
                                                                                                                                                                                                                         Misc-difference
                                                                                                                                                                                                                                                                                                                                                                  AAR75178 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                     (FARH ) HOECHST JAPAN
                                                                                          17-SEP-1993;
                                                                                                                                                                                                                                                        Bos taurus
                                                                                                                                                                                                                                                                                                       Partial peptide of HMW kiningeen fragment 1.2
                                                                                                                                                                                                                                                                                                                            05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-158909/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-SEP-1993;
                                                                                                                                                                                                                                                                                    high molecular weight; kininogen; fragment; 1.2; 1; 2; partial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARH ) HOECHST JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                     27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HKNKGKKNGKHNGWK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                  hknkgknngkhydwr 41
                                                                                                                                                                                                                                                                          treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            41 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                          93JP-0230616
                                                                                                            93ЛР-0230616
                                                                                                                                                                                                                                                                         agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93JP-0230616.
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                                                                                                                                                                                 69
                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                         /label=
                                                                                                                                                                                          'label= Val
                                                                                                                                                                                                               'label=
                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71.48;
73.38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         KK.
                                                                                                                                                                                                                                                                         bovine; growth
                                                                                                                                                                       Lys or Arg
                                                                                                                                                                                                                Pro,
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                                                                                                                                                                                            or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                         promotion; fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.00076;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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RESULT 15
AAW07625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                         The present peptide, and its claimed fragments, are derived from residues 402-498 of the human high polymer quininogen L-chain are useful in cell adhesion, cancer metastasis or platelet aggregation inhibitors, and in wound, inflammatory disease, arteriosclerosis or glomerular nephritis treating agents. The present peptide was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75178 is a partial peptide corresponding to bovine kininogen fragment 1.2, amino acids 387-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compones. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                           Cell adhesion inhibiting peptide(s), used as cancer metastasis
Sequence
                                                                                                                                               Claim 3; Page 2; 14pp; Japanese.
                                                                                                                                                                            inhibitor - comprises partial amino acid sequence of human high polymer quininogen L chain
                                                                                                                                                                                                                                          WPI; 1996-421988/42.
                                                                                                                                                                                                                                                                                                                                                                                               JP08208692-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; high polymer; quininogen; L-chain; cell adhesion; cancer metastasis; platelet aggregation; inhibition; wound; inflammatory disease; arteriosclerosis; glomerular nephritis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             on fibroblasts.
                                                                                                                                                                                                                                                                                                      28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                   28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                                                 13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human high polymer quininogen L-chain derived peptide
                                                                                                                                                                                                                                                                      (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        96 hknkgknngkhydwr 110
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20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                      94JP-0259451
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13..20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers 1..13
                                                                                                                                                                                                                                                                                                                                                                                                                           /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.4%; 73.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                        "claimed peptide (claim 6)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "claimed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0.0021;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         (claim 1)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 110;
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                                                                                                  l from
ain. They
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Query Match

66.3%;

Score 65;

DΒ

17;

Length 20;

		Search completed: July 6, 2001, 09:09:19 Job time: 125 sec	Best Local Similarity 100.0%; Pred. No. 0.002; Matches 11; Conservative 0; Mismatches 0; Qy 1
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Result
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Maximum DB
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Perfect score:
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                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                Score
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 ,
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167
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                                                                                                                                                                                                Length DB
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Arabidopsis thalia			Arabidopsis thalia	Arabidopsis thalia	Streptococcus pyog	Partial peptide of	Haemophilus influe	Human high molecul	Human high polymer				-	-	tha	0		Arabidopsis thalia				Arabidopsis thalia	high	Light chain of hum	ς,	Partial peptide of	Human high molecul		Partial peptide of	tide	high polym	Human two-chain hi	

## ALIGNMENTS

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RESULT
AAY81996
  A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                 WPI; 2000-376483/32.
                                                                                                                                                                                                                        Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                   05-NOV-1999;
                                                                                                                                                                               WO200027866-A1
                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                             Human high molecular weight kininogen domain 5
                                                                                                                                                                                                                                                                                                                            AAY81996;
                                                                                                                                                                                                                                                                                                                                                AAY81996 standard; peptide;
                                                                            (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                               10-NOV-1998;
                                                                                                                                                         18-MAY-2000.
                                                                                                                                                                                                                                                                                                     16-OCT-2000 (first entry)
                                                                                                               98US-0107833.
                                                                                                                                   99WO-US26419.
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                                                                                                                                                                                                                                                                               fragment #5
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Best Local Similarity
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The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a
                                                                   Claim 4; Page 36; 41pp; English
                                                                                                                                                                                     WPI; 2000-376306/32.
                                                                                                                                                                                                                                Colman WR, Mousa AS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000
                                                                                                                                            Method
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                                                                                                                                                                                                                                                                              (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
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ial cell migration
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Pred. No. 2e-17;
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                                                                                                                                       proliferation, using
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Best Local S
Matches 28
           The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting engothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                (DUPO)
                                                                                                                                                                                        Claim
                                                                                                                                                                                                                      Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                    Colman WR,
                                                                                                                                                                                                                                                                     WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                 09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; high molecular weight kininogen; glyco
plasma kallikrein; heavy chain; light chain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain of human high molecular weight kininogen
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COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                   UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                  MOUSA A S.
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                                                                                                                                                                                     Page
inhibiting angiogenesis.
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endothelial cell migration;
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Best Local :
                04-SEP-2000
                                               AAY93347;
                                                                          AAY93347 standard;
                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                           fragment 1, amino acids 458-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                            AAR75186
                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1995-158909/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28-MAR-1995.
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                                                                                                                                                                                                                    28; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                          is a partial peptide corresponding to human kininogen
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                                                                                                                                                                                                                                   Score 167; DB 1
Pred. No. 5e-17;
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Pred. No. 4.9e-17;
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            Homo sapiens
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Query Match
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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                            Light chain of human
                                                                                                                                                            04-SEP-2000
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                                                                                                                                                                                                                                                           AAY93351 standard; peptide;
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(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
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les 28; Conserv
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                                                                                                         high molecular weight kininogen analogue
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                                                                                                                                                   17-SEP-1993;
                                                                                                                                                                                                        28-MAR-1995
                                                                                                                                                                                                                                                                                                          Homo sapiens
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Best Local Similarity
Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for
                                                                    The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARR75181 is a partial peptide corresponding to human kininogen fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsus. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                           Claim
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that inhibit endothelial cell migrafice -
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                                                                                                                                                                                                             WPI; 2000-376306/32.
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(COLM/)
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                                                                                                                                         9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28;
                                                                                                                                                                                                                                                                               DUPONT PHARM COLMAN W R.
                                                                                                                                                                                                                                                                                                          UNIV TEMPLE
                                                                                                                                                                                                                                                                   MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                         Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131 AA;
                                                                                                                                                                                                                                       Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; ilarity 100.0%; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                         38;
                                                                                                                                                                                                                                                                                                                                   98US-0107844
                                                                                                                                                                                                                                                                                                                                                              99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation;
                                                                                                                                        41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          peptide;
                                                                                                                                                                                                                                                                                             S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese.
                                                                                                                                        English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 167; DB 16;
Pred. No. 1.1e-16;
D; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  a partial peptide of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                using compound
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Query Match
Best Local S
Matches 28
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                          of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                     The present sequence represents the light chain of human high molecul weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the name to a constitution of the method of the name to be seen that the method of the name to be seen the seen that the name to be seen that the name that the name to be seen that the name to be seen that the name that the name to be seen that the name to be seen that the name that the name to be seen that the name that the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (COLM/)
                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY93342 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibiting endothelial cell proliferation. The compounds used for inhibiting angiogenesis. The compounds can also inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
  28; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUPONT PHARM CO. COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             186 AA;
                                                                                                                   255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of.
  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               human high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0107844.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41pp; English.
                      100.0%;
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  0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
Score 167; DB 21;
Pred. No. 2.4e-16;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 167; DB 21;
Pred. No. 1.7e-16;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                            Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                            255;
                                                                                                                                                                                                                                                                                                                                                                                                                            high molecular
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be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     186;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
0
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RESULT 1 AAY93345

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AAY93345 standard; peptide; 47

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EQQHGLGHGHKFKLDDDLEHQGGHV 28

eqqhglghghkfkldddlehqgghv

25

Mismatches

Indels

0,

Gaps

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RESULT :
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Hest Local
                              Query Match
                                                                                                               The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kbg glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to used for inhibiting angiognesis. The compounds can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                          (DUPO)
                                                                         Sequence
                                                                                                                                                                                                                                                                                            Claim 11; Page 40-41; 41pp; English.
                                                                                                                                                                                                                                                                                                                         Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration -  \\
                                                                                                                                                                                                                                                                                                                                                                                                Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasma kallikrein; heavy chain;
endothelial cell proliferation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-SEP-2000
                                                                                                      inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain
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   l Similarity
25; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                            MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                          DUPONT PHARM CO-
COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UNIV TEMPLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard;
                                                                         179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                Mousa AS
 86.8%; So llarity 100.0%; I Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     of human high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0107844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                Score
Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light chain; analogue; angiogenesis;
endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
             145; DB 21
. No. 2.3e-1
                               21;
                            Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     analogue
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RESULT 12
AAY8198
ID AAY819
XX AAY819
XC AAY819
XY 16-OCT
XX TX
DE Human
XX Human;
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                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                            Matches
                               Human two-chain high molecular weight kiningeen domain 5 fragment #7
                                                                                                                        AAY81998 standard;
                                                                                                                                                                                                                                                                                                                                                           The present sequence represents a fragment of the light chain of huma high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                16-OCT-2000
                                                                                            AAY81998;
                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 3; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration  \begin{tabular}{ll} \hline \end{tabular} 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colman WR, Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Light chain of human high molecular weight kininogen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                04-SEP-2000
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       10-NOV-1998;
                                                                                                                                                                                                                            12 GHKFKLDDDLEHQGGHV 28
                                                                                                                                                                                              Local
high molecular weight kininogen; HK,
                                                                                                                                                                                                                                                          l Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                     47
                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                             (first entry)
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                                                                                                                        peptide;
                                                                                                                                                                                                                                                     58.,
100.08; F1
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                                                                                                                                                                                                                                                                        Score 98; Pred. No.
                                                                                                                          AA
                                                                                                                                                                                                                                                                        DB 21; 1
2.8e-07;
                                                                                                                                                                                                                                                                                      Length 47;
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В
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                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell proliferation the compostion may be recombinant peptides, an atural peptides, or synthetic peptides. They may also be chemically extended using for example.
28-SEP-1995;
                            13-AUG-1996.
                                                           JP08208692-A.
                                                                                         Homo sapiens
                                                                                                                     Human; high polymer; quininogen; L-chain
                                                                                                                                               Human high polymer quininogen L-chain derived
                                                                                                                                                                               04-FEB-1997 (first entry)
                                                                                                                                                                                                              AAW07627;
                                                                                                                                                                                                                                        AAW07627 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376483/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 synthesised, using, for example,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             McCrae RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                1 ghkfkldddlehqggh
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95JP-0276418
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Best Local Similarity
Matches 14; Conserv
                             AAR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity.
Sequence
                                                                                                               Claim
                                                                                                                                    A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                           WPI; 1995-158909/21.
                                                                                                                                                                                                  (FARH ) HOECHST JAPAN KK
                                                                                                                                                                                                                            17-SEP-1993;
                                                                                                                                                                                                                                                                               28-MAR-1995
                                                                                                                                                                                                                                                                                                       JP07082172-A.
                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                      high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                               Partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example; Page 8; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cell adhesion inhibiting peptide(s), used as cancer metastasis inhibitor - comprises partial amino acid sequence of human high polymer quininogen L chain
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4 hgheqqhglghghk 17
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41 AA;
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2.4e-06;
                                  growth promotion activity
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Query Match Best Local Similarity

50.9%; 55.6%;

Score 85; Pred. No.

DB 16; 1.7e-05;

Length

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                                                                                           Sequence
                                                                                                               on fibroblasts.
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                                                                                                                                                                                      Claim
                                                                                                                                                                                                        A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
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wound treating agent; !
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two-chain high molecular weight kininogen; HKa;
anglogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                         WPI; 2000-376483/32.
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Best Local
  The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. HKa or a
                                                                                                                   Claim
                                                                                                                                                                             A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                    WPI; 2000-376483/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting anglogenesis. Anglogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit anglogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell approach section for example cellides. They may also be chemically example cellides are because the composition of the composition o
                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human high molecular weight kininogen domain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; high molecular weight kininogen;
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nilarity 100.
Conservative
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                                                                                                              52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                peptide;
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ches 0;
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AAY93345
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Best Local
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high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for
                                                                                                                                                                             Claim 3; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                                        Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \, -
                                                                                                                                                                                                                                                           WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                         Colman WR,
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(DUPO ) DUPONT PHARI
(COLM/) COLMAN W R.
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                                                                                                                                            present sequence represents a fragment of the light chain of human
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COLMAN W R.
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Pred. No.
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                                                                            The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method and the compounds can be used for inhibiting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                       Sequence
                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                         Method for inhibiting endothelial cell proliferation, using that inhibit endothelial cell migration \,\cdot\,
                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  inhibiting endothelial cell proliferation. The compounds used for inhibiting angiogenesis. The compounds can also inhibit migration of endothelial cells to vitronectin.
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                                                                                                                                                                                                                                                                4;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16;
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n; heavy chain; light chain; analogue; angiogenesis;
proliferation; endothelial cell migration; vitronectin.
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Pred. No. 4.1e-09;
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                                                                                                                                                                                                         to endothelial cells,
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Query Match Best Local Similarity

Score 94; Pred. No.

DB 21; 4.9e-09;

Length

RESULT AAR75186

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1 GHKFKLDDDLEHQGGH 16

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                                                                                               high molecular weight kininogen. High molecular weight kininogen is a 120 kbg glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrain into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                        Sequence
                                                                                                                                                                                                                                                                                               Claim 6;
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                                                                                                                                                                                                                                                                                                                                                                                                    Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY93348 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                             (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                 (MOUS/) MOUSA A S.
             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G
                                                                                                                                                                                                                                                                 present sequence represents an analogue of the light chain of human
                                                                                                                                                                                                                                                                                                                                                                        2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ghkfkldddlehqggh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        16;
   l Similarity
16; Conser
                                                                                                                                                                                                                                                                                               Page
                                                                         62
                                                                                                                                                                                                                                                                                                                                                                                                    Mousa AS
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                         AA;
                                                                                                                                                                                                                                                                                               37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98US-0107844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-US26377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide;
             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              င္ပ
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   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
             Score 94; DB 21;
Pred. No. 5.6e-09;
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   Mismatches
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                           Length 62;
 Indels
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0,
                                                                                                                                                                                                                                                                                                                                           compound
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Gaps
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0;
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RESULT
AAY93347
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                                                                                                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                  fragment 1, amino acids 458-520. Partial peptides of bovine and human kininogen fragment 1, amino acids 458-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion action on fibroblasts
 10-NOV-1998;
                 09-NOV-1999;
                                                WO200027415-A2
                                                                        Synthetic.
                                                                                     plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                              Human; high molecular weight kininogen;
plasma kallikrein; heavy chain; light cl
                                                                                                                   Light chain of human high molecular weight kininogen analogue
                                                                                                                                     04-SEP-2000
                                                                                                                                                     AAY93347;
                                                                                                                                                                    AAY93347
                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                      A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                 18-MAY-2000
                                                               Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                        Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                              (FARH ) HOECHST JAPAN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high molecular wound treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75186 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial peptide of human HMW kininogen fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75186;
                                                                                                                                                                                                             17
                                                                                                                                                                                                                          1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                    7
                                                                                                                                                                                                           1995-158909/21
                                                                                                                                                                                                                                           16;
                                                                                                                                                                    standard; peptide;
                                                                                                                                                                                                                                                                                                                                                        Page 8;
                                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                           Conservative
                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                  AΑ;
98US-0107844
                 99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                              93JP-0230616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             agent;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    weight;
                                                                                                                                                                                                                                                                                                                                                        gpp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide; 63 AA
                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                        Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kininogen;
                                                                                                                                                                                                                                                                                                       because they have growth promotion activity
                                                                                                                                                                    83
                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                        Score 94; DB 10,...
Pred. No. 5.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            growth
                                                                                                                                                                    AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           agment; 1.2; 1; 2; partial; promotion; fibroblast.
                                                                                              chain;
                                                                                                      glycoprotein;
                                                                                                                                                                                                                                                        Length 63;
                                                                                                                                                                                                                                          Indels
                                                                                                     endothelial cell;
                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                         Gaps
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δõ
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RESULT
AAY93351
ID
AAY9
XX
AC
AAY9
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Matches 16; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local
Colman WR,
                                                             (UTEM )
                                                                                                                                                                                                                                                                                                                                                            Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                                           10-NOV-1998;
                                                                                                                                                                                 09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that
                                                                                                                                                                                                                           18-MAY-2000
                                                                                                                                                                                                                                                               WO200027415-A2
                                                                                                                                                                                                                                                                                                                            Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Light chain of human high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
                                                                                                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAY93351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Analogues of high molecular weight kininogen are used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
                                          MOUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibit migration of endothelial cells to vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               φ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         od for inhibiting endothelial cell proliferation, using compound inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ghkfkldddlehqggh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   <u>ن</u>
                                                           ) UNIV TEMPLE.
) DUPONT PHARM |
) COLMAN W R.
                                        MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mousa AS
  Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,
                                                                                                                                           98US-0107844
                                                                                                                                                                               99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide;
                                                                                  င္ပ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 94; DE
Pred. No. 7.8
0; Mismatches
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A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .8e-09;
s 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                              analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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WPI; 2000-376306/32

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RESULT
AAR75181
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Best Local S
Matches 16
                                                      human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compones. The fragments are useful in wound treating because they have growth according to the component.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kbg glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to the third the compounds can also be used to the thirt with the compounds can also be used to the thirt with the compounds can also be used to the thirt with the compounds can also be used to the thirt with the compounds can also be used to the thirt with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can also be used to the thirty with the compounds can be used to the thirty with the compounds can also be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the can be used to the thirty with the compounds can be used to the thirty with the compounds can be used to the thirty with the can be used to 
Sequence
                                           on fibroblasts.
                                                                                                                                                                                                  Claim 7;
                                                                                                                                                                                                                                                                                                                                                       (FARH ) HOECHST JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JP07082172-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   05-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75181 standard; peptide; 131-AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                       AAR75181
                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     wound treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          high molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Partial peptide of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                       wound treating agent contg. a partial peptide of kininogen ave growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                              1995-158909/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8
                                                                                                                                is a 1.2,
                                                                                                                                                                                              Page 7; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
  131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                              partial peptide corresponding amino acids 390-520. Partial
  A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weight; kininogen; fragment; 1.2; 1; 2; partial;
agent; human; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                   93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                            93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                       KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HMW kininogen fragment 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
                                                                                                                                                  to human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                              kininogen
of bovine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94
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16;

Conservative

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Indels

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Gaps

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GHKFKLDDDLEHQGGH 16 ghkfkldddlehqggh

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RESULT 10
AAY93353
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Query Match
Best Local S
Matches 16
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Best Local Similarity
                                                                                              The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kbm glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                       Sequence
                                                                                                                                                                                                                                                                                           Claim 11;
                                                                                                                                                                                                                                                                                                                        Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                 Colman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; high molecular weight kininogen; glycoprotein; plasma kallikrein; heavy chain; light chain; analogue,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain of human high molecular weight kininogen analogue.
                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-376306/32.
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                 WR,
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                                                                                                                                                                                                                                                                                         Page 40-41; 41pp; English
                                                                       179 AA;
                                                                                                                                                                                                                                                                                                                                                                                                 Mousa AS
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             100.0%;
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Score 94; DB
Pred. No. 1.9
0; Mismatches
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Pred. No. 1.3e-08;
Pred. No. 1.3e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A
             ; DB 21;
. 1.9e-08;
                           Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 131;
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AAY93342
ID AAV
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ID 1
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  DEX DXXX
                                                                                                                                                 Вþ
                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                         The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                            04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration -
  Light chain
                                                      AAY93342;
                                                                              AAY93342 standard;
                                                                                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Colman WR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93349 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000
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                                                                                                                                                                                                                Local Similarity
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                                                                                                                                              ghkfkldddlehqggh 31
                                                                                                                                                                        GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  9; Page 38; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high molecular weight kininogen; glycoprotein; endothelial kallikrein; heavy chain; light chain; analogue; angiogenes:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DUPONT PHARM CO
COLMAN W R.
MOUSA A S.
                                                                                                                                                                                                                                                                    186
  of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mousa AS;
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                           (first entry)
                                                                                                                                                                                                                                                                    A,
human high molecular weight kininogen.
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                                                                               protein;
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Pred. No.
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                                                                                                                                                                                                    Mismatches
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AAW07628
ID AAW(
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                                                                                                                                                                                                                                             RESULT
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Best Local (
                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for kininogen analogues. The method and the compounds can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                               04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                kininogen analogues. The method and the compounds can be inhibiting endothelial cell proliferation. The compounds used for inhibiting angiogenesis. The compounds can also
28-SEP-1995;
                          13-AUG-1996
                                                    JP08208692-A
                                                                                                        Human; high polymer;
                                                                                                                                   Human high polymer quininogen L-chain derived peptide
                                                                                                                                                                                         AAW07628;
                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-1999;
                                                                                                                                                                                                                   AAW07628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Method
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                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           that inhibit
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                                                                                                                                                                                                                                                                                                               1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                                                                                                                                                      ghkfkldddlehqggh 100
                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         for inhibiting endothelial cell proliferation, using compound whibit endothelial cell migration -
                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                              (first entry)
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95JP-0276418.
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                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                        100
                                                                                                        quininogen; L-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CO
                                                                                                                                                                                                                                                                                                                                                        .08;
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                                                                                                                                                                                                                                                                                                                                                        Score 94;
Pred. No.
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s 0;
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                                                                                                                                                                                                                                                                                                                                                                    Length
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be used to
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AAY81993
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Best Local S
Matches 13
      The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kB glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising part or all of the present
                                                                                                                   A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                          Human; high molecular weight kininogen; HKa;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
                                                                                  Claim
                                                                                                                                                                                                                                                                  05-NOV-1999;
                                                                                                                                                                                                                                                                                                                  WO200027866-A1
                                                                                                                                                                                  McCrae RK;
                                                                                                                                                                                                                                                                                           18-MAY-2000
                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present peptide is derived from residues 402-498 of the human high polymer quininogen L-chain. It was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cell adhesion inhibiting peptide(s), used as cancer metastasis inhibitor - comprises partial amino acid sequence of human high
sequence may be used
                                                                                                                                                                                                        (UTEM ) UNIV TEMPLE.
(MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                            10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                          Human high molecular weight kininogen domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                 rheumatoid arthritis;
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|fkldddlehgggh 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Page 8; 14pp; Japanese.
                                                                                  Page 28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20
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                                                                               52pp;
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                                                                                                                                                                                                                                                                                                                                                                 endothelial
a pharmaceutical composition for inhibiting
                                                                                 English
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Pred. No.
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2.6e-06;
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AAY79183
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Best Local S
Matches 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It calso occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid
HSCs (PHSCs) such as umbilical cord cells, bone marrow cells and foetal liver cells. The encoded proteins are growth factors, transcription factors, splicing factors, capping factors, transporproteins, translation factors or replication factors that modulate
                                                   The present sequence is that of a mouse haematopoietic stem cell (HSC) specific protein. It is an example of claimed HSC-specific proteins (see AAY94077-131), redicted from novel isolated HSC-specific nucleic acids (see AAZ94077-131). The HSCs are especially primitive
                                                                                                                         Claim 21;
                                                                                                                                                 Hematopoietic stem cell signaling proteins modulating replication a differentiation for treating immune system disorders and leukaemia
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Misc-difference 523
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CC HSC activity, especially differentiation or replication. The CC invention provides claimed methods: for identifying PHSC-specific CC nucleic acids; for generating a stem cell/progenitor cell from CC PHSCs; for identifying the presence of a PHSC in a sample; for CC identifying the presence in a sample of a compound that modulates CC activity; for using such a compound to trapt an immune system CC condition, especially leukaemia; for introducing exogenous nucleic CC acid into a HSC; and for ex vivo expansion of HSCs. Also claimed CC are vectors, host cells, and an antibody that specifically binds a XX Squence 631 AA;

Ouery Match 47.9%; Score 45; DB 21; Length 631; Best Local Similarity 50.0%; Pred. No. 18; Matches 8; Conservative 2; Mismatches 6; Indels 0; Gaps 0; 1 GHKFKLDDDLEHQGGH 16 Db 351 ghrfkrsditkkqdgh 366

Search completed: July 6, 2001, 09:09:18
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Query Match 45.7%; Score 43; DB 2; Length Best Local Similarity 58.3%; Pred. No. 2.8; Matches 7; Conservative 2; Mismatches 3; Independent of the control of	US-08-825-14  US-08-825-14  US-08-825-14  Sequence 14, Application US/08820825  Patent No. 5945309  GENERAL INFORMATION: APPLICANT: VI, GUO-LIANG APPLICANT: VI, GUO-LIANG APPLICANT: VI, GUO-LIANG APPLICANT: DILLON, PATRICK TITLE OF INVENTION: CYTOSTATIN III  NUMBER OF SEQUENCES: 15  CORRESPONDENCE ADDRESS: ADDRESSES: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE CITY: ROCKVILLE STATE: MD  COUNTRY: USA 2IP: 20850 COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PATENTION UNBER: US/08/820,825 FILING DATE: 19-MAR-1997 CLASSIFICATION UNBER: US/08/820,825 FILING DATE: 19-MAR-1997 CLASSIFICATION UNBER: US/08/820,825 FILING DATE: 19-MAR-1997 CLASSIFICATION UNBER: BF22 TELECOMMUNICATION INFORMATION: NAME: BROOKES, ANDERS A. REGISTRATION INFORMATION: TELEPAN: (301) 309-8512 INFORMATION FOR SEQ ID NO: 14: SEQUENCE CHARACTERISTICS: LEMGTH: 106 amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acids TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein US-08-820-825-14	ALIGNMENTS	28 36 38.3 3712 2 US-08-222-617A-4 29 36 38.3 3712 2 US-08-222-617A-25 30 36 38.3 3727 2 US-08-222-617A-27 31 36 38.3 3778 2 US-08-222-617A-27 31 36 37.2 86 4 US-08-905-223-420 32 35 37.2 123 2 US-08-97-972-1 34 35 37.2 447 1 US-08-33-485-67 35 37.2 447 1 US-08-33-485-67 36 35 37.2 447 1 US-08-899-324-33 37 37 2 447 1 US-08-899-324-33 38 37 2 447 1 US-08-899-324-33 38 37 2 447 1 US-08-899-324-33 38 37 2 447 1 US-08-899-324-33 39 37 2 53 2 US-08-899-324-33 39 37 37 2 53 2 US-08-616-392C-4 40 35 37.2 583 2 US-08-616-392C-4 41 35 37.2 583 2 US-08-616-392C-4 42 34 36.2 123 4 US-08-844-188-36 43 36.2 123 4 US-08-844-188-36 44 36.2 123 4 US-08-844-188-36 45 34 36.2 154 1 US-08-102-942A-5
ngth 106; Indels 0;			Sequence
Gaps 0;			4, Appli 25, Appl 27, Appli 27, Appli 420, Appli 67, Appli 67, Appl 67, App

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Best Local Similarity
Matches 7; Conserv
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                             APPLICANT: Ni, Jian
APPLICANT: Yu, Guo-Liang
APPLICANT: Gentz, Reiner
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: CYTOSTATIN I
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
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APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
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LENGTH: 106 amino acid
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NAME: BROOKES, ANDERS A.
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APPLICATION NUMBER: 08/820,825
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     9410 KEY WEST AVENUE
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                                                                                                                                                                                                                                                                                                                                        Conservative
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58.3%;
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                                                                                                                                                                                                                                                                                                                                                        Score 43;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                                        Mismatches
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US-08-470-298B-2
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Best Local Similarity
7; Conserve
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: NI, JIAN
APPLICANT: GENTZ, REINER
APPLICANT: YU, GUO-LIANG
APPLICANT: ROSEN, CRAIG /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                  STREET: 9410 KEY
CITY: ROCKVILLE
STATE: MD
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ZIP: 20850
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                  301-309-8512
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPACTION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA: NAME: Benson, Robert H
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PF1
TELECOMMUNICATION. INFORMATION:
TELEPHONE: 301-309-8504 APPLICATION NUMBER: US/00
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Robert H US/08/409,731A PF175 Score 43; 1 Pred. No. 2 DB 1; Length 107;

Mismatches

0;

Gaps

0;

Sequence 2, Application US/08470298B Patent No. 5844081 COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION UNMEE: US/08/470,298B
FILING DATE: 06-JUN-1995
CIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 9F175D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
THELEPAX: 301-309-8513 TITLE OF INVENTION: CYTOSTATIN I NUMBER OF SEQUENCES: 12 CORRESPONDENCE ADDRESS: ADDRESSEE: HUMAN GENOME SCIENCES, INC. STREET: 9410 KEY WEST AVENUE

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Best Local Similarity 58...
7; Conservative
Sequence 2, Application US/08820825 Patent No. 5945309
                                                                                                                                                                  Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 301-610-5772
                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: p-43,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 107 amino acids
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                                                                                         APPLICATION NUMBER: FILING DATE: 13-FEE CLASSIFICATION: 420
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CITY: ROCKVILLE
STATE: MARYLAND
                                                                                                                                                  Local Similarity tes 7; Conserv
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                                                                                                                     5 KLDDDLEHQGGH 16
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Yu, Guo-Liang
Rosen, Craig A
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Pred. No. 2.9;
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Pred. No. 2
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Best Local Similarity 58.3%;
                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvu
TITLE OF INVENTION: HUMAN RETINOID BINDING PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
AMBE: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,37
REFERENCE/DOCKET NUMBER: P
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MEDIUM TYPE: Floppy disk
COMPUTER: IEM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/899,031
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 309-8504
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CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                                                                                                                       STATE: C
COUNTRY:
                                                                                                                                                                                       CITY: Palo Alto
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FILING DATE:
                                                                                                                                        ZIP: 94304
                                                                                                                                                                                                         ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 KPDKEIEHQGNH 49
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   amino acid
   GY: linear
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9410 KEY WEST AVENUE
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                                                                                                                                                       USA
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 Herewith
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Pred. No. 3
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3.7;
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Best Local :
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                                TELEFAX: (301) 309-8512 INFORMATION FOR SEQ ID NO: 2:
                                                             NAME: BROOKES, ANDERS A.
REGISTION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
                  SEQUENCE CHARACTERISTICS:
                                                                                                                                               FILING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                 PRIOR APPLICATION DATA: APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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APPLICANT: DILLON, PATRICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: NI, JIAN APPLICANT: YU, GUO-LIANG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LIBRARY: Since
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                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                   CLASSIFICATION:
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REGISTRATION NUMBER: 30
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135 amino acids
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58.3%;
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RESULT 10
US-08-423-752-10
: Sequence 10, Application US/08423752
: Patent No. 6022949
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                                                                                                                                                                                                                       ; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-492-459-10
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Best Local Similarity 50...
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Takashi
                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
                                                                                      1352 HKFHLDQAVEEEGSN 1366
                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: May 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/243,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington STATE: D.C. COUNTRY: U.S.A.
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FILING DATE: June 20, 1995
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46.78;
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Pred. No. 1.
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Maximum DB seq length: 2000000000
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1: pir1:*
2: pir2:*
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  July 6, 2001, 09:18:01 ; Search time 73.59 Seconds (without alignments) 16.562 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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94
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Copyright (c) 1993 - 2000 Compugen Ltd
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	42 40 42.6 1733 2 527939 tensin - chicken 43 40 42.6 1744 2 A54970 tensin, cardiac mu 44 40 42.6 1785 2 553976 probable membrane 45 40 42.6 1792 2 A57075 tensin - chicken (
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: 219241	RESULT 1  KGHUH1  KGHUH1  KININOGEN, HMW precursor [validated] - human  kininogen II; low molecular  N;Contains: bradykinin (kalildin I); HMW kininogen II; low molecular  C;Species: Homo sapiens (man)  C;Species: Homo sapiens (man)  C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A31905; A34030;  R;Ohkubo, II; Kurachi, K; Takkasawa, T; Shiokkawa, H; Sasaki, M.
, , , , , , , , , , , , , , , , , , ,	Biochemistry 23, 5691-5697, 1984 A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide A;Reference number: A90490; MUID:85122621 A;Accession: A01279 A;Accession: A01279 A;Molecule type: mRNA
or by chance to have a constraint being printed, are distribution.	A;Residues: 1-389 <ohk> A;Cross-references: GB:K02566; NID:g177889 A;Cross-references: GB:K02566; NID:g177889 R;Takagaki, Y.; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A;Reference number: A92544; MUID:85234582 A;Accession: A25276</ohk>
Description	A; Molecule type: mRNA A; Residues: 1-592, 'I', 594-644 <tak></tak>
kininogen, HMW pre	A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 R:Auerswald, E.A.: Roessler, D.: Mentele, R.: Assfalg-Machleidt, I.
probable acidCoA	
nucleophosmin NO38	A;Title: Cloning, expression and characterization of human kininogen domain 3. A:Reference number: S32422: MUID:93223854
mannopine biosynth	A;Accession: S32422
repressor protein	A: Molecule type: mRNA A: Rolecule type: mRNA Control of the type: mRNA A: Residues type: m
K-kininogen, LMW p	A; Note: differences are due to known cloning artifacts
kininogen, HMW I p	Eur. J. Biochem. 152, 307-314, 1985
hypothetical prote	A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270
aspartate carbamoy	A;ACCESSION: A91133 A;Molecule type: protein
aspartate carbamoy	A; Residues: 379-644 <lot></lot>
ORF MSV077 hypothe	R; Reliermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W.
site-specific DNA- skeletal muscle ab	Eur. J. Biochem. 154, 471-478, 1986 A:Title: Completion of the primary structure of human high-molecular-mass kininggen
probable transcrip	A; Reference number: A24871; MUID: 86108361
YOR1 protein - yea hypothetical prote	A; Accession: A24871 A; Molecule type: protein
hypothetical prote	A; Residues: 'z', 20-380 < KEL1>
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frezzled protein-1	human high molecular mass kin
dom-3 protein - Ca	A; Accession: A27899

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A;Molecule type: protein
A;Molecule type: protein
A;Residues: 450-452,'X',454,'X',456 <LIT>
R;Straczek, J.; Maachi, F.; le Nguyen, D.; Becchi, M.; Heulin, FEBS Lett. 373, 207-211, 1995
A;Title: Purification from human plasma of a tetrapeptide that A;Reference number: S68059; MUID:98033974
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A; Residues: 380-389 <SAS>
A; Residues: 380-389 <SAS>
R; Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turi
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A; Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs)
A; Reference number: S02482; MUID:89076517
A; Accession: S02482
A; Molecule type: protein
A; Residues: 1-19;189-192;310-314;381-389 <LEN1>
R; Matsumura, Y; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of interpretable in the company of the company 
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A; Residues: 379-389; K', 390-407; Q', 409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli,
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin moiety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
A; Accession: A27699
A; Molecule type: protein
A; Residues: 380-389 <MIN>
A; Residues: 380-389 <MIN>
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A:Residues: 264-359,'N',361-375 <LEN2>
R:Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A:Title: Human mast cell tryptase isoforms:
A:Reference number: S55239; MUID:95251593
A;Title: Structural organization of the human kininogen A;Reference number: A92545; MUID:85234583 A;Contents: annotation; gene organization
                                                                                                                                                                                                  A; Accession: S68059
A; Molecule type: protein
A; Residues: 431-434 <STR>
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FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C
A;Reference number: S14303; MUID:91192133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Experimental source: urine
A;Note: this peptide had Pro-383 modified
A;Accession: B61495
A;Molecule type: protein
A;Residues: 381-389 <KAT2>
A;Experimental source: urine
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Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin
A;Reference number: A4030; MUID:88106632
A;Accession: A34030
A;Molecule type: protein
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R;Maeda, H.; Matsumura, Y.; Kato, H.
R;Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin in A;Reference number: A31905; MUID:89034061
A;Accession: A31905
A;Molecule type: protein
                                                                                                                           R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, J. Biol. Chem. 260, 8610-8617, 1985
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A; Residues: 380-389 <KAT1>
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                                                                                                                                                                   Y.; Miyata, T.; Nakanishi,
                                                                                   gene and a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              M.H.; Nabet,
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A:Cross-references: GDB:125256; OMIM:228960
A:Map position: 3q27-3q27
A:Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C:Superfamily: kininogen; cystatin homology
C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
F:1-18/Domain: signal sequence #status experimental <MAT2>
F:19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>
F:19-379/Domain: cystatin homology <CY1>
F:19-379/Domain: cystatin homology <CY1>
F:142-253/Domain: cystatin homology <CY2>
F:264-375/Domain: cystatin homology <CY3>
F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F:380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <CH>
F:390-644/Domain: dystatin homology <CY3>
F:390-644/Domain: maccomplex in the status experimental <CH>
F:381-389/Product: low molecular weight growth promoting factor #status experimental F:38-341-434/Product: low molecular weight growth promoting factor #status experimental F:38-34,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond F:383/Modified site: carbohydrate (Asn) (covalent) #status experimental F:389-390/Cleavage site: Met-Lys (kallikrein) #status experimental F:389-390/Cleavage site: A-hydroxyproline (Pro) (partial) #status experimental F:331-33,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F:331-33,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F:3601,533,542,546,557,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status experimental F:361-364-3658,577,571,593,628/Binding site: carbohydrate (Ser) (covalent) #status experimental F:361-364-3658,571,571,593,628/Binding site: carbohydrate (Ser) (covale
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A;Reference number: A91455; WIID:90255622
A;Reference number: A91455; WIID:90255622
C;Comments: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the same
C;Comment: Kininogen is a Cysteine proteinase inhibitor, takes part in initiation of C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein L homolog - My
C; Species: Mycoplasma
C; Date: 17-Nov-1995 #s
C; Accession: H64231
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C; Superfamily:
                                                                                                                                                                                                                 A;Status: preliminary; nucleic acid A;Molecule type: DNA
                                                                                                                                                                                                                                                                                  A;Title: The minimal gene complement of Mycoplasma genitalium A;Reference number: A64200; MUID:96026346
A;Accession: H64231
                                                                                                                                                                                                                                                                                                                                                                                                , C.A.; Venter, J.C.
Science 270, 397-403, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: nvalle
R;Fraser, C.M.; Gocayne, J.D.;
Nguyen, D.; U
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                                  A; Genetic code:
                                                                                                          A;Cross-references: GB:U39709; GB:L43967; NID:g1045984; A;Experimental source: strain G-37
                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-414 <TIGR>
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F;577/Binding site: carbohydrate
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hypothetical protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0
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Pred. No. 1.5
); Mismatches
                                                                                                                                                                                                                                                   sequence not shown; translation not shown
MG096
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50.0%;

Score 47;

DB 2;

Length 414;

Qy

В

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nucleophosmin NO38 - African clawed frog
NyAlternate names: nucleolar protein NO38
C;Species: Xenopus laevis (African clawed frog)
C;Date: 31-Dec-1993 #sequence_revision 03-Nov-1995 #text_change 03-Nov-1995
C;Accession: S18971; A41730
R;Peculis, B.A.; Gall, J.G.
submitted to the EMBL Data Library, September 1990
A;Reference number: S18971
A;Accession: S18971
                                            Query Match
Best Local Similarity
Thes 7; Conserve
                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 5-296 < PE2>
                                                                                                                                                                                                                                                                                               A;Residues: 1-296 <PEC>
R;Peculis, B.A.; Gall, J.G.
J. Cell Biol. 116, 1-14, 1992
J. Cell Biol. 2003 Comparison of the nucleolar protein NO38 in amphibian oocytes.
A;Reference number: A41730; MUID:92112947
A;Accession: A41730
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C;Keywords: acid-thiol ligase
F;70-533/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision
C;Accession: T34850
                                                                                                                                                         C; Superfamily: nucleophosmin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMI
A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z21559
A; Accession: T34850
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                                                                                                                                                                             A; Gene: NO38
                                                                                                                                                                                                                      A; Note:
                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
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                                                                                                                                                                                              Genetics:
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58.3%;
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Pred. No.
                                                                              Score 43; DB Pred. No. 16;
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                                                                                                 RESULT
S01433
repressor protein C - phage phi-C31 C;Species: phage phi-C31 C;Date: 30-Sep-1989 #sequence_revision C;Accession: S01433; S38912 R;Sinclair, R.B.; Bibb, M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mannopine biosynthesis protein mas1'
C;Species: Agrobacterium rhizogenes
C;Date: 09-Mar-1996 #sequence_revision
C;Accession: I39727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data A; Reference number: Z20034 A; Accession: T25435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein T28H10.1 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #te: C;Accession: T25435
                                                                                                                                                                             В
                                                                                                                                                                                                                δÃ
                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: short-chain alcohol dehydrogenase homology F;200-377/Domain: short-chain alcohol dehydrogenase homol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-430 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: 139720; A; Accession: 139727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R; Hansen, G.; Larribe, M.; Vaubert, D.; Tempe, J.; Biermann, Proc. Natl. Acad. Sci. U.S.A. 88, 7763-7767, 1991
A;Title: Agrobacterium rhizogenes pr81816 T-DNA: Mapping and A;Reference number: 139720; MUID:91352070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        В
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A;Molecule type: DNA
A;Residues: 1-299 <WIL>
A;Cross-references: EMBL: Z75551; PIDN:CAA99933.1; GSPDB:GN00023; CESP:T28H10.1
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                                                                                                                                                                                                                                                                                                                                                                                                          A; Note: encoded within the T-DNA (transferred DNA) segment of the plasmid; this segme
                                                                                                                                                                                                                                                                                                                                                                                                                              A; Genome: plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: mas1'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:M60490; NID:g142245; PIDN:AAA22101.1; PID:g142253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Map position: 5
A;Introns: 57/2; 116/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Gene: CESP:T28H10.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: clone T28H10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                            disease
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Best Local :
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Best Local Similarity 40.0
Matches 6; Conservative
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Pred. No.
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Pred. No.
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                                                                                                                                                                                                                                                        Mismatches
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                                        30-Sep-1989 #text_change 04-Mar-2000
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24;
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R;Fung, W.P.; Schreiber, G.

J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the genes for majo A;Reference number: A92653; MUID:87250580
A;Reference number: A92653; MUID:87250580
A;Recession: C27115
A;Molecule type: DNA
A;Residues: 1-290 <FUN>
R;Residues: 1-290 <FUN>
R;Regeyama, R; Kitamura, N; Ohkubo, H.; Nakanishi, S.
R;Itle: Differing utilization of homologous transcript
A;Reference number: A25488; MUID:87137465
                                                                                                                                                                                                                                                                                                                                                                                                       K-kininogen, LMW precursor - rat (fragments) C;Species: Rattus norvegicus (Norway rat) C;Date: 31-Mar1989 #sequence_revision 31-Ma C;Accession: C27115; A25488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           K-kininogen, HMW precursor - rat (fragment)
(;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-Sep-1993
C;Accession: C25486
R;Kitagawa, H; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen generates and evolu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Gene: c
C;Superfamily: phage phi-C31 repressor
C;Keywords: DNA binding; transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              망
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A: Molecule type: DNA
A: Residues: 1-264 <KIT>
C: Comment: The nucleotide
C: Superfamily: kininogen;
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A; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Accession: C25486
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A; Residues: 1-683 <HAR>
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A; Residues: 1-683 <SIN>
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A;Title: The repressor gene (c) of the Streptomyces temperate phage phi-c31: nucleotide A;Reference number: S01433; MUID:89039715
A;Accession: S01433
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Thes 7; Conservative
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70.08;
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Pred. No. 17;
1; Mismatches
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Pred. No.
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on 31-Mar-1989 #text_change
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Chater, K.F.
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                                                           initiation sites
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                                                           rat
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A;Title: Differing expression patterns and evolution of A;Reference number: A92625; MUID:87137443

A;Reference number: A92625; MUID:87137443

A;Recession: A25486

A;Molecule type: mRNA

A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for residue C;Superfamily: kininogen; cystatin homology

C;Keywords: alternative splicing

F;1-18/Domain: signal sequence #status predicted <SIG>F;1-18/Domain: cystatin homology <CY1>
F;19-639/Product: kininogen, HWH I #status predicted <MAF:19-131/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
Query Match
Best Local Similarity
Thehes 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
C;Access
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J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the genes for A;Reference number: A92653; MUID:87250580
A;Accession: A27115
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C;Superfamily: kininogen;
F;19-65/Domain: cystatin }
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-48 <KAG>
A:Cross-references: GB:J02662; NID:g205071; PIDN:AAA41483.1; PID:g205072
C:Superfamily: kininogen; Cystatin homology
F:19-65/Domain: Cystatin homology (fragment) <CYS>
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A; Residues: 1-315 <FUN>
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Status: not compared with
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              рЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N;Contains: bradykinin
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Best Local :
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 GHKHKLDDLKQQRDDGYNYRHPMGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GHKFKLDD------DLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GHKFKLDD------DLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chem. 262, 2190-2198,
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homology (fragment)
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40.0%;
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                        ; Score 42.5; D
; Pred. No. 45;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 42.5; I
Pred. No. 20;
1; Mismatches
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Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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                                                                                           Length 639;
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Conservative

5;

Indels

9;

Gaps

1;

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A; Residues: 458-498 (HAN)

R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.;

J. Biol. Chem. 262, 2768-2779, 1987

A; Title: Bovine high molecular weight kininogen. The
A; Reference number: A92627; MUID:87137530

A; Accession: A29559

A; Molecule type: protein
A; Residues: 'Z',20-123,'I',125-127,'I',129-378 <SUE:
A; Residues: 'Z',20-123,'I',125-127,'I',129-378 <SUE:
Continuous (Continuous)

R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Note: article in Japanese C:Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is imported by kallikrein, is a potent vasodilator, it is a protein vasodilator, it is a protein vasodilator, it is present in the kininogen prior to the release of bradykinin. C:Superfamily: kininogen; cystatin homology C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; duple cysteine cysteine proteinase inhibitor; duple cysteine cysteine cysteine proteinase inhibitor; duple cysteine c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Title: The amino acid sequence of the light chain of human high-molecular-mass A;Reference number: A91153; MUID:86030770
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984
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                                                                                                                 F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;241-252/Domain: cystatin homology <CY2>
F;243-374/Domain: cystatin homology <CY2>
F;253-374/Domain: cystatin homology <CY2>
F;379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;389-621/Product: bradykinin (kallidin I) #status experimental <BDY>
F;389-621/Product: HMW kininogen I light chain #status experimental <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-621/Product: HMW prokininogen I #status predicted <MAT>
F;19-379/Product: HMW kininogen I heavy chain #status experi
F;417-488/Region: glycine/histidine/lysine-rich F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) \#status ex F;27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide
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A; Residues: 1-621 <KIT>
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R; Han, Y.N.; Komiya, M.; Iwi
J. Biochem. 77, 55-68, 1975
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J. Biochem. 67, 313-323, 1970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kininogen,
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Inin (kallidin); kininogen I; kininogen II; prokininogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.; Tanaka, T.; Nawa, H.; Nakanishi,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of bovine high-molecular-weight kininogen. Am
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                                             A; Map position:
C; Superfamily:
                                                                                                                                   A;Gene: VC0796
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R; D'Angelo, M.;
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F:87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental F;136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental F:197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F:378-379/Cleavage site: Met-Lys (kallikrein) #status experimental F;382/Modified site: 4-hydroxyproline (Pro) #status predicted F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental F;389.406,512/Binding site: carbohydrate (Ser) (covalent) #status experimental F;399.400,520,524,536,548,553,570/Binding site: carbohydrate (Thr) (covalent) #status experimental F;498-499/Cleavage site: Arg-Thr (kallikrein) #status experimental
  A; Experimental source:
                    A;Molecule type: DNA
A;Residues: 1-356 <HEI>
A;Cross-references: GB:AE004166;
                                                                                                                    A; Title: DNA Sequence of both chromosomes of the cholera pathogen A; Reference number: A82035; MUID:20406833 A; Accession: F82277
                                                                                                                                                                                                                                        R;Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin,
                                                                                                                                                                                                                                                                                          C;Species: Vibrio cholerae
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
C;Accession: F82277
                                                                                                                                                                                                                                                                                                                                                                 citrate (pro-3S)-lyase ligase VC0796 [imported] - Vibrio cholerae (strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: ATSP:F25L23.130
A;Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-335 < DAN>
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submitted to the Protein Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein F25L23.130 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change
                                                                                             A; Status: preliminary
                                                                                                                                                                                          1, R.R.; Mekalanos, J.J.; Venter, J.C.; Fraser,
Nature 406, 477-483, 2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 225012
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          142 KFSADDPIQHEG
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GB:AE003852; NID:g9655259; O1; strain N16961; biotype
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Pred. No.
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May 2000
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52;
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  PIDN: AAF93960.
El Tor
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H.; Dragoi, ]
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                         GSPDB:GN
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(pro-3S)-lyase ligase

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aspartate carbamoyltransferase (EC 2.1.3.2) - garden pea
(:Species: Pisum sativum (garden pea)
(:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 29-Sep-1999
(:Accession: T06484
R.Williamson, C.L.; Slocum, R.D.
Plant Physiol. 105, 377-384, 1994
A.Title: Molecular cloning and characterization of the pyrB1 and pyrB2 genes encoding as A; Reference number: Z15710; MUID:94302176
A; Reference number: Z15710; MUID:94302176
A; Accession: T06484
A.Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecular type: mRNA
A; Residues: 1-386 <WILD
A; Residues: 1-386 <WILD
A; Experimental source: cv. Wando, leaf
C; Gene-tics:
A; Cross references: EMBL:M96981; NID:9495658; PIDN:AAA62443.1; PID:9495659
A; Experimental source: cv. Wando, leaf
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                                                                                                                                                                                                                                                                                                                                              A;Gene: pyrB1
C;Superfamily: ornithine carbamoyltransferase; aspartate/ornithine carbamoyltransferase
C;Keywords: pyrimidine nucleotide biosynthesis; transferase
Search completed: July 6, 2001, 09:18:02 Job time: 648 sec
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity 54.9
Matches 6; Conservative
                                                                                                                      1 GHKFKLDDDLEHQ 13
| ||:||| :| |
75 GQKFQLDDVIEAQ 87
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33 HQLTVDDDVEH 43
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US-09-060-410-2; Sequence 2, A
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Best Local Similarity 40...
Thes 7; Conservative
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SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 42.68;
Best Local Similarity 37.58;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: NOVEL COMPOUNDS
FILE REFERENCE: GP-30010
CURRENT APPLICATION NUMBER: US/09/136,652A
CURRENT FILING DATE: 1998-08-19
EARLIER APPLICATION NUMBER: EP 974019473.3
EARLIER FILING DATE: 1997-08-19
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: MARTIN, XAVIER APPLICANT: BORON, WALTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: BRILL, ANTOINE APPLICANT: KHANDOUDI, NASSIRAH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                tent No. 6165461
      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: DBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1352 HKFHLDQAVEEEGSN 1366
                                                                                                                                                                                                                                                           APPLICANT: Chen, Zhu
APPLICANT: Berman, Kevin
TITLE OF INVENTION: TAO PROTEIN KINASES AND METHODS
TITLE OF INVENTION: THEREFOR
                                                                                                                                                                                                                                                                                                                                APPLICANT:
                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  410 GENVQMNGDTPHDGGH 425
                                                                                                                               COUNTRY: US
ZIP: 98104
                                                                                                                                                                                              STREET:
                                                                                                                                                                                CITY: Seattle
                                                                                                                                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHKFKLDDDLEHQGGH 16
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                                                                                                                                                             Washington
                                                                                                                                                                                                                                                                                                                                                                                                Application US/09060410
                                                                                                                                                                                            6300 Columbia Center,
                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                         Hutchinson, Michele
                                                                                                                                                                                                                                                                                                                                               Cobb, Melanie
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                                                                                                                                                                                                            SEED and BERRY LLP
14-APR-1998
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46.7%;
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Pred. No.
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Pred. No. 1
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                                                                                                                                                                                              701 Fifth Avenue
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1.3e 7; Indels
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TYPE: amino acid;
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-410-2
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US-08-67.9-635A-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SESTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION MUMBER: US/08/679,635A
FILING DATE: 10-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/08679635A Patent No. 5985643
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEPAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                        TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                       NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Tomasz, Alexander
APPLICANT: Delencastre, Herminia
TITLE OF INVENTION: AUXILIANY GENES AND PROTEINS OF
TITLE OF INVENTION: METHICILLIN RESISTANT BACTERIA AND ANTAGONISTS THEREOF
NUMBER OF SEQUENCES: 17
                                                                                                     MOLECULE TYPE:
                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                      HYPOTHETICAL:
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NAME: Maki, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 860
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STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                       TOPOLOGY:
                                                                                                                                     STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 07601
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nes 7; Conserv
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                                                                                                                                                                        LENGTH:
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58.3%;
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 Score
Pred.
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Pred. No. 1.6e+02;
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 38;
No.
 DB 2; · Length 463; le+02;
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; TYPE: amino acid
; STRANDEDNESS: sing
; TOPOLOGY: linear
; MOLECULE TYPE: pepti
US-08-423-752-10
                                                                                                                                                                                                                                                                                                                                                        RESULT 11
US-08-945-994-3
                                                                                                                                                                                                                                                                                                 Sequence 3, Application US/08945994 Patent No. 6043051 GENERAL INFORMATION:
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APPLICANT: Takashi OKADO et al.

TITLE OF INVENTION: A GENE CODING FOR A PROTEIN REGULATING TITLE OF INVENTION: AUREOBASIDIN SENSITIVITY

TITLE OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
              COMPUTER: IBM Compatible OPERATING SYSTEM: MS-DOS SOFTWARE: Wordperfect 5.1 CURRENT APPLICATION DATA:
                                           ZIP: 2000

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IBM Compatible

COMPUTER: MC-NOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE: May 16, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr
REGISTRATION NUMBER: 33,3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/243,403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
FILING DATE: April 18, 19
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MEDIUM TYPE: Diskette, 5.25 inch, 500 kb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
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REFERENCE/FOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                  APPLICANT: Takashi OKADO et al TITLE OF INVENTION: PROMOTER
                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                       STATE: D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                      CITY: Washington STATE: D.C.
                                                                                                                                                                                        STREET:
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                                                                                                                     ZIP: 20006
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805 Fifteenth Street, N.W., #700
                                                                                                                                                                                          E: Wenderoth, Lind & Ponack, L.L.P. 2033 K Street, N.W., #800
                                                                                                                                         U.S.A.
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linear
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US/08/945,994
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Pred. No. 1.2e+02;
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; MOLECULE TYPE: US-08-945-994-3
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Matches
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INFORMATION FOR SEQ ID NO:
                              INFORMATION FOR SEQ ID NO: 2.
SEQUENCE CHARACTERISTICS:
LENGTH: 1477 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1352 HKFHLDQAVEEEGSN 1366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: WAITEN M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                             REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION: TELEPHONE: 202-371-8850
                                                                                                                                                                                                                           CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                            SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1477
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                           STATE: D.C.
COUNTRY: U.S.A.
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STRANDEDNESS: sin
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TYPE: amino acid
STRANDEDNESS: sin
                                                                                                                                                             NAME: Warren M. Cheek, Jr. REGISTRATION NUMBER: 33,367
                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
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                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                 20005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takashi OKADO et al.

VENTION: GENE REGULATING AUREOBASIDIN SENSITIVITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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N: 435
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 single
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                               inch,
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1.2e+02;
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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STS_MOUSE
STV_METUS
TRC5_ECOLI
TRC5_CANMA
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P08979 bacteriopha
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DISULFIDE BONDS.
Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
"Disulfide bonds in bovine HMW kininogens.";

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	and kininogens."			chain of human	en A., Foertsch B.		kininogen.";	okawa H.,		kininogèn gene	., Takagaki Y.,			rekininogens. Primary		LMW).	ı; Hominidae;	Vertebrata;	PUNTETRAG	date) update)	644 AA.	•	MENTS							
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOW PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PIM: BRADYKININ IS RELEASED FROM KININGGEN
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SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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M11437; AAB59550.1;
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Fraser C.M., Gocayne J.D., White O., Adams M.D., Clayton R.A., Fleischmann R.D., Bult C.J., Kerlavage A.R., Sutton G., Kelley J. Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J. Nguyen D.T., Utterback T.R., Saudek D.M., Phillips C.A., Merrick Tomb J.-F., Dougherty B.A., Bott K.F., Hu P.-C., Lucier T.S., Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.; "The minimal gene complement of Mycoplasma genitalium."; Science 270:397-403(1995).
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CYSTATIN-LIKE 3.
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MISSING (IN ISOFORM LAW).
T -> I (IN REF. 1).
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N-LINKED
N-LINKED
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Pred. No.
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3132B4CBAF8FBB7E CRC64;
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Best Local S
Matches 7
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ACT_SITE
                                                                                                              PROSITE; Plasmid;
                                                                                                                                                                                                                                                             modified and this statement is not removed entities requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         differentiation.";
Proc. Natl. Acad. Sci. U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hansen G., Larribe M., Vaubert D., Tempe J., Biermann B.J., Montoya A.L., Chilton M.D., Brevet J.; "Agrobacterium rhizogenes pRi8196 T-DNA: mapping and DNA sequence functions involved in mannopine synthesis and hairy root
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Agrobacterium rhizogenes Plasmid pRi8196.
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01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                         EMBL; M60490; AAA22101.1;
                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch)
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                                                                                                                                                                                      HSSP; P14061;
                                                                                                                                                                  InterPro; IPR002198; -
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een the Swiss Institute of Bioinformatics and the Eb
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996 (Rel. 34, Last sequence update)
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SYNTHESIS REDUCTASE (EC 1.-.-).
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PS00061; ADH_SHORT;
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430 AA;
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Query Match

45.78;

Score 43;

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Length 430,

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RESULT
KNG_RAT
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Matches 7
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Matches 8; Conservative
                                        KNG_RAT
STANDARD;
P08934; P08933;
01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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P08979;
                                 KNG.
                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
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Rattus norvegicus (I
Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                         Transcription regulation; SEQUENCE 683 AA; 74077
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PIR; S01433; S01433
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Gene 147:29-40(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE=94374705; PubMed=8088546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteriophage phi-C31.
Viruses; dsDNA viruses,
Lambda phage group.
NCBI_TaxID=10719;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Sequence of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "The repressor gene (c) of the Streptomyces temperate phage phi c31: nucleotide sequence, analysis and functional cloning."; Mol. Gen. Genet. 213:269-277(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nucleotide
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                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
(Rat).
a; Chordata;
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b; Mismatches
 Craniata; Vertebrata;
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17;
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                                                                                                                                                                                                                                                                                                                                                     HAW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HMM-KININGEN INHIBITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING BACTOR ACTION); (5)
LAM-KININGEN IS IN CONTRAST TO HMM-KININGEN NOT INVOLVED IN BLOOD
                                                                                                                                                        between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Rageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
"Differing utilization of homologous transcription initiation si
of rat K and T kininogen genes under inflammation condition.";
J. Biol. Chem. 262:2345-2331(1987).
-i- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Furuto-Kato S., Matsumoto A., Kitamura N., Nakamura I., Furuto-Kato S., Matsumoto A., Kitamura N., Nakamura I., Primary structures of the mRNAs encoding the rat precursors for Primary structural relationship of kininogens bradykinin and T-kinin. Structural relationship of kininogens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         major acute phase
inhibitor.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (LMW ISOFORM)
MEDLINE=86008264; PubMed=2413018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=87137465; PubMed=3818598;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Fung
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Differing expression patterns and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-87137443; PubMed-3029068;
Kitagawa H., Kitamura N., Hayashida H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mammalia; Eutheria;
NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 1-41 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Structure and expression of the genes for protein (thiostatin) and kininogen in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=87250580; PubMed=2439509;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN-BUFFALO
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                                                                                                                                                                                                                                                                       CLOTTING.
SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
                                                                                                                                        European
                                                                                                                                                                                                   SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                  PTM: BRADYKININ IS MISCELLANEOUS: RAT
                                                                                                                                                                                                                                   HMW/LMW KININOGENS
L29428;
M11884;
M14369;
M14369;
                                                                                                                                                     SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              family.";
                                                                                                         non-profit institutions as long and this statement is not removed.
                                                                                              requires
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                                                                            equires a license agreement (S email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schreiber G.;
                                                                                                                        Bioinformatics Institute. There are no restrictions profit institutions as long as its content is in
AAA41486.1;
AAA41487.1;
AAA41484.1;
AAA41485.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262:9298-9308(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-Liver;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260:12054-12059(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            262:2190-2198(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     N.A
                                                                                                                                                                                                                             RELEASED FROM KININOGEN BY PLASMA KALLIKREIN. EXPRESS FOUR TYPES OF KININOGENS: THE CLASSICAL AND TWO ADDITIONAL LAW-LIKE KININOGENS: T-I AND
ALT_SEQ
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                                                                                           (See
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the rat.";
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                                                                                                                                                                                                                                                                                                              (SHOWN
                                                                                         http://www.isb-sib.ch/announce/
                                                                                                        Usage
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RESULT 6
CRBB_CHICK
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Best Local S
Matches 10
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01-OCT-1996 (Rel. 3
01-OCT-2000 (Rel. 4
BETA CRYSTALLIN A2
                                                                                                                                                                                                                                                   CRBB_CHICK
P55164;
01-OCT-1996
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CONFLICT
SEQUENCE
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                            SEQUENCE FROM N.A.
STRAIN-WHITE LEGHORN; TISSUE-Lens;
MEDLINE-96296047; PubMed-8674507;
Duncan M.K., Banerjee-Basu S., McDermott J.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
CARBOHYD
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CARBOHYD
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DOMAIN
"Sequence and expression B3-crystallins.";
                                                                                                                                         Archosauria;
                                                                                                                                                          Eukaryota;
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                                                                                                          NCBI_TaxID=9031;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
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34, Last sequence up
40, Last annotation
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61
70933
                                                                                                                                         Neognathae;
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Neognathae; Galliformes; Phasianidae;
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CYSTATIN-LIKE 2
CYSTATIN-LIKE 3
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N-LINKED (GLCNAC. . . .) (POTENTIAL).
VSPSYIARVQEERDPGNEQGFIHGHGWLHAKQ -> RLLNS
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D3172DF94FF56AF5
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(GLCNAC...
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                             Piatigorsky
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                                                                                                                                         Euteleostomi;
idae; Phasianinae;
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Best Local S
Matches 7
                                                                                       MEDLINE=87137530; PubM
Sueyoshi T., Miyata T.
Miyata T., Iwanaga S.;
                                                                                                                                                                         Nature
[2]
                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P01044;
21-JUL-1986
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DOMAIN
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DOMAIN
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                                                     "Bovine high molecular weight kininogen. positions of carbohydrate chains and dis
                                                                                                                                                     SEQUENCE OF 19-378
                                                                                                                                                                                          "Ritamura N., Takagaki Y., Furuto S., Tana
"A single gene for bovine high molecular
weight kininogens.";
Nature 305:545-549(1983).
                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
MEDLINE-84014106; PubMed-6571699;
                                                                                                                                                                                                                                                                                                                                                                                                                             BRADYKININ]
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01-JUN-1994
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                                  chain portion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   KININOGEN, HMW I
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                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                     Bovidae; Bovinae;
                                                                                                                                                                                                                                                                                                                                                                                                            Bos taurus (Bovine).
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                Biol.
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by non-profit institutions as long
ified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE BETA/GAMMA-CRYSTALLIN FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRUCTURE OF BETA-CRYSTALLIN OLIGOMERS SEEMS TO BE STABILIZED THROUGH INTERACTIONS BETWEEN THE N-TERMINAL ARMS (BY SIMILARITY). DOMAIN: HAS A TWO-DOMAIN BETA-STRUCTURE, FOLDED INTO FOUR VERY SIMILAR GREEK KEY MOTIFS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eye Res. 62:111-119(1996).
FUNCTION: CRYSTALLINS ARE THE DOMINANT S
OF THE VERTEBRATE EYE LENS.
SUBUNIT: HOMO/HETERODIMER, OR COMPLEXES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _BOVIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PS00225;
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147
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(Rel. 01, Last seq
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CRYSTALLINS ARE THE DOMINANT STRUCTURAL
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                262:2768-2779(1987)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                               . 01, Last sequence update)
. 29, Last annotation update)
PRECURSOR (THIOL PROTEINASE INHIBITOR) [CONTAINS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Duplication
                                                                                                                                  PubMed=3546295;
                                                                                                                                                                                                                                                                                                                                                       Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CRYSTALLIN_BETAGAMMA;
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99
104
146
                                                                                                              T., Hashimoto
                                                                                                                                                                                                                                                                                                                                                                    Chordata; Craniata;
Cetartiodactyla; Rur
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.7%;
77.8%;
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Pred. No.
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                                                                                                                                                                                                                               Tanaka T.,
ular weight
                                                       disulfide bridges
                                                                                                                                                                                                                                                                                                                                                                      Ruminantia;
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                                                                                                              Kato H., Hayashida H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                      Vertebrata;
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                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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CARBOHYD
DISULFID
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CARBOHYD
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CHAIN
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DOMAIN
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                                                                        CARBOHYD
                                                                                                                                                                                                                                                               PROSITE; PS00287; CYSTATIN; 2. Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
DISULFIL
                                           CARBOHYD
                                                       CARBOHYD
                                                                                                                                                DOMAIN
                                                                                                                                                                                                          CHAIN
                                                                                                                                                                                                                       SIGNAL
                                                                                                                                                                                                                                                                                            Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN.
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PIR; A29559; A29559.
                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01491; CAA24735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Studies on the primary structure of bovine h kininogen. Amino acid sequence of a fragment peptide') released by plasma kallikrein."; J. Biochem. 77:55-68(1975).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 67:313-323(1970).
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"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
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MEDLINE=70180420; PubMed=4986212;
                                                                                                                                                                                                                                                  Thiol protease inhibitor; Bradykinin;
                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000010;
                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 458-498
                                                                                                                                                                                                                                   nflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=75170265; PubMed=1169237;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND FLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PERTIDE BRADXKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FUNCTION: (1) KININGENS ARE INHIBITORS OF THIOL PROTEASES; (2 HMW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UI
TO RESIDUE 400.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Y.N., Komiya M., Iwanaga S., Suzuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       non-profit institutions as long
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389
19
136
258
19
87
136
168
197
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27
82
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18
621
378
388
621
135
257
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378
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168
197
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                                                                                                                                                                                                                                    Signal
             OR 169.
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
INTERCHAIN.
                                                                                                                CYSTATIN-LIKE CYSTATIN-LIKE CYSTATIN-LIKE
                                                                                    PYRROLIDONE CARBOXYLIC N-LINKED (GLCNAC. . .)
                                                                                                                                                           BRADYKININ.
LIGHT CHAIN
                                                                        PARTIAL.
                                                                                                                                                                                         HEAVY CHAIN.
                                                                                                                                                                                                          KININOGEN,
                                                                                                                                                                                                                                                    Blood
                                                                                                                                                                                                          MMH
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                                                                                                                                                                                                                                                  coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ALTERNATE MRNA
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L outstation -
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RESULT 8
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C: IF FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

C: IF FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

C: HELPING TO POSITION OPTIMALLY PREKALLIKEEIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBOLY-AND PLASMIN-CIC INDUCED AGGREGATION OF THROMBOLY-ES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS; (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRICRESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PEREMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTACLANINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDICENSURY (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, (5) LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD CLOTTING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
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01-0CT-2000 (Rel
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                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
                                                                                              the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takano M., Kondoh J., Yayama K., Okamoto H.; "Molecular cloning of cDNAs for mouse low- and high- molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (IS
STRAIN=C57BL/6 x CBA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KININOGEN PRECURSOR
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nes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 GHKFKLDDDLEHQGGH 16
                                                                                                                                                    SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
; D84435;
; D84415;
                                                                                                                          SWISS-PROT entry is copyright. It is produced through
                                                                                                           the Swiss Institute of Bioinformatics
                                                                  non-profit institutions as long and this statement is not removed
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141
205
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228
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621 AA;
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BAA19743.1;
BAA19742.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (ISOFORMS HMW AND LMW).
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Rodentia;
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Yayama K., Okamoto H.;
                                                      rest is not removed. Usage has the agreement
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Pred. No.
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Sciurognathi;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                661
                                                     (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB
22;
                                                                                            There are no restrictions
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Best Local
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Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 1.
Glycoprotein; Plasma; Repeat; T
Bradykinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                   VE4_HPV65
Q07873;
Q1-OCT-1994
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SEQUENCE
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the European Bioinformatics Institute. Tuse by non-profit institutions as long modified and this statement is not remove.
                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                Egawa K., Delius H., Matsukura T., Kawashima M., de Vill
"Two novel types of human papillomavirus, HPV 63 and HPV
comparisons of their clinical and histological features
                                                                                                                                                                                       MEDLINE-93276568; PubMed-8389082; Delius H., Matsukura T.,
                                                                                                                                                                                                                                                                                        Human papillomavirus type 65 Viruses; dsDNA viruses, no R
                                                                                                                                                                                                                                                                                                                                               01-OCT-1994
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
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CHAIN
                                                                                                            sequences to other HPV types.";
Virology 194:789-799(1993).
                                                                                                                                                                                                                                                                      NCBI_TaxID=28312;
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661 .
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                   Created)
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BY SIMILARITY.
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Pred. No. 2
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774460258D58796E CRC64;
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KININOGEN HEAVY CHAIN
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 not removed.
                                                                                                                                                                                                                                                                                        stage;
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                                                                                                                                                                                                                                                                                                                                                                                                                              213
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                                                                                                                                                                                                                                                                                                                                               update)
                   There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28;
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Usage
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                                                                                                                                                                                         de Villiers E.M.;
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for
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RESULT 1
PYB1_PEA
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Best Local Similarity
Matches 8; Conserv
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Best Local
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SEQUENCE
                                                                                                                                                                                                                                                                                                 PYB1_PEA STANDARD; PRT; 386 AA. 043086; 043086; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) ASPARTATE CARBAMOYLTRANSFERASE 1 PRECURSOR (EC
                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                     Pfam; PF00185; OTCace; 1.
PRINTS; PR00100; AOTCASE.
PRINTS; PR00101; ATCASE.
PROSITE; PS00097; CARBAMOYLTRANSFERASE;
                                                                                                                                                                               or send an
                                                                                                                                                                                                  modified
                                                                                                                                                             EMBL; M96981; AAA62443.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                 Pisum sativum (Garden pea).
Eukaryota: Viridiplantae; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE 21:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                           TRANSIT
                                                                                           Pyrimidine biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                               Magnoliophyta; eud:
Fabales; Fabaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSCARBAMYLASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; x70829; CAA50175.1;
                                                                                   Multigene
                                                                                                                                           [nterPro;
                                                                                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3888;
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                                                                                                                                                                                                                                               PATHMAY: SECOND STEP IN PYRTMIDINE BIOSYNTHESIS.
SUBUNIT: HOMOTRIMER (POTENTIAL).
SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
                                                                                                                                                                                                                                                                                   ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
ENZYME REGULATION: ALLOSTERICALLY REGULATED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GHKFKLDDDLEHQG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                             non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
                                                                                                                                          IPR002029; -.
IPR002082; -.
                                                                                   family.
                                                        386
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           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                            TISSUE=Leaf;
                                                                  386
                  43.6%;
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                                                                                            Transferase;
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         Score 41; DB
Pred. No. 18;
2; Mismatches
          ?;
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                                                        ASPARTATE CARBAMOYLTRANSFERASE A9440F45474E29F4 CRC64;
                                                                           CHLOROPLAST (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41;
Pred. No.
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18;
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Rosidae; eurosids I;
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01-JUN-1994 ()
01-JUN-1994 ()
01-OCT-2000 ()
MODIFICATION ()
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SEQUENCE
                                                      _LACLA
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PYB3_PEA
Q43064;
15-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Characterization of a cDNA encoding a third aspartate transcarbamoylase (pyrB3) from pea.";
(In) Plant Gene Register PGR96-063.
-!- CATALYTIC ACTIVITY: CARBAMOYL-PHOSPHATE + ASPARTATE ORTHOPHOSPHATE + N-CARBAMOYLASPARTATE.
                                                                                   MTL1_LACLA P35516;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00101; ATCASE PROSITE; PS00097; CARBAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002082; -.
Pfam; PF00185; OTCace;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pisum sativum (Garden pea)
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
ASPARTATE CARBAMOYLTRANSFERASE 3 PRECURSOR (EC 2.1.3.2) (ASPARTATE
TRANSCARBAMYLASE 3) (ATCASE 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pyrimidine biosynthesis; Transferase; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pyrimidine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Magnoliophyta; eudicotyledons; core eudic
Fabales; Fabaceae; Papilionoideae; Pisum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ATCASES/OTCASES FAMILY.
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                                                                                                                                                                                                                                                                                           8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR00100; AOTCASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                                                                                                                                                                  391
(Rel. 29, Created)
(Rel. 29, Last sequence update)
(Rel. 40, Last annotation update)
N METHYLASE LLAI (EC 2.1.1.72) (ADENINE-SPECIFIC
                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                         STANDARD;
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                                                                                                                                                                                                                                                                                           Score 41; DB Pred. No. 19; 2; Mismatches
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There are no restrictions
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YOR1_YEAST
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Best Local :
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                                                                                                                                                              OLIGOMYCIN RESISTANCE YOR1 OR YGR281W.
                                                                                                                                                                         01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
15-JUL-1998 (Rel. 36, Last annotation
OLIGOMYCIN RESISTANCE ATP-DEPENDENT PR
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                                                                                                                                   Saccharomyces cerevisiae (Baker's Eukaryota; Fungi; Ascomycota; Sacc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PIR; A47029; A47029.

REBASS; 3437; M.LlaI.

InterPro; IPR002052; -

InterPro; IPR0020294; -

Pfam; PF02086; MethyltransfDl2;
  cerevisiae
                                       Katzmann D.J., Hallstrom T.C., Voet M.,
Volckaert G., Moye-Rowley W.S.;
                                                                                                                        Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                Transferase; Methyltransferase; Restriction system; Repeat; SEQUENCE 622 AA; 72512 MW; 69A817F46BE9C772 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- CATALYTIC ACTIVITY: S-ADENOSYL-L-METHIONINE + DNA ADENINE = S-ADENOSYL-L-HOMCOYSTELNE + DNA 6-METHYLAMINOPURINE.
-!- SIMILARITY: CONTAINS TWO COPIES OF A SEGMENT OF FOUR AMINO ACIDS WHICH IS CHARACTERISTIC OF ADENINE-SPECIFIC METHYLASES.
(YOR1) is required for oligomycin resistance cerevisiae.";
                                                                SEQUENCE FROM N.A. MEDLINE=96069397; PubMed=8524254;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00092; N6_MTASE; 1.
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NCBI_TaxID=1360;
                       Expression of an ATP-binding cassette transporter-encoding gene
                                                                                                                                                                                                                                             YOR1_YEAST
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FÜNCTION: METHYLATION OF SPECIFIC BOTH RESTRICTION AND MOLFICATION NONPALINDROMIC SEQUENCE.
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Saccharomycotina; Saccharomycetes;
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32;
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STRAIN-5288C / FY1679;
MEDLINE-97245295; PubMed=9090054;
Volckaert G. Voet M., Robben J.;
Volckaert G. Voet M., Robben J.;
"Sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the sequence analysis of a near-subtelomeric 35.4 kb DNA segment on the sequence of the se
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HSSP; P13569; 1NBD.
SGD; S0003513; YOR1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
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-!- SIMILARITY: BELONGS TO THE ATP-BINDING TRANSPORT (ABC TRANSPORTERS). MDR SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Yeast 13:251-259(1997).
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000257;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                         _HUMAN
TISSUE-Fetal brain;
MEDLINE-97459707; PubMed-9315667;
Satijn D.P.E., Olson D.J., van der Vlag J., Hamer K.M., Lambrechts C. Satijn D.P.E., Ouson D.J., Sewalt R.G.A.B., van Driel R., Otte A.P.;
                                                                                                                                                                                                                                                                  01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last seq
01-0CT-2000 (Rel. 40, Last seq
CHROMOBOX PROTEIN HOMOLOG 4 (PO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       member of the mouse polycomb transcriptional repressor complex.";
J. Mol. Biol. 273:993-1003(1997).
-I- FUNCTION: INCOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY
                                                                                                                                                                   Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae;
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InterPro; IPR000953;
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Satijn D.P.E., Otte A.P., Berns A., van Lohuizen M.;
"MPC2, a new murine homolog of the Drosophila polycomb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHROMOBOX PROTEIN HOMOLOG 4 (POLYCOMB 2 HOMOLOG) (PC2) (MPC2). CBX4 OR MPC2.
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MEDLINE=98035734; PubMed=9367786;
                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                NCBI_TaxID=9606;
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Mol. Cell. Biol. 17:4105-4113(1997).
-!- FUNCTION: INVOLVED IN MAINTAINING THE TRANSCRIPTIONALLY REPRESSIVE
STATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED
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Pfam; PF00385; chromo;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=97342649; PubMed=9199346; Satijn D.P.E., Gunster M.J., van der Vlag J., Hamer K.M., Schul Alkema M.J., Saurin A.J., Freemont P.S., van Driel R., Otte A.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Interference with the expression of a novel human polycomb protein, hPc2, results in cellular transformation and apoptosis."; Mol. Cell. Biol. 17:6076-6086(1997).
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-!- SIMILARITY: CONTAINS 1 'CHROMO'
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Hilton H., Gaut B.S.;
Hilton in maize an "Speciation and domestication in maize an evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998).
EMBL; AF064213; AAC31456.1; -.
HSSP; P50477; ICAU.
Mendel; 31892; Zeama; 1188; 31892.
InterPro; IPR000901; -.
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NCBI_TaxID=4578;
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Pfam; PF00546; SeedStore_7s; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
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SEQUENCE 236 AA; 27019 MW; 1F3D9BD
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Q9SBF1
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Best Local Similarity
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                                                Matches
                                                           Query Match
Best Local
                                                                                                                                                                                             SEQUENCE FROM N.A.
Hilton H., Gaut B.S.;
"Speciation and domestication in maize and its wild relatives:
"Speciation and domestication in maize and its wild relatives:
evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998).
Genetics 0:0-0(1998).
GENBL; AF064218; AAC31461.1; -
                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                             Zea mays subsp. mays (maize).
Eukaryota; Viridiplantae; Embryoph;
Magnoliophyta; Liliopsida; Poales;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-007-2000 (TrEMBLrel. 15, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Interpro; IPR001113; -. Pfam; PF00546; Seedstore_7s; 1. PROSITE; PS00867; CPSASE_2; UNKNOWN_1. NON_TER 239 239 SEQUENCE 239 AA; 27384 MW; 628924A
                                                                                                                                  Pfam; PF00546; Seedstore_7s; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                 InterPro; IPR000901; -.
InterPro; IPR0011113; -.
Pfam; PF00546; Seedstor
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Eukaryota; Viridiplantae; Emb
Magnoliophyta; Liliopsida; Po
Andropogoneae; Zea.
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01-NOV-1998 (TrEMBLrel. 08, Created)
01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                          NON_TER
                                                                                                                                                                                                                                                                                                                                              GLOBULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                              Q9SBF1;
                                                                                                                                                                                                                                                                                                                                                                                                           Q9SBF1
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Mendel; 31895; Zeama;1188;31895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF064216;
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                                                                                                                                                                                                                                                                                   NCBI_TaxID=4578
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DDNLHHHGGH
                      DDDLEHQGGH 16
                                                                                                                                                                                     P50477; 1CAU
                                             7; Conserv
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                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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70.0%;
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70.0%;
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; Poales; Poaceae; PACC clade; Panicoideae
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; Poales; Poaceae; PACC clade; Panicoideae;
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                                                          Score 45;
Pred. No.
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Pred. No.
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                                               Mismatches
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17;
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                 RXMEDLINE-20196006; PubMed=10731132;

RX MEDLINE-20196006; P.G., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Burdon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeifer B.D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier R., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Fletschmann W.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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Q9VDL1;
01-MAY-2000
01-MAY-2000
01-MAY-2000
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01-OCT-2000
01-OCT-2000
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopteryota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AK000062; BAA90919.1; -
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01-OCT-2000 (TrEMBLrel. 15, Last se
01-OCT-2000 (TrEMBLrel. 15, Last a
CDNA FLJ20055 FIS, CLONE COL00943.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BERKELEY;
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Mammalia; Eutheria;
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Tanaka T., Nakamura Y., Isogai T., Sugar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=COLON;
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nes 8; Conserv
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Primates;
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50.0%;
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Last sequence update)
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Last annotation update)
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Sugano S.;
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A Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
A Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
Bibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).
BEMBL, AE003731; AAF55780.1;
BEBL; AE03731; AAF55780.1.
SEQUENCE 279 AA, 30634 MW; 1AE724980AF18201 CRC64;
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01-MAY-1999
01-MAY-1999
01-MAY-2000
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01-MAY-1999 (TrEMBLrel. 10, Last sequence
01-MAY-2000 (TrEMBLrel. 13, Last annotatio
PUTATIVE LONG-CHAIN-FATTY-ACID-COA LIGASE.
                                                                                                                                                                                                                       the 8
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Oliver K., Ha
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Streptomyces coelicolor.
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NCBI_TaxID=1902;
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                                                   PROSITE;
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Kinashi H., Hopwood D.A.;
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                                                                                                                               set of ordered cosmids and a detailed genetic and physical map 8 Mb Streptomyces coelicolor A3(2) chromosome.";
1. Microbiol. 21:77-96(1996).
BL; ALO35478; CAB36604.1;
SP; P08659; ILCI.
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     AA;
                                                     AMP-binding; 1.
55; AMP_BINDING;
  59034 MW;
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57.1%;
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Last annotation update)
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Pred. No.
  CEB7374431F28CE5 CRC64;
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Query Matcl

46.8%;

Score 44;

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Length 541;

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RESULT
Q9VEA9
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Beston K.Y., Benos P.V., Berman B.P., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E.; Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Dodson K., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K.J., Evangelista C.C., Ferrac C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J. H., Gu Z., Guan P., Harris M.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., Glasser K.,
RA Hostin D., Houston K.A., Howland T.J., Wei M., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shieb B.C., Siden-Kianos I., Simpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y. Wassarman D.A., Weiner E., Wang A.H., Wang X.,
RA Wang Z.-Y. Wassarman D.A., Weinstock G. M., Weissenbach J.,
RA Ylriskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Ra Keinert M., Shong F. N., Zhong W., Zhong G., Zhoo Q., Z
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Q9VEA9;
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01-MAR-2001 (TrE
CG7156 PROTEIN.
CG7156.
                                                                                                                        "The genome sequence of Drosophila Science 287:2185-2195(2000).

EMBL; AE003721; AAF55518.1; -.

FlyBase; FBgn0038588; CG7156.

InterPro; IPR000719; -.
                                         SMART; SM00312; PX;
                                                                 PROSITE;
                                                                                   Pfam; PF00069;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                    InterPro; IPR000719; -.
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81 AA; 77072 MW;
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                                                             PROTEIN_KINASE_DOM; 1.
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01-MAR-2001 (
EMB|CAB67623.
                                                                                            SEQUENCE
                                                                                                          Peculis B.A., Gall J.G.;
"Localization of the nucleolar protein J. Cell Biol. 116:1-14(1992).
EMBL; X56039; CAA39511.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 physically assigned P1 and TAC clones."; DNA Res. 5:379-391(1998).
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STRAIN=COLUMBIA;
MEDLINE=99156233; PubMed=10048488;
Asamizu E., Sato S., Kaneko T., Nal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-MAR-2001
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                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
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                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                               NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                                                    Xenopus laevis (African clawed frog)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     144
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(TrEMBLrel. 16, Last annotation update)
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                                                                                            32886 MW;
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    45.7%;
58.3%;
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50.0%;
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    Score
Pred.
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Pred. No.
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                                                                                                                                                        amphibian oocytes.";
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Best Local
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                                              Bacteriophage phi-C31.
Viruses; dsDNA viruses, lambda phage group.
NCBI_TaxID=10719;
[1]
                                                                                                                         Q9T215
Q9T215;
Q9T215;
01-MAY-2000
01-MAY-2000
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Q22856;
01-NOV-1996
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Riiken L., Roopra A., Saunders D., Shownkeen I
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M. Weinstock L., Wilkinson-Sproat J., Wohldman P.,
"2.2 M. Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
Submitted (JUN-1998) to the EMBL/GenBank/DDBJ databases.
             Smith M.C.
                       SEQUENCE FROM N.A.
STRAIN-NORWICH STOCK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
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01-OCT-2000
                                                                                                                 REPRESSOR.
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                                                                                                                                                                                                                                                                                                                                           InterPro; IPR002582;
Pfam; PF01648; ACPS;
                                                                                                                                                                                                                                                                                                                                                               Nature 368:32-38(1994).
EMBL; Z75551; CAA99933.1;
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les 6; Conserv
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Caenorhabditis.
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                                                                                                                                                                                                                                                                                   Score 43;
Pred. No.
                                                                              stage;
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annotation update)
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                                                                              Tailed phages; Siphoviridae;
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Q9L800
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Best Local S
Matches 8
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Matches 7
        009016
009016;
01-JUL-1997
01-JUL-1997
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01-0CT-2000
01-MAR-2001
                                                                                                                                          2663
                                                                                                                                                                                                                                                                                     PRINTS; PR00313; CABNDNGRPT.
PROSITE; PS00310; EF_HAND; UNKNOWN_1.
PROSITE; PS00330; HEMOLISIN_CALCIUM; 4.
SEQUENCE 2747 AA; 280202 MW; 208FE380E44A5F37
                                                                                                                                                                                                                                                                                                                                                                                                                        Braun M., Frey J., Kuhnert P.;
"280 kDa RTX protein of Aeromonas.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF218037; AAF27914.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9L800;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Smith M.C.M., Burns N., Wilson R.N., Gregory M.A.;
"The complete genome sequence of the Streptomyces temperate phage C31:
evolutionary relationships to other viruses.";
Nucleic Acids Res. 27:2145-2155(1999).
EMBL; AJ006589; CAA07123.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-ATCC 33658;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00353; hemolysinCabind;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=645;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria;
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MEDLINE=99238410; PubMed=10219087;
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MEDLINE=99162580; Pub
                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR001343; -.
InterPro; IPR002035; -.
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SEQUENCE FROM
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                                                                                                                                                                         1 GHKFKLDDDLEHQGGH 16
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rix R.W., Smith M.C.M., Burns N., Ford M.E.,
the world's a phage.";
. Natl. Acad. Sci. U.S.A. 96:2192-2197(1999)
                                                                                                                                         GDKLDLSDLLDHDGSH 2678
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7; Conservative
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Proteobacteria;
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        (TrEMBLrel. 04, (TrEMBLrel. 04,
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70.08;
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16,
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Pred. No. 4.26
1; Mismatches
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                                                          126
                                                                                                                                                                                                   DB 2; Len
. 4.2e+02;
. 7;
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1e+02;
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                                                                                                                                                                                                        0;
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                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                      0;
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Q9VXP2
        Query Match
Best Local Similarity
watches 10; Conserv
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RA Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Ge Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N., Kalpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
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NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-MAR-2001 (TrEMBLrel. 16,
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musce
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RHP OR CG8497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RHP PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q9VXP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9VXP2
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K-KININOGEN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AF003623; AAC09070.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jacob H.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harris E.L., Grigor M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=97468288;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           KNGK.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GHKFKLDD------DLEHQGGH 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GHQLKLDDLKQQREDGYDHRHPVGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ogen genes allow mapping Genome 8:791-792(1997).
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126 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PubMed=9321484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        14092 MW;
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Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 42.5;
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         exon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9CCDF8751DA49C88 CRC64;
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RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Meunt S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Noy M., Murphy B., Murphy L., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Sylrakas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhong G., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RT Sclence 287:2185-2195(2000).
REA Wall, AE003500; AAF48516.1; -.
REA PLUBEG. EPD.003507; AAF48516.1; -.
                                                                                                                 Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
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                                                                                                                                                                                                                                                             FlyBase; FBgn0026374; Rhp. InterPro; IPR000861; -. InterPro; IPR001478; -. Pfam; PF00595; PDZ; 1. Pfam; PF02195; HRI; 1. SMART; SM00228; PDZ; 1. SEQUENCE 718 AA; 80826 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XYY9;
01-NOV-1999
01-NOV-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edwards K.A., Kaneshiro K., Yamamoto D.;
"Mutations in the Drosophila Rhophilin gene at 13E.";
Submitted (FEB-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AF132025; AAD31273.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Eterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequ
01-MAR-2001 (TrEMBLrel. 16, Last anno
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InterPro; IPR001478; -.
Pfam; PF00595; PDZ; 1.
SMART; SM00228; PDZ; 1.
SMART; SM00228; PDZ; 1.
85EQUENCE 648 AA; 72858 MW; 85EE4EBC6947D45D CRC64;
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559 DDDEEHDGGY 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7227;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity nes 7; Conserv
                                  7 DDDLEHQGGH 16
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                                                                                                                                                                                                                                                                   80826 MW; AF9DD0C57132AA31 CRC64;
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70.0%;
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70.08;
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Last annotation update)
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                                                                                                                                              Score 42; DB 5;
Pred. No. 1.6e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 42; DB 5;
Pred. No. 1.4e+02;
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                                                                                                                     Mismatches
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                                                                                                                                                                       Length 718,
                                                                                                                 2; Indels
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Search completed: July 6,

2001,

09:25:55

Job time: 991 sec

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ACCOMPANDA 
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CH38_DF
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                                                                                                                                                                                                                                                                             Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Manatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards J., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA George R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barndon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Harli J.F., Agbayani A., An H.-J., Andrews.-Pfannkoch C., Baldwin D.,
RA Abril J.F., Agbayani A., An H.-J., Andrews.-Pfannkoch C., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Benock J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Bays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dorlor K.J., Evangelista C.C., Ferraz C., Ferriar S., Fleischmann W.,
RA Fosler C., Gabrat W. A., Ferraz C., Ferriar S., Fleischmann W.,
RA Fosler C., Gabrat W.
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Best Local :
         Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischman Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D., Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S. M., Mov M. Mirshky D.
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01-APR-1988 (Rel.
01-OCT-2000 (Rel.
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CP38 OR S38 OR CG1121.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-87246506; PubMed-3036489;
Spradling A.C., de Cicco D.V., Wakimoto B.T., Levine J.F.,
Kalfayan L.J., Cooley L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHORION PROTEIN S38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CH38_DROME
P07183; Q9W3E5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Amplification of the X-linked Drosophila chorion gene cluster requires a region upstream from the s38 chorion gene."; EMBO J. 6:1045-1053(1987).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7227
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   S.M.,
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ANTIFUNGAL PROTEIN.
2 x 7 AA REPEATS OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
Murphy L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Best Local S
Matches 7
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A Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
A Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
A Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
A Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
A Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
A Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
A Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.
A Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287.2185-2195(2000).
                                                                                                                                                               Mau B., Shao Y.; "The complete genome sequence of Science 277:1453-1474(1997).
                                                                                                                                                                                                                MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T.
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., M
Gregor J., Davis N.W., Kirkpatrick.H.A., Goeden M.A.,
                                                             Chung E., Allen E., Araujo R., Aparicio A., Davis K., Duncan M. Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O., Lew H., Namath A., Oefner P., Roberts D., Schramm S., Davis R.W.; Submitted (JAN-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                        Escherichia coli.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1997
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P77485;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID-562;
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                                                                                                                                                                                                                                                                                                                                                                                                             YBCZ.
                                                                                                                                                                                                                                                                                                                                                                                                                           PROBABLE
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EMBL; AE003444; AAF46383.
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                            FUNCTION: PROBABLE MEMBER OF A TWO-COMPONENT REGULATORY SYSTEM YBCZ/YLCA. MAY ACTIVATE YLCA BY PHOSPHORYLATION.
               SUBCELLULAR LOCATION:
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997 (Rel. 35, Last sequence update)
997 (Rel. 35, Last annotation update)
SENSOR PROTEIN YBCZ (EC 2.7.3.~).
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               INTEGRAL MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                        gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                  Escherichia coli K-12.";
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(See http://www.isb-sib.ch/announce/
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2.9;
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Smith H.O.,
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Pterygota; Ne
Ephydroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P25123; Q26302;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
GAMMA-AMINOBUTYRIC-ACID RECEPTOR BETA SUBUNIT PRECURSOR (GABA(A)
RECEPTOR) (CYCLODIENE RESISTANCE PROTEIN).
                                                                                         This SWISS FROM the Swiss Institute of Bioinformathe European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                   "Molecular cloning and transformation of cyclodiene Drosophila: an invertebrate gamma-aminobutyric acid receptor locus.";
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DOMAIN
                   EMBL; M69057; AAA28556.1; EMBL; S61113; AAB26669.1;
                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GAB_DROME
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           PIR;
                                                      entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                             MEDLINE=93260477; PubMed=7684073; Ffrench-Constant R.H., Rocheleau
                                                                                                                                                                                                                                                                                                                                                                                                       ffrench-Constant R.H., Mortlock D.P.,
Macintyre R.J., Roush R.T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A. MEDLINE=91334435; .PubMed=1651498;
                                                                                                                                                                                                                                                                                                 "Drosophila gamma-aminobutyric acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly)
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nes 8; Conser
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                                                                                                                                                                 SIMILARITY: BELONGS TO THE LIGAND-GATED CAUTION: IT IS UNCERTAIN WHETHER MET-1,
                                                                                                                                                                                                            CHLORIDE CHANNEL.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
OF
                                                                                                                                                       INITIATOR
                                                                                                                                                                            CHLORIDE IONOPHORE COMPLEX.
SIMILARITY: BELONGS TO THE LIGAND-GATED IONIC
                                                                                                                                                                                                     THE CYCLODIENE/PICROTOXININ BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; X16827; CAA34727.1;
S08137; S08137
           A41145; A41145
                                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the El
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Musc
a; Drosophilidae; Drosophila.
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BD7BFDF649EB1D50 CRC64;
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TRANSMEM
                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entre the European Bioinformatics Institute. There are no resta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1995 (Rel. 31, Created)
01-FEB 1995 (Rel. 31, Last sequence up
30-MAY-2000 (Rel. 39, Last annotation
ANTIFUNGAL PROTEIN PRECURSOR (AFP)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR002289; -. Pfam; PF00065; neur_chan; 1. PRINTS; PR00252; NRIONCHANNEL. PRINTS; PR00253; GABAARECEPTR. PRINTS; PR01160; GABAARBETA. PROSITE; PS00236; NEUROTR_ION_CHANNEL; 1.
                         modified
                                         use
                                                                                                                                                                                                                                                       J. Biol. Chem.
                                                                                                                                                                                                                                                                                           "Purification, cl
protein from the
                                                                                                                                                                                                                                                                                                                                                   TISSUE=Fat body;
MEDLINE=93280179; PubMed=8505329;
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Oestroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sarcophaga
Eukaryota;
                                                                                                                                  -!- TISSUE SPECIFICITY: HEMOLYMPH.
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                                                                                                                                                        SUBUNIT: HOMODIMER. TISSUE SPECIFICITY:
                                                                                                                                                                                                                FUNCTION: THIS PROTEIN INHIBITS THE GROW FUNGAL SPECIES. THE ANTIFUNGAL ACTIVITY
                                                                                                                                                                                                ENHANCED BY THE PRESENCE OF SARCOTOXIN IA
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   non-profit institutions as long
and this statement is not removed
requires a license agreement (See
                                                                                                                                                                                                                                                                                                                                                                                                                                        peregrina (Flesh fly) (Boettcherisca peregrina (Flesh fly) (Boettcherisca peregrina Hexapoda; Metazoa; Arthropoda; Tracheata; Hexapoda; Neoptera; Endopterygota; Diptera; Brachyce; Sarcophagidae; Sarcophaga.
                                                                                                                                                                                                                                                                                                                               Kurata S., Natori S.;
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he hemolymph of Sarcophaga
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                                                                                                                                                                                                                                                                                         cDNA cloning of an antifungal haga peregrina (flesh fly)
(See http://www.isb-sib.ch/announce/
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MEDLINE-91172321; PubMed=1672445;
Vollbrecht E., Veit B., Sinha N.,
Vollbrecht E., Veit B., 
  <del>-</del> <del>-</del> <del>-</del> <del>-</del>
                                                                                                                                                        Smith L.G., Green B., Veit B., Hake S.;
"A dominant mutation in the maize homeobox gene, Knotted-1, ectopic expression in leaf cells with altered fates.";
Development 116:21-30(1992).
                                                                                                                                                                                                                                                                                                           Nature
[2]
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01-MAR-1992
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Magnoliophyta; Liliopsida;
Andropogoneae; Zea.
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                FUNCTION: POSSIBLE TRANSCRIPTION FACTOR THAT REGULATES GENES INVOLVED IN DEVELOPMENT. MUTATIONS IN KN-1 ALTER LEAF DEVELOPMENT. FOCAL OF CELLS ALONG THE LATERAL VEIN DO NOT DIFFERENTIATE PROPERLY BUT CONTINUE TO DIVIDE, FORMING KNOTS. MAY PARTICIPATE IN THE SWITCH FROM INDETERMINATE TO DETERMINATE CELL FATES. PROBABLY BINDS TO THE DNA SEQUENCE 5'-TGAC-3'.

SUBCELLULAR LOCATION: NUCLEAR.
                                                                                                                                                                                                                                                                                                                                                 developmental gene
family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HGHGHGRDKHTNKDKNN 511
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                                                                                                                                                                                                                                                                                                                          350:241-243(1991).
                                                                                                                                                                                                                                                                 в73;
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61
639
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(Rel.
(Rel.
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82
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402
                                                                                                                                                                                                                                                                                    EXPRESSION
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          . 21, Last sequence up. 38, Last annotation KNOTTED-1.
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70
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EXPRESSED IN APICAL MERISTEMS OF VEGETATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Embryophyta; Tracheophyta; Spermatophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Poales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BY SIMILARITY
BY GICNAC
N-LINKED (GICNAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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Pred. No.
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CYSTATIN-LIKE
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E -> K (IN REF. 2).
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N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
VSPSYIARVQEERDPGNEQGPIHGHGWLHAKQ -> RLLNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CEYKGRLLKAGAGPAPERQAEASTVTP (IN ISOFORM
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INTERCHAIN (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -> K (ÎN REF. 2).
D3172DF94FF56AF5 CRC64;
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is a
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                                                                                                                                                                                                                                                                                                                                                                  member of a maize homeobox
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0.027;
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Best Local
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01-APR-1990
01-OCT-1994
                                                                                                                                                                                                                                                                                                                                                        2C_DICDI
P15648;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA_BIND
SEQUENCE
         This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outset the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                     homologous proteins.";

Mol. Microbiol. 4:129-135(1990).

-i- DEVELOPMENTAL STAGE: EXPRESSED
                                                                                                                                                                           "Two cyclic AMP-regulated
                                                                                                                                                                                                                                                                   Eukaryota; Mycetozoa;
                                                                                                                                                                                                                                                                              Dictyostelium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                   MEDLINE=90205618;
                                                                                                                                                                                                                   STRAIN-AX2
                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=44689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a coetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict
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                                                                                                                                                                                                                                                                                                        2C PROTEIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MaizeDB; 65584; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; X61308; CAA43605.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities
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                                                                                                                                                                                                                                                                                                                                                                                                                                  15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 HGHGHGKH
                                                                                      SIMILARITY: TO PROTEIN 7E.
                                                                                                 EXPRESSION CEASES UPON CELL BY EXOGENOUS CAMP.
DOMAIN: MAY FORM AN EXTENDED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MERISTEM DURING DEVELOPMENT. DOWN-REGULATED AS LEAVES AND FLORAL ORGANS ARE INITIATED.
SIMILARITY: BELONGS TO THE TALE/KNOX FAMILY OF HOMEOBOX PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AND FLORAL STEMS AS WELL AS IN THE UNDERLYING GROUND MERISTEM. SPECIFICALLY EXPRESSED IN VASCULAR BUNDLES DEVELOPING BOTH IN TI LEAF AND STEM. URRY LOW LEVELS OF EXPRESSION IN LEAVES.

DEVELOPMENTAL STAGE: EXPRESSED THROUGHOUT APICAL AND VEGETATIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S14283; S14283.
                                                                                                                                                                                                                                                                                                                                                                                                                                  HGHGHGQH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 l Similarity
7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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359
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(Rel.
(Rel.
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92
264
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homeobox;
                                                                                                                                                                                                                                                                  discoideum (Slime mold).
cetozoa; Dictyosteliida; Dictyostelium.
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a license agreement (See http://www
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14,
30,
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rds A.J., Jagger P.,
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87.5%;
                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Transcription regulation; Nuclear protein. POLY-HIS.
                                                                                                                                                                           genes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 51; DB
Pred. No. 1.2;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1:
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POLY-LYS.
ELK DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOMEOBOX (TALE-TYPE).
800FFD82082400FB CF
                                                                                                                           DISAGGREGATION
                                                                                                                                                                              from
                                                                                                  COIL
                                                                                                                           ONLY LATE IN DEVELOPMENT. ITS SAGGREGATION BUT IS FULLY RESTORED
                                                                                                                                                                          , Bleasby A., F
Dictyostelium
                                                                                                                                                                                                                                                                                                                  update)
                                                                                                   STRUCTURE
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Best Local S
Matches 11
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SEQUENCE
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CHAIN
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DOMAIN
"Primary structures of the mRNAs encoding the rat precursors is bradykinin and T-kinin. Structural relationship of kininogens major acute phase protein and alpha 1-cysteine proteinase
                                                            gene
                                                                         SEQUENCE FROM N.A. (ISOFORMS HAW AND LAW MEDLINE=87137443; PubMed=3029068; Kitagawa H., Kitamura N., Hayashida H.,
                                                                                                                                                 01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN; 1.
                        MEDLINE=86008264; PubMed=2413018;
Furuto-Kato S., Matsumoto A., Kitamura N.,
                                                                                                              Eukaryota;
Mammalia; I
                                                                                                                                    KNG
                                                                                                                                                                       KNG_RAT
P08934; P08933;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bradykinin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glycoprotein; Plasma; Repeat;
                                        SEQUENCE
                                                                  "Differing expression
                                                                                                      NCBI_TaxID=10116;
                                                                                                                           Rattus norvegicus (Rat)
                                                                                                                                          KININOGEN
                                                                                                                                                                                                                                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                    CARBOHYD
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                                                     Biol.
                                                                                                                                                                                                                               2 HGHGHGKHKNKGKKN
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                                                     family.";
iol. Chem.
                                                                                                                                                                                                                   HGHGKGKHTNKDKNS
                                                                                                                                                                                                                                                     Similarity
                                      FROM N
                                                                                                             Eutheria;
                                                                                                                                          PRECURSOR
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IPR003243;
                                                                                                                                                                                                                                                                                433
661
                                                                                                                     Metazoa;
                                                                                                                                                                                                                                              71.4%;
nilarity 73.3%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blood coagulation;
                                                                                                                                                                                                                                                                                                               19
380
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389
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327
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401
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                                                     262:2190-2198(1987).
                                                                                                                                                                              STANDARD;
                                      Þ
                                                                                                                                                                                                                                                                                                               661
73102
                                                                                                             Chordata;
Rodentia;
                                                                                                                                         0, Last annotation update)
[CONTAINS: BRADYKININ].
                                                                                                                                                                                                                                16
                                                                   patterns and
                                                                                                                                                                                                                                                                                   MW.
                                                                                                                                                                                                                                                                                                                                         INTERCHAIN (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                              Score 70; DB
Pred. No. 0.00
1; Mismatches
                                                                                                                                                                                                                                                                                MISSING (IN ISOFORM), 774460258D58796E
                                                                                                                                                                                                                                                                                                       N-LINKED (GLCNAC. . .) (POTENTIAL).
VSPPYIAAEQEENDAETEOGPTHGHGWLHEKQ ->
CEYKGRLSKAGAEPAPERQAESSQVKQ (IN ISOF
                                                                                                                                                                                                                                                                                                  EMW)
                                                                                                                                                                                                                                                                                                                                                                                                                 CYSTATIN-LIKE HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                CYSTATIN-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                              KININOGEN LIGHT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             KININOGEN HEAVY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thiol protease inhibitor; Vasodilator; Inflammatory response; Signal;
                                                                                                             Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rat
                                                                                                                                                                              PRT;
                                                                   a H., Miyata T., evolution of th
                                                                                                                                                       update)
                                                                                                                                                                                                                                                                                         (IN ISOFORM LMW).
                                                                                        (MMT
                                                                                                                                                                              639
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                                                                                                                                                                                                                                                             DB
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                       Nakanishi S.;
                                                                   of the
                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN.
                                                                                                                                                                                                                                                            Length 661;
                                                                                                                                                                                                                                                                                  CRC64;
                                                                         Nakanishi S.;
                                                                   rat kininogen
                                                                                                                                                                                                                                                                                                        (IN ISOFORM
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          with
                                                                                                              Rattus
                                                                                                                                                                                                                                                                                                               RLLRA
                                                                                                                                                                                                                                              0;
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RA Kageyama R., Kitamura N., Onkubo H., Nakanishi S.;

RY "Differing utilization of homologous transcription initiation sites

RY "Differing utilization of homologous transcription initiation.";

RY Of rat K and T kininogen genes under inflammation condition.";

RY OF TAT K and T kininogen genes under inflammation condition.";

RY J Biol. Chem. 262:3345-2351(1987).

CC -!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROFEASES; (2)

CC -!- FUNCTION: (1) KININOGEN SARE INHIBITORS OF THIOL PROFEASES; (2)

CC -!- FUNCTION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO

CC HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO

CC FACTOR XII; (3) HAW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-

CC INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE

CC INDUCED AGGREGATION OF FIRELASED FROM HAW-KININOGEN SHOWS A VARIETY OF

CC INDUCED AGGREGATION OF HYPOTENSION, (4C) NATRIURESIS AND

CC CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND

CC CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND

CC CONTRACTION, (4C) INDUCTION OF NOCICEPTORS (4E) IT IS A

MEDIATOR OF INFLAMMATION AND CAUSES (4EI) INCREASE IN VASCULAR

CC PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF

CC OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS

CC OTHER MEDIATORS OF INFLAMMATION OF HYPOTENSION;

CC INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION);

CC INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION);

CC KININOGEN IS IN CONTRAST TO HAW-KININOGEN NOT INVOLVED IN BLOOD
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or send a
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J. Biol.
                                                                 CHAIN
CHAIN
                                                                                                                                                 pfam; pF00031; cystatin; 3.
pRINTS; pR00334; KINIMOGEN.
pROSITE; pS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease
Bradykinin; Blood coagulation; Inflammatory
Alternative splicing; Multigene family.
                                                                                                                                                                                                                                                                                                                                   PIR; A25486; A25486.

PIR; A28055; A28055.

InterPro; IPR000010; -.

InterPro; IPR002395; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L29428; AAA41486.1; -.
EMBL; M11884; AAA41487.1; -.
EMBL; M14369; AAA41484.1; -.
EMBL; M14369; AAA41485.1; AL/
EMBL; M16455; AAA41482.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fung W.-P., Schreiber G.; "Structure and expression of the genes for major acute phase alpha "rotein (thiostatin) and kininogen in the rat.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                + +
                                  PEPTIDE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      s SWISS-PROT entry is copyright. It is produced ween the Swiss Institute of Bioinformatics and European Bioinformatics Institute. There are a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
TISSUE SPECIFICITY: PLASMA.
EYM: BRADYKLNIN IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
MISCELLANGOUS: RAT EXPRESS FOUR TYPES OF KININOGENS: THE CLASSIC
MISCELLANGOUS: AND TWO ADDITIONAL LMW-LIKE KININOGENS: T-I A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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BRADYKININ.
KININOGEN LIGHT CHAIN
                                                              KININOGEN.
KININOGEN HEAVY
                                                                                                                                                                                 protease inhibitor; Vasodilator;
ammatory response; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (See http://www.isb-sib.ch/announce/
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HWW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HWW-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOTYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STINULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIODROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kato H.,
"Studies
                                                                                                  CARBOHYD
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                                                                                                                                                                                                                                                                           Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                          Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN;
                                                                                                                                                                                                                                                                                                                                                                                    PIR; A01281; KGBOH1.
PIR; A29559; A29559.
                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                   CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; V01491; CAA24735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Studies on the primary structure of bovine high-molecular-we kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
                                                                                                                                MOD_RES
                                                                                                                                                                                                         PEPTIDE
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InterPro; IPR002395; -
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PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LINE=75170265; PubMed=1169237;
Y.N., Komiya M., Iwanaga S., Suzuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TO RESIDUE 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACTION;
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N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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PYRROLIDONE CARBOXYLIC
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CYSTATIN-LIKE
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RESULT 4
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008677; 00
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                   EMBL; D84435; BAA19743.1;
EMBL; D84415; BAA19742.1;
MGD; MGI:1097705; Kng.
                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                    entities requires a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6 x CBA; TISSUE=Liver;
Takano M., Kondoh J., Yayama K., Okamoto H.;
"Molecular cloning of cDNAs for mouse low- a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U1-UCT-2000 (Rel. 40, Last annotation update)
KININOGEN PRECURSOR [CONTAINS: BRADYKININ].
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01-OCT-2000 (Rel.
01-OCT-2000 (Rel.
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[1]
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LAW-KININGEN INHIBITS THE AGGRECATION OF THEMOEDCYTES; (6) LAW-
KININGEN IS IN CONTRAST TO HAW-KININGEN NOT INVOLVED IN BLOOD
CLOTTING (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LAW; ARE
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS
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                                                                                                            s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                    UE SPECIFICITY: PLASMA.
BRADYKININ IS RELEASED FROM KININOGEN
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93.8%;
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Pred. No.
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1.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and high- molecular
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                                                                                                                                                                                                                                                                                                                       BY PLASMA KALLIKREIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 621
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HWY-KININGEN PROTEASES; (2)
HWY-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HWW-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOLYTES; (4) THE ACTIVE
PERTIDE BRADYKKINI THAT IS RELEASED FROM HWY-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF THYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACCITION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine h
kininogen. Amino acid sequence of a fragment
peptide') released by plasma kallikrein.";
J. Biochem. 77:55-58(1975).
                                Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSTTE: PS000287; CYSTATIN; 2.
Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                [5]
SEQUENCE OF 456-496
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"Primary structure of bovine plasma high-molecular-weight kininogen.
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus of the bradykinin moiety.";
J. Blochem. 79:1201-1222(1976).
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MEDLINE=70180420; Pu
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"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the hea
                                                                                                                                                                                                                                                                                                                                                    EMBL; V01492;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=75170265; PubMed=1169237;
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                                                                                                                                                          InterPro; IPR000010; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        bonds and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HAW II AND LAW II KININOGEN PRECURSORS PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TO RESIDUE 398
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                                                                                                                                                                                                                                                                                                                    V01492; CAA24736.1; -.
V01492; CAA24737.1; ALT_SEQ.
   protease inhibitor;
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on the structure of bovine kininogen: cleavages of disulfide of methionyl bonds in kininogen-II.";
m. 67:313-323(1970).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         262:2768-2779(1987).
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   Bradykinin; Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bovine high-molecular-weight fragment ('histidine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               There are no restrictions
      coagulation;
Signal;
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Best Local Similarity
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KNH1_BOVIN
P01044;
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CHAIN
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DOMAIN
                                    Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid
positions of carbohydrate chains and disulfide bridges i
                                                                                                                                              Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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SEQUENCE OF 378-393
MEDLINE=70180420; Po
                                                    Sueyoshi T., Miyata
Miyata T., Iwanaga S
                                                                                                                        SEQUENCE FROM N.A. MEDLINE=84014106; PubMed=6571699;
                                                                                                                                                                       Eukaryota;
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                              chain
                                                                           SEQUENCE OF 19-378
                                                                                          Nature 305:545-549(1983).
                                                                                                   weight
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                                                                                                                                                                                Bos taurus
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                                                                   MEDLINE-87137530;
                                                                                                         Kitamura N., Takagaki Y., Furuto S., Tanaka T.,
"A single gene for bovine high molecular weight
                                                                                                                                                                                                                                                                          474
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                                                                                                                                                                                                                                                                          KHGHGHGKHKNKGKNN 489
                              portion.
                        Chem.
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257
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1141
1141
                       262:2768-2779(1987)
                                                                                                                                                                                                                                     STANDARD;
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                                                                    PubMed-3546295;
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 PubMed=4986212
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93.8%;
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N-LINKED (GLCNAC
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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ion update)
                                     disulfide bridges in
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                                                            Kato H., Hayashida
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1.5e-06;
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molecular
                                              sequence,
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PIR; A01279; KGHUH1.

PIR; A25276; A25276.

PIR; A01280; KGHUL1.

PIR; B25276; B25276.

PIR; S02482; S02482.

SWISS-2DPAGE; P01043;
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EMBL; M11526
EMBL; M11528
EMBL; M11438
EMBL; M11438
EMBL; M11521
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EMBL; M11523
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EMBL; M11525
EMBL; M11526
EMBL; M11526
                   CHAIN
                                                                                                                                          Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN;
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HELPING TO POSITION OPTIMALLY PREMALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROWBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS; (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRITRESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULATION OF MOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELEAXING FACTOR ACTION), (5)
LMM-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMM-
KININOGEN IS IN CONTRAST TO HMM-KININOGEN NOT INVOLVED IN BLOOD
                                                             SIGNAL
                                                                                                                             Glycoprotein;
                                                                                 Alternative
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                                                                                                                                                                                                            InterPro; IPR000010; -.
InterPro; IPR002395; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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M11521;
M11522;
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M11524;
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M11437;
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                                                                                                  Blood coagulation;
                                                                               splicing.
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AAB59550.1;
AAB59550.1;
AAB59551.1;
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                 KININOGEN HEAVY CHAIN
                                                                                                Thiol protease inhibitor; Vasodilator; inflammatory response; Signal;
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Best Local
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21-JUL-1986 (Rel. (
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea

Bovidae; Bovinae; Bos.

NCBI_TaxID=9913;
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MEDLINE-87137530; PubMed=3546295;
Sueyoshi T., Miyata T., Hashimoto
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CARBOHYD
                             "A single gene for bovine weight kininogens.";
Nature 305:545-549(1983).
                                                    Kitamura N.,
                                                           SEQUENCE FROM N.A. MEDLINE=84014106; PubMed=6571699;
                                                                                                                     BRADYKININ
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 Hashimoto N.,
                                            Furuto S., Tanaka T.,
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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Pred. No. 2.8e-07;
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    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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plasmodium
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A; Introns: 91/9; 127/1; 193/2
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enorhabditis elegans
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Sophila melanogaster
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                                                                                                                                                                                                                                                                                                                                  ces: FlyBase:FBgn0004244
Macetylcholine receptor
Inotransmitter receptor; transmembrane protein
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                                                                                                                                                                                                                 HGKH 9
amka M.L.; Lipshitz, H.D. 2129-21410, 1997.
                                         9 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R.H.; Mortlock D.P.; Shaffer, C.D.; MacIntyre, R.J.; Roush, R.T. Sci. U.S.A. 88, 7209-7213, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             #sequence_revision 10-Apr-1992 #text_change 21-Aug-1998
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                                                                                   fruit fly (Drosophila melanogaster)
                                                                                                                                                                                                                                              51.0%; Score 50; DB 77.8%; Pred. No. 10; tive 1; Mismatches
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                                                                                                                                                               A; Description: probably function as a transcription factor C; Keywords: nucleus; zinc finger
                                                                                                                                                                                                                                                                                                                              A;Accession: T13893
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                    A; Title: Control of germ-band retraction in Drosophila by the zinc-finger protein HIN A; Reference number: 217807; MUID: 97330681
                                                                                                                                                                                                      C; Function:
                                                                                                                                                                                                                                            A;Gene: hindsight
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A; Residues: 1-1920 <Y
                                           Query Match
Best Local Similarity b/..
Thes 7; Conservative
                                                                                                                                                                                                                      Cross-references: FlyBase:FBgn0003053
                                                                                                                                                                                                                                                               Genetics:
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1136 НСНСНСКН 1143
                      2 HGHGHGKH 9
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87.5%;
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                                                                      Indels
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Search completed: July 6, 2001, 09:18:02 Job time: 648 sec

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R;Meisel, L.; Lam, E. Plant Mol. Biol. 30, 1-14, 1996 Plant Mol. Biol. 30, 1-14, 1996 A;Title: The conserved ELK homeodomain of KNOTTED-1 contains two regions that signal A;Reference number: S65139; MUID:96197395 A;Accession: S65139
A;Status: nucleic acid sequence not shown; not compared with conceptual translation A;Molecule type: mRNA A;Residues: 247-326 <MEI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein peb - fruit fly (Drosophila melanogaster) (;Species: Drosophila melanogaster C;Date: 13-Aug-1999 #sequence_revision 13-Aug-1999 #text_change 13-Aug-1999 C;Accession: T13594 R;Ferraz, C.; Vidal, S.; Brun, C.; Bucheton, A.; Demaille, J.G. submitted to the EMBL Data Library, October 1998 A;Description: Sequencing the distal X chromosome of Drosophila melanogaster. A;Reference number: Z17692
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A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-125 <SCH>
A;Cross references: EMBL:AL355927; GSPDB:GN00116; NCSP:BlD1.100
A;Experimental source: BAC clone BlD1; strain OR74A
C;Genetics: A;Gene: NCSP:BlD1.100
A;Map position: 6
                                                                                                                                                                                                                                                                                                                                                              N;Alternate names: homeotic protein Knotted-1
C;Species: Zea mays (maize)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 15-Oct-1999
C;Accession: S14283; S65139
R;Vollbrecht, E; Veit, B; Sinha, N.; Hake, S.
Nature 350, 241-243, 1991
                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-359 <VOL>
A;Residues: 1-359 <VOL>
A;Cross-references: GB:X61308; GB:X57672; NID:g22350; PIDN:CAA43605.1; PID:g22351
A;Note: DNA was also sequenced
                                                                                                                                                                                                                                                                                           A;Title: The developmental gene Knotted-1 is a member of a maize A;Reference number: S14283; MUID:91172321
A;Accession: S14283
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A;Cross-references: FlyBase:FBgn0003053
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A; Residues: 1-1891 <FER>
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mes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 HGHGHG-KHKNKGKK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 HGHGHGKHKNKG 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HDHGRGRKHGNKGKK 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       289/3
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8; Conservative
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73.3%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 54; DB Pred. No. 7.6; 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 54.5;
Pred. No. 0.
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.57;
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A;Description: involved in the regulation of vegatative development; may A;Note: primarily expressed in meristematic cells of vegetative tissues; A;Note: intercellular transport into epidermal cells has been proposed C;Superfamily: unassigned homeobox proteins; homeobox homology C;Keywords: DNA binding; homeobox; nucleus; transcription regulation F;265-324/Domain: homeobox homology <HOX>
                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, November 1996 A; Reference number: Z20428 A; Accession: T27840
                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein ZK39.2 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene 2C protein - slime mold (Dictyostelium discoideum)
C;Species: Dictyostelium discoideum
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 29-Oct-1999
                                                                                                                                                                                 A;Cross-references: EMBL:282093; PIDN:CAB05018.1; GSPDB:GN00019; CESP:ZK39.2 A;Experimental source: clone ZK39
                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1~229 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Two cyclic AMP-regulated genes from Dictyostelium discoideum encode homologo A;Reference number: S08136; MUID:90205618
A;Accession: S08137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: S08137
R;Ramji, D.P.; Richards, A.J.; Jagger, P.; Bleasby, A.; Hames, B.D. Mol. Microbiol. 4, 129-135, 1990
                                                                                                    A; Map position: 1
A; Introns: 28/1; 55/3; 111/1
                                                                                                                                           C; Genetics:
A; Gene: CESP: ZK39.2
                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Gene: 2C
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A; Residues: 1-98 < RAM>
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A;Introns: 126/3; 167/3; 216/1; 293/3
                                                                                                                      A; Map position:
                                                                                                                                                                                                                                                                                                                                             R;Kershaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                  T27840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Cross-references: EMBL: X16827; NID: g7161;
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Best Local Similarity
Matches 8; Conserv
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Best Local
                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 HGHGHGKHKNKGK 14
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7; Conserv
  Conservative
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                    51.0%;
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87.5%;
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Pred. No.
                    Score 50;
Pred. No.
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Mismatches
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                    4.2;
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                                       DB 2;
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4.6
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N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
R;Kitagawa, H; Kitamura, N.; Hayashida. u · · · · · · · · · · · J. Biol. Chem. 262
                                                                                                                                                                                                                                                                                                                                                                                                                               F:1-18/Domain: signal sequence #status predicted <SIG> F;19-639/Product: kininogen, HMW I #status predicted <MAT> F;19-131/Domain: cystatin homology <CY12> F;142-253/Domain: cystatin homology <CY2> F;264-375/Domain: cystatin homology <CY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution A;Reference number: A92625; MUID:87137443
A;Accession: A25486
A;Molecule type: mRNA
A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for resiculation of the codon codon 
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J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family.
A;Reference number: A92625; MUID:87137443
A;Accession: C25486
A;Molecule type: DNA
A;Mol
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c;Species: Rattus norvegicus (Norway rat)
c;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-Sep-1993
C;Accession: C25486
           RESULT
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Best Local
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93.8%;
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                                                                                                                                                                                                                                                                                             Score 64;
Pred. No.
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Pred.
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0.11;
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                                                                                                                                                                                                                                                                                                                        Length 639;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          of the rat kininogen gene family.
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R-kininogen, LMW precursor - rat (fragments)

C;Species: Rattus norvegicus (Norway rat)

C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 20-Aug-1999

C;Accession: C27115; A25488

R;Fung, W.P.; Schreiber, G.

R;Fung, W.P.; Schreiber, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: not compared with conceptual translation A;Molecule type: DNA A;Residues: 1-315 <FUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: A27115
R;Fung, W.P.; Schreiber, G.
J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the genes for major acute phase alpha-1-protein A;Reference number: A92653; MUID:87250580
A;Accession: A27115
A;Accession: A27115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GB:J02662; NID:g205071; PIDN:AAA41483.1; PID:g205072 C;Superfamily: kininogen; cystatin homology F;19-65/Domain: cystatin homology (fragment) <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Reference number: A92653; MUID:87250580
A;Accession: C27115
A;Molecule type: DNA
A;Residues: 1-290 <FUN>
R;Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation sites of rat K
A;Reference number: A25488; MUID:87137465
A;Accession: A25488; MUID:87137465
A;Accession: A25488
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-48 <KAG>
A;Residues: 1-48 <KAG>
                                  A; Reference number:
                                                            R;Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, submitted to the Protein Sequence Database, May 2000
                                                                                                                                         C;Species: Neurospora crassa
C;Date: 02-Jun-2000 #sequence_revision
C;Accession: T49356
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        major acute phase alpha-1 protein 1 - rat (fragments)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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A; Accession: T49356
                                                                                                                                                                                                                                                   hypothetical protein B1D1.100 [imported] - Neurospora crassa
                                                                                                                                                                                                                                                                                             T49356
                                                                                                                                                                                                                                                                                                                                RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Genetics:
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Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                  225022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 60;
Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Nyakatu

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...omment: Bradykinin, released from kininogen by ka xyproline residue is present in the kininogen prior C;Superfamily: kininogen; cystatin homology C;Keywords: alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Reference number: A94300
A;Contents: annotation; disulfide bonds
A;Contents: annotation; disulfide bonds
A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is importance.
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, in the kininogen prior to the release of bradykinin.
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A;Reference number: A91938
A;Accession: A91938
A;Molecule type: protein
A;Residues: 456-496 <AA2>
R;Sueyoshi, T; Miyata, T; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwana J. Biol. Chem. 262, 2768-2779, 1987
J. Biol. Chem. 262, 2768-2779, 1987
A;Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of R;Reference number: A92627; MUID:87137530
A;Recession: B29559
A;Molecule type: protein
A;Residues: 'Z',20-104,'E',106-256,'XX',257-376 <SUE>
A;Reference number: A92627; MUID:87137530
A;Recession: B29559
A;Roccession: B29559
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J. Biochem. 79, 1201-1222, 1
A; Title: Primary structure of A; Reference number: A91941; A; Accession: A91941
В
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A;Title: Disulfide bonds in
A;Reference number: A94300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 'Z', 20-104, 'E', 106-256, 'XX', 257-376 R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Eur. J. Biochem. 152, 307-314, 1985
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A; Residues: 387-
                                                                                                                                                                                                                                                                                                                 136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental; 197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental; 197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental; 386-377/Cleavage site: Met-Lys (kallikrein) #status experimental; 386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental; 396,400,404,510/Binding site: carbohydrate (Ser) (covalent) #status experimental; 397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status experimental; 397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status experimental; 496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          418-488/Region: glycine/histidine/lysine-rich
19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimer
27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :19-619/Product: HMW kininogen II #status predicted <MAT>
:19-376/Product: HMW kininogen II heavy chain #status experimental <HCH:
:19-130/Dommain: cystatin homology <CVI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Superfamily: kininogen; cystatin homology 
Keywords: alternative splicing; blood coagulation; cysteine 
1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                           Matches
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87,158,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status experimental
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     141-252/Domain: Cystatin homology <CY2>
261-372/Domain: Cystatin homology <CY3>
377-386/Product: Lysyl-bradykinin (kallidin II) #status experimental <KBH
378-386/Product: bradykinin (kallidin I) #status experimental <BDY>
388-386/Product: HMW kininogen II light chain #status experimental <LCH>
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Biochem. 77, 55-68, 1975
   474
                                                                                                                                                                                    Local
                                                                   1 KHGHGHGKHKNKGKKN 16
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   KHGHGHGKHKNKGKNN
                                                                                                                                                                             Similarity
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                                                                                                                                                                             94.9%;
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MUID:76260155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bovine HMW kininogens
                                                                                                                                       Score 93; DB
Pred. No. 8.9e
0; Mismatches
                                                                                                                                           0;
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Suzuki, T
                                                                                                                                                                             DB 1;
8.9e-06;
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tatus experimental <BDY>
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                                                                                                                                                                                                               Length 619
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                                                                                                                                   Gaps
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RESULT

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 458-498 < HANN
R; Sueyoshi, T; Miyata, T; Hashimoto, N; Kato,
J. Biol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N;Contains: bradykinin (xallium,, ......)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (lattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01281; A91923; A91938; A29559
C;Accession: A01281; A91923; A91938; A29559
R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, Nature 305, 545-549, 1983
Nature 305, 545-549, 1983
                                                                                                                                                                                                                                                                                                                   F:19-130/Domain: cystatin homology <CYI>
F:141-252/Domain: cystatin homology <CYI>
F:246-374/Domain: cystatin homology <CYI>
F:263-374/Domain: cystatin homology <CYI>
F:379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F:389-621/Product: htm kininogen I light chain #status experimental <LCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Superfamily: kininogen; cystatin homology C;Keywords: alternative splicing; blood coagulation; c F;1-18/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of C;Comment: The plycine/histidine/lysine-rich region of HMW kininogen light chain is i C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass A;Reference number: A91153; MUID:86030270
A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: protein A; Residues: 378-393 <KAT>
R; Han, Y.N.; Komiya, M.;
                                                                                     F;136/Binding site: carbohydrate (Thr) (covalent) (partial) #statu
F;197/Binding site: carbohydrate (Asn) (covalent) (partial) #statu
F;378-379/Cleavage site: Met-Lys (kallikrein) #status experimental
                                                                                                                                                                                     F;417-486/Region: glycine/histidine/lysine-rich F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status ex; F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status ex; F;27-591.82-93.106.125.141.144.205-217.228-247,263-266.327-339,350-369/Disulfide | F;87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R:Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1948
A;Title: Disulfide bonds in bovine HMW kininogens.
A;Reference number: A94300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Han, Y.N.; Komiya, M.; Iwa
J. Biochem. 77, 55-68, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;19-621/Product: HMW kininogen I #status predicted <MAT>
F;19-379/Product: HMW kininogen I heavy chain #status experimental <HCH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 'Z', 20-123,'I', 125-127,'I', 129-378
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kato, H.;
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A; Residues: 1-621 <KIT>
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                                                             F;382/Modified site: 4-hydroxyproline (Pro) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xyproline residue is present in the kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Note: article in Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Accession: A29559
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                              /Cleavage site:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HMW I precursor -
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923; MUID:70180420
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                              (kallikrein)
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                                  #status experimental
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experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              potent vasodilator of bradykinin.
                                                                                                                              experimental
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de bond
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A; Residues: 1-19,189-192;310-314;381-389 <LEN1>
R; Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A; Title: Isolation and identification of hydroxyproline analogues of bradykinin in h
A; Reference number: A61495; MUID:88211869
A; Accession: A61495
A; Molecule type: protein
A; Residues: 380-389 <KAT1>
A; Residues: 380-389 <KAT1>
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Note: this peptide had Pro-383 modified to 4-hydroxyproline
A; Accession: C61495
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A; Accession: C61495
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R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in A;Reference number: S02482; MUID:89076517
A;Accession: S02482
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A; Residues: 379-389', K', 390-407, 'Q', 409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, A.G.
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin moiety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
A; Accession: A27699
A; Molecule type: protein
A; Residues: 380-389 <MINN-
R; Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A; Title: Purification and identification of [hydroxyproly1(3)] bradykinin in ascitic
A; Reference number: A31905; MUID:89034061
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y
J. Biol. Chem. 260, 8610-8617, 1985
A;Title: Structural organization of the human kininogen
A;Reference number: A92545; MUID:85234583
                                                                                                                                                                             A; Molecule type: protein
A; Residues: 450-452,'X', 454,'X', 456 < LIT>
R; Straczek, J; Maachi, F; le Nguyen, D;
FEBS Lett. 373, 207-211, 1995
A; Title: Purification from human plasma of A; Reference number: S68059; MUID: 96033974
A; Accession: S68059
                                                                                                                                                                                                                                                                                                                                                                                A; MoLecule type: protein
A; Residues: 264-359, 'N', 361-375 < LEN2>
R; Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A; Title: Human mast cell tryptase isoforms:
A; Reference number: S55239; MUID:95251593
A; Accession: S55239
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FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C :
A;Reference number: S14303; MUID:91192133
A;Accession: S14447
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A;Recession: A31905
A;Molecule type: protein
A;Residues: 381-389 <AMEDIAN A; Ideishi, M.; Arakawa, K.
Biochem: Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin
A;Reference number: A34030; MUID:88106632
A;Accession: A34030
A;Molecule type: protein
A;Molecule type: protein
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                                                                                                                                                     protein
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                                                                                        Takagaki, Y.; Miyata,
                                                                                                                                                                                                                                    tetrapeptide
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                              gene and
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                                 model for its evolut
                                                                                        T.; Nakanishi,
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A;Gene: GDB: KNG
A;Gene: GDB: KNG
A;Gross-references: GDB:125256; OMIM:228960
C;Keywords: God:12525; Old Color Cystatin homology
C;Keywords: Alternative septimental <MAT2>
F;J9-644/Product: HMW kininogen II forminogen II status experimental <HCH>
F;J80-389/Product: Lysyl-bradykinin (kallidin II) #status experimental <HCH>
F;J80-644/Domain: Gystatin homology <CY2>
F;J81-389/Product: Lysyl-bradykinin (kallidin II) #status experimental <HCH>
F;J81-389/Product: Lysyl-bradykinin (kallidin II) #status experimental <HCH>
F;J81-389/Product: Lysyl-bradykinin (kallidin II) #status experimental <HCH>
F;J81-344/Product: Lysyl-bradykinin (kallidin II) #status experimental <HCH>
F;J81-344/Product: Lysyl-bradykinin (kallidin II) #status experimental F;J81-349/Product: Lysyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-bradyl-brad
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kalliddin); kininogen I; kininogen II; prokinin C;Species: Bos primigenius taurus (cattle) C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun C;Date: A01282; A91941; A91938; B29559 R;Kitamura, N: Takagaki, Y:; Furuto, S:; Tanaka, T:; Nawa, H.; Nakani: Nature 305, 545-549, 1983
A; Molecule type: protein A; Residues: 376-391 < KAT>
                                                                       A; Accession: A91923
                                                                                                           A; Title: Studies on the structure of bovine kininogen: A; Reference number: A91923; MUID:70180420
                                                                                                                                                                                       R; Kato, H.; Nagasawa, S.; Suzi
J. Biochem. 67, 313-323, 1970
                                                                                                                                                                                                                               A;Cross-references: GB:V01492; GB:K01758; R;Kato, H.; Nagasawa, S.; Suzuki, T.
                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-619 < KIT>
                                                                                                                                                                                                                                                                                                                                                                              A;Title: A single gene for bovine high molecular weight A;Reference number: A93317; MUID:84014106 A;Accession: A01282
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C;Genetics:
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A;Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from t C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in init C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in light C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent v xyproline residue is present in the kininogen prior to the release of brady
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kininogen,
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1.8e-06;
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Listing firs
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Maximum DB seq length: 200000
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Perfect score:
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Pred. No. is the number score greater than or e and is derived by analy
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PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match Length
July 6, 2001, 09:18:02; Search time 73.59 Seconds (without alignments)
16.562 Million cell updates/sec
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Gapop 10.0 , Gapext 0.5
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1 KHGHGHGKHKNKGKKN 16
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Copyright (c) 1993 - 2000 Compugen Ltd
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45.5	46	46	46	46	46	46	46	46	46	46	46.5	47	47	47
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S58327	A54063	T43236	T15506	T08684	T26757	T26756	T49164	S71224	T29574	JQ2266	S65780	D96786	T08132	JC5822
cobalt accumulatio	TATA-binding prote	carboxypeptidase C	hypothetical prote	hypothetical prote	•	hypothetical prote	zinc transporter-l	xyloglucan endo-1,	hypothetical prote	cold acclimation p	glycine/proline-ri	protein F10A5.15 (	oleosin-like prote	NADH dehydrogenase

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US-08-933-774-7

Sequence 7, Application US/08933774A Patent No. 6025137

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TYPE: PRT
ORGANISM: Homo sapiens
US-08-933-774-7
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/623,679
FILING DATE: 29-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/412,431
FILING DATE: 29-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fasse, J. Peter
REGISTRATION NUMBER: 32,983
REFERENCE/DOCKET NUMBER: 07334/004001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 7
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APPLICANT: Shyjan, Andrew W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/08/933,774A CURRENT FILING DATE: 1997-09-19 EARLIER APPLICATION NUMBER: US 08/623,679 EARLIER FILING DATE: 1996-03-29 EARLIER APPLICATION NUMBER: US 08/412,431 EARLIER FILING DATE: 1995-03-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS, PREVENTION TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION FILE REFERENCE: 07334/004003
                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSIT
TITLE OF INVENTION: DIAGNOSTI
TITLE OF INVENTION: PROGRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
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ZIP: 02110-2804
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STATE: MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            225 Franklin Street
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Pred. No.
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Search completed: July Job time: 190 sec

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   В
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US-08-933-774-9
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                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
APPLICANT: Shyjan, Andrew W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS,
TITLE OF INVENTION: AND TREATMENT OF TUMOR PROGRESSION
FILE REFERENCE: 07334/004003
CURRENT PELLORATION NUMBER: US/08/933,774A
CURRENT FILING DATE: 1997-09-19
EARLIER APPLICATION NUMBER: US/08/623,679
EARLIER APPLICATION NUMBER: US/08/412,431
                                                                   Best Local Similarity
Matches 9; Conserv
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                                                                                                   Query Match
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Matches 9; Conservative
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355 KGGRGKGKKKKGK 368
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                     1 KHGHGHGKHKNKGK 14
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Pred. No.
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CURRENT APPLICATION DATA:

SOFTWARE:

PatentIn Release #1.0, Version #1.30

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS/ASCII

COMPUTER READABLE FORM:

MEDIUM TYPE:

Floppy disk

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JS-08-938-534-28
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Best Local Similarity
Matches 8; Conserv
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TELEX: 79-002
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                  SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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LENGTH: 1085 amino aci
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PRIOR APPLICATION UDMBER: SN 08/326,781
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APPLICATION NUMBER:
                          ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Gottschling, Daniel E. APPLICANT: Singer, Miriam S.
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OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
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STRANDEDNESS: si
NAME: Parker, David REGISTRATION NUMBER:
                                             FILING DATE:
                                                            FILING DATE: APPLICATION NUMBER:
                                                                                                                           CLASSIFICATION:
                                                                                                                                       APPLICATION NUMBER: US/0
FILING DATE: 26-SEP-1997
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                                                                                                                                                                                                                                                                                 UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                             Singer, Miriam S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                               Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               October 20, 1994
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                                               October 20, 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.9%;
61.5%;
                                                                                                                                                                                                                                                                                                                                                                                              Telomerase Compositions and Methods
                                                                                                                                                                                    Release #1.0, Version #1.30
                                                            SN 08/326,781
                                                                                            08/431,080
                                                                                                                                                       US/08/938,534
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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US-08-623-679-7
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                                                                                               US-08-623-679-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7, Application US/08623679 Patent No. 5674739
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                                                                                                                                                                          TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Shyjan, A TITLE OF INVENTION: TITLE OF INVENTION: TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                   FILING DATE: 29-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/412,431
FILING DATE: 29-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: ARTELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/623,679
                                                                                                                                                           SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 617/542-5070
                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    521 KSGKSHIEHKNKG 533
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: USA
7TP: 02110-2804
                                                                                                                                                                                                    TELEPHONE: 617/542-30
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Fish & .....
emperg: 225 Franklin Street
                                                                                                                                                                                                                                                                     NAME: Fasse, J. Peter REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid STRANDEDNESS: si
                                                                                                                            TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
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                                                                                                              TOPOLOGY:
                                                                                                                                         LENGTH:
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                                                                                                                          amino acid
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                               64.3%;
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61.5%;
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                                                                                                                                                                                                                                                                   32,983
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Pred. No.
                                 Pred. No. 1.6e+02;
                                              Score 44;
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                                            DB 1;
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                                            Length 1497
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Conservative

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US-09-208-742-2

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RESULT 9
US-08-646-715-20
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Best Local Similarity
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Best Local
                                                                                                                                        Matches
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
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                                                                               1163 KHKHRHSKDKDKERKD 1178
                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino aci
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                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A
REGISTRATION NUMBER: 36,627
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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STATE: California
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                                                                                                                                        Local Similarity
nes 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 94111-4187
                                                                                                      1 KHCHCHCKHKNKCKKN 16
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                                                                                                                                                                                                                                                       amino acid
    Application US/08646715
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                                                                                                                                                                                                                                                                      1213 amino acids
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VERWION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
VERWION: MOCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
EQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comai, Lucio
Dynlact, Brian D.
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Comai,
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Tanese, Naoko
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SYSTEM: PC-DOS/MS-DOS
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53.3%;
                                                                                                                                                    46.9%;
                                                                                                                                     Score 46; DB Pred. No. 70; 3; Mismatches
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70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            ; MOLECULE TYPE: protein US-08-646-715-20
                                                                                                                                                                            sequence 28, Application US/08431080 Patent No. 5698686
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GENERAL INFORMATION
                                                                                                 GENERAL INFORMATION:
APPLICANT: Gottsching, Daniel E.
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Co
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
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                                                                                                                                                                                                                                                                                        1163 KHKHRHSKDKDKERKD 1178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS
LENGTH: 1213 amino aci
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APPLICATION NUMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                   CORRESPONDENCE ADDRESS
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TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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APPLICANT:
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                                                 STREET:
                                                                 ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
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                               Houston
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                 TEXAS
                                                 E: Arnold, White & Durkee P.O. Box 4433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1213 amino acids
UNITED STATES OF AMERICA
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Tanese, Naoko
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Comai, Lucio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 398-3249
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                                                                                                                                                                                                                                                                                                                                                                      46.9%;
                                                                                                   Telomerase Compositions and Methods 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Release #1.0, Version #1.25
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                                                                                                                                                                                                                                                                                                                                                                      Score 46;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TEST, ALBRITTON & HERBERT
er, Suite 3400
                                                                                                                                                                                                                                                                                                                                                      core 46; DB ced. No. 70; Mismatches
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TELEPHONE:

415/705-8410

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В
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                                                                                                                                          ; TOPOLOGY: unknown
; MOLECULE TYPE: pept:
US-08-072-064-8
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                                                            Matches
                                                                           Query Match
Best Local Similarity
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Best Local 9
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                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
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LENGTH: 637 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: FFRENCH-CONSTANT, RICHARD H. APPLICANT: JACKSON, MEYER B.
                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
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457 ЕНСИСНЕНН 465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/072,064 FILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00574
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STATE: California
                                                                                                                                                                                                        LENGTH:
                                                                                                                                                                                                                                                                        TELEPHONE:
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                            1 KHGHGHGKH 9
                                                                                                                                                                                         1: 637 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                    CARROLL, PETER G.
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415/397-8338
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VENTION: DRUG AND PESTICIDE SCREENING
                                                              Conservative
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Pred. No.
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Pred. No.
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                                                                                          DB 3;
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Best Local Similarity
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                                            SOFTWARE: FastSEQ
SEQ ID NO 2
                                                                                                                                                                                                           Sequence 2, Application US/09208742 Patent No. 6174679
                                                                                       APPLICANT: Kaufmann, Joerg
TITLE OF INVENTION: CIF150/hTAFII150 is Necessary
TITLE OF INVENTION: Cycle Progression
FILE REFERENCE: 1453.002
CURRENT APPLICATION NUMBER: US/09/208,742
CURRENT FILING DATE: 1998-12-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (203)268-1951
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                             NUMBER OF SEQ ID NOS:
ORGANISM: human
                             ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: CR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203)268-1951
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OPERATING SYSTEM: MS-DOS
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08558
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ORIGINAL SOURCE:
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: October 4th ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                               457 ЕНСНСНН 465
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CLASSIFICATION:
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CITY: Trumbul
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TENTION: MOLECULAR CLONING AND TRANSFORMATION OF CYCLODIENE RESISTAN
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                                                               Windows Version 3.0
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77.8%;
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US-08-072-064-1

Sequence 1, Applic Patent No. 6008046

Application US/08072064

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                                                             ARPLICANT: FERENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
APPLICANT: JACKSON, MEYER B.
APPLICANT: DRUG AND PESTICIDE SCREENING
                                                                                                                                                                                                                                                                                                                                                       Matches
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TELEPAX: 415/397-8338
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
                                                      CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: peptide ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00574
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32.
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PRIOR APPLICATION DATA:
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APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
NUMBER OF SEQUENCES: 20
                                                                                                                                                                                                                                                                            457 ЕНСИСНСКИ 465
STREET:
CITY: S
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nes 7; Conserv
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FILING DATE: 19930602
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                                      DDRESSEE:
                                                                                                                                                                                                                                                                                                                   1 KHGHGHGKH 9
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                   220 Montgomery Street, Suite 2200
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                                      PETER G. CARROLL
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Pred. No. 11;
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US-08-072-064-6
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Best Local Similarity
7; Conserv
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                                                                                                                                                                                                                                                      COUNTRY: United States
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy d:
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                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-0CT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CORRENT APPLICATION DATA:
ANDITOWNITCH STATEMENT APPLICATION UNITED.
                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: FFRENCH-CONSTANT, RICHARD H.
APPLICANT: JACKSON, MEYER B.
TITLE OF INVENTION: DRUG AND PESTICIDE SCREENING
                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: PETER G. CARROLL
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REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/705-8410
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COMPUTER READABLE FORM:
TYPE: Floppy disk
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   457 EHGHGHGHH 465
                                                                                                                                      APPLICATION NUMBER: US/08/072,064 FILING DATE: 19930602 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PETER G. CARROLL
STREET: 220 Montgomery Street, Suite 2200
CITY: San Francisco
                  REFERENCE/DOCKET NUMBER:
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5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
    Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd
    DB
US-08-137-614A-26
US-08-072-064-1
US-08-072-064-6
US-08-072-064-6
US-08-072-064-8
PCT-US-20-8558-1
US-09-208-742-2
US-08-646-715-20
US-08-646-715-20
US-08-933-774-9
US-09-397-318A-6
US-09-397-570-4
US-09-057-570-7
US-08-758-250-7
US-09-057-570-7
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Query Match
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Matches 7; Conserv

Conservative

Score 50; DB Préd. No. 11; Mismatches

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Length 617; Indels

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US-08-137-614A-26  Sequence 26 Application US/08137614A  Sequence 26 Application US/08137614A  Patent No. 5487976  GENERAL INFORMATION: APPLICANT: Soderlund, David M. APPLICANT: Soderlund, Douglas C. APPLICANT: Henderson, Joseph E. TITLE OF INVENTION: Gene Encoding An Insect TITLE OF INVENTION: Gamma-Aminobutyric Acid (G NUMBER OF SEQUENCES: 31 CORRESPONDENCE ADDRESS: ADDRESSEE: Nixon, Hargrave, Devans & Doyle STREET: Clinton Square, P.O. Box 1051 CITY: Rochester STATE: New York COUNTRY: USA ZIP: 14603 ZIP: 14603 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COUNTRY: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1. CURRENT APPLICATION NUMBER: US/08/137,614A FILING DATE: 15-OCT-1993 CLASSIFICATION NUMBER: 34,103 REGISTRATION NUMBER: 34,103 REGISTRATION NUMBER: 34,103 REGISTRATION NUMBER: 34,103 REGISTRATION NUMBER: 363-1636 TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1600 INFORMATION FOR SEQ ID NO: 26: SEQUENCE CHARACTERISTICS: LENGTH: 617 mnino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-137-614A-26	28. 42 42.9 456 4 US-08-709-974A-11 29 41 41.8 542 1 US-08-382-505-2 30 41 41.8 542 1 US-08-38-709-3 31 41 41.8 542 1 US-08-623-679-3 32 41 41.8 903 1 US-08-750-332-1 34 41 41.8 903 1 US-08-750-332-1 35 40.5 41.3 800 1 US-08-750-532-4 36 40.5 41.3 800 1 US-08-785-052-4 40 40.8 13 1 US-08-784-077A-6 38 40 40.8 13 1 US-08-484-184-2 39 40 40.8 13 1 US-08-484-980-6 42 40 40.8 13 1 US-08-484-950-6 42 40 40.8 13 1 US-08-484-950-6 42 40 40.8 13 1 US-08-484-950-6 43 40 40.8 13 1 US-08-484-950-6 42 40 40.8 13 1 US-08-269-929-6 43 40 40.8 13 1 US-08-269-929-6 44 40 40.8 13 1 US-07-694-983-12 45 40 40.8 15 1 US-07-694-983-12
(GABA) Receptor Subunit	Sequence 11, Appl Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 3, Appli Sequence 1, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 2, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 11, Appli Sequence 11, Appli Sequence 11, Appli Sequence 12, Appli

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Search completed: July Job time: 992 sec
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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
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RA Cherry J.M., Cawley S., Dahlke C., Daveloport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveloport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveloport L.B., Dietz S.M.,
RA Cherry J.M., Cawley S., Dahlke C., Daveloport L.B., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McShrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry D.M., Melson D.L.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Rainzolo M., Pitman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainzert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Rainzolo M., Pitman G.S., Sanders R.D.C., Scheeler F., Shen H.,
RA Rainzert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang S.H., Wang X., Rabin W., Smith H.O.,
RA Globs R.A., Palaco G., Dann M., Strong S., Yao Q.A.,
RA Yel S., Yao G. D., Romp J., Romp J., Romp J., Nander S., Smith H.O.,
RA Shen S., Sanda M., Shong W., Zhou S., Zh
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE003678; AAF54238.1; -.
F1yBase; F9gn0037885; CG11718.
SEQUENCE 819 AA; 92141 MW; E7F295E74FE2A72B CR
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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MEDLINE=20196006; PubMed=10731132;
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Pred. No. 6.4;
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Post-processing: Minimum Match 0%
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Perfect score:
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US-08-594-031-102
US-08-872-979-8
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US-08-117-952-788
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US-08-750-717-2
US-08-983-534-3
US-09-204-764-3
US-09-203-7162-2
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US-09-203-7162-3
US-07-885-089B-30
US-07-885-089B-18
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US-09-077-977A-1
US-08-484-438-40
5514582-43
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US-08-737-715-2
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 US-07-885-089B-37
US-07-885-089B-36
US-07-885-089B-34
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                       Sequence 1, Appli
Sequence 40, Appl
Patent NO. 5214582
Patent NO. 5202428
Sequence 37, Appl
                                                                                        Sequence 2, Appli
Sequence 12, Appl
Sequence 30, Appl
Sequence 33, Appl
Sequence 16, Appl
Sequence 18, Appl
Sequence 18, Appl
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Sequence 100, Appli
Sequence 100, App
Sequence 102, App
Sequence 702, App
Sequence 787, App
Sequence 788, App
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NUMBER OF SEQUENCES: 6

CURRENT APPLICATION NUMBER: US/07

APPLICATION NUMBER: US/07

FILING DATE: 01-JUL-1987

SEQ ID NO:2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 1
5268270-2
                                                                                                                                                                                                                                                                                                                   US-08-468-558-5
                                                                                                                                                                                                                                                                                                                                                                                              Q
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                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
Matches '10; Conserv
                                                                                                                                                                                                                                                                                         Sequence 5, Application US/08468558 Patent No. 5877280
                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, V
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,558
FILING DATE: 06-JUN-1995
CILECTET ATTON. 425
                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                       APPLICANT: Wetmur, James G.
TITLE OF INVENTION: Cloning and Expression of Thermostable
TITLE OF INVENTION: MutS Genes and Proteins and Uses Therei
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSE: Hamilton Brook Smith & Bayrolds D C
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                  COUNTRY: Ut
ZIP: 02173
                                                                                                                                                           STATE:
                                                                                                                                                                        CITY: Lexington
                                                                                                                                                                                   ADDRESSEE:
STREET: Tw
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 1507
                                                                                                                                            Massachusetts
: United States of America
                                                                                                                                                                                   Two Militia Drive
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                      US/08/468,558
                                                                                                                                                                                               Brook,
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	37	37	37	37	37	3 <b>7</b>	37	37	37	37	37	37	37	37	37	37	37	37
	37.8			37.8														
	542	542	542	533	462	384	384	384	384	352	352	286	263	252	247	247	226	192
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ALIGNMENTS .	US-08-933-774-3	US-08-623-679-3	US-08-412-431-3	US-08-225-488-2	US-08-484-438-42	PCT-US92-09124-2	US-09-066-481-2	US-08-445-342A-2	US-07-783-706-2	US-08-913-581-2	US-08-785-052-2	US-09-203-716-1	US-07-906-983-2	US-07-885-089B-7	US-07-885-089B-8	US-07-885-089B-2	US-07-885-089B-35	US-08-208-008C-9
	Sequence 3, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 42, Appl	Sequence 2, Appli	Sequence 1, Appli	Sequence 2, Appli	Sequence 7, Appli	Sequence 8, Appli	Sequence 2, Appli	Sequence 35, Appl	Sequence 9, Appli					

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;Patent No. 5268270
; APPLICANT: Meyer, Thomas F.;
; TITLE OF INVENTION: PROCESS
301 HDNAGTVKGNGEHH-WKT 317
              1 HKNKG--KKNGKHNGWKT 16
                                                                                                                              Thomas f.; Halter, Roman; Pohlner, Johnnnes N: PROCESS FOR PRODUCING PROTEINS USING GRAM
                                                                       43.4%;
                                                                                                                                                                                                US/07/171,872
                                                                       Score 42.5; DB 6;
Pred. No. 1.5e+02;
                                                           Mismatches
                                                                                       DB 6;
                                                                                       Length 1507;
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                                                         Gaps
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Smith & Reynolds,

Proteins and Uses Therefor

Version

#1.

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; MOLECULE TYPE: protein US-08-737-715-2
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Best Local Similarity
Watches 8; Conserve
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                                             Matches
                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 5: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                              TELEFAX: (202)293-7860
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
SEQUENCE 1382 amino acid
                                                                                                                                                                                                                                                         NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-861-6240
                                                                                                                                                                                                                                                                                                                     FILING DATE: 12-MAY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Ebina, Yousuke
TITLE OF INVENTION: MUTANT HUMAN INSULIN RECEPTOR DNA
NUMBER OF SEQUENCES: 5
                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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                                           Local Similarity nes 7; Conserv
                                                                                                                                                      TOPOLOGY:
                                                                                                                                                                 TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: FILING DATE: 12-NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: 'D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Washington
                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
1 HKNKGKKNGK 10
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amino acid
GY: linear
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                                                                                                                                                                                  1382 amino acids
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2100 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                (202)293-7860
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                                             Conservative
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                                                                                                                                                     linear
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72.78;
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                                                          Score 41; I
Pred. No. 2
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Pred. No.
                                             Mismatches
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2.3e+02;
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                                                                      Length 1382;
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                                           Indels
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                                           0;
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                                          Gaps
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Best Local Similarity
"-+ches 5; Conserv:
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                                                                                                                                           US-08-594-031-102
                                                                                                                                                             RESULT
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US-08-594-031-100
                                                                                                           Sequence 102, Application US/08594031 Patent No. 5783182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 100, Appl Patent No. 5783182
                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO:
              APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: PAYOR
                                                                                                                                                                                                                                                                                                                                                                      MOLECCE NO
ANTI-SENSE: NO
ANTI-SENSE: NO
TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 20004-2400
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1363 HMNGGKKNGR 1372
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                          114 DGKHHGWR 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM COMPUTER: IBM COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET: 1299 Peni
CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Remenick, James REGISTRATION NUMBER: :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/0 FILING DATE: 30-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ Version 1.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                           8 NGKHNGWK 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: BAKER & BOTTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
1299 Pennsylvania Avenue, N.W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            376 amino acids
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                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                single
                                                                                                                                                                                                                                                                                       40.8%;
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                                                                                                                                                                                                                                                                                       Score 40;
Pred. No.
                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                      DB 1;
92;
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskette

20004-2400

COUNTRY:

USA

COMPUTER:

IBM Compatible

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Query Match
Best Local Similarity
Thes 5; Conserv
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; ORIGINAL SOURCE:
US-08-594-031-102
                                                                                                                                                                                                                                                                                                                                                                         US-08-872-979-8
                                                                                                                                                                                                                                                                                                                                                        Sequence 8,
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    squence 8, Application US/08872979 stent No. 6074844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/872,979
FILING DATE: Herewith
                                                                                                                                                                                                                                                            APPLICANT: Lal, Preeti
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW HUMAN MEMBRANE FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
                                                                                                                                                                                                                              NUMBER OF SEQUENCES: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: DOS
SOFTWARE: FastSEO Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                      COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                            APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                      114 DGKHHGWR 121
                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                     STREET: 3174 POI
CITY: Palo Alto
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 30-JAN CLASSIFICATION: 435
                                                                                                    MEDIUM TYPE: Diskette
                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                 ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                     94304
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                                                                                                                                                                    CA
                                                                                                                                                                                                   E: Incyte Pharmaceuticals, Inc
3174 Porter Drive
                                                                                                                                                     USA
                                                                                                                                                                                                                                                                                                           Hillman, Jennifer L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-terminal
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Pred. No. 92;
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US-08-872-979-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 787, Application US/08117952 Patent No. 5851760
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Best Local Similarity
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                                                                                 TELEFAX: 619-546-9392
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
                                                                                                                                      REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P4
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,952
FILING DATE: 07-SEP-1993
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
                                                                                                                                                                         APPLICATION NUMBER: US 0)
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Reiter, Stephen E.
REGISTRATION NUMBER: 31,
                                                                                                                                                                                                                                                                CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86 KKKNKKKGKEKGGK 99
                                                                                                                       TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Pretty, Schroeder, Brueggemann & Clark STREET: 444 South Flower Street, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                                                                                                                                               90071
                                 amino acid
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                                                   60 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Evans, Glen A.
Smith, Michael W
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GenBank
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57.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      METHOD FOR GENERATION OF SEQUENCE
                                                                                                                                                                                                                                               US 08/078,471
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Pred. No.
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1e+02;
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Best Local Similarity
Whiches 8; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-117-952-788
               Sequence 4, Application US/08477451 Patent No. 5928865
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                                                                                                                                                                                                                  Query Match
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Reiter, Stephen E. REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
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CORRESPONDENCE ADDRESS: Pretty, 8
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APPLICANT: Smith, Michael W.
TITLE OF INVENTION: METHOD FOR GENERATION OF SEQUENCE
TITLE OF INVENTION: SAMPLED MAPS OF COMPLEX GENOMES
                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                 Local Similarity les 8; Conserv
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                   10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/117,952 FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
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internal
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53.3%;
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Pred. No.
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Best Local Similarity
Matches 6; Conserv
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ZIP: 94608-2916
ZOMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS
MS-DOS/MS-DOS/MS-DOS
                                                                                                                                                                                                                                                                                  APPLICANT: MOORMANN, Robertus J. M.
APPLICANT: VAN RIJN, Petrus A.
TITLE OF INVENTION: Nucleotide Sequen
TITLE OF INVENTION: Strains, Polypept
TITLE OF INVENTION: Thereof for Diagn
TITLE OF INVENTION: Infections
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
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APPLICATION NUMBER: US/0
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
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TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                    COMPUTER READABLE FORM:
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NAME: McClung, Barbara G
REGISTRATION NUMBER: 33,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE:
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                                                                                                                                                                      COUNTRY: USA
ZIP: 22202
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              APPLICATION NUMBER: FILING DATE: 24-DEC
                                                                                                                                                                                                            STATE: Virginia
                                                                                                                                                                                                                              CITY: Arlington
                                                                                                                                                                                                                                                ADDRESSEE: YOUNG & THOMPSON STREET: 745 South 23rd Street
CLASSIFICATION:
                                                                                                                              MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                            Nucleotide Sequences of Pestivirus
Strains, Polypeptides Encoded by These Sequences and Use
Thereof for Diagnosis and Prevention of Pestivirus
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Pred. No.
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PRIOR APPLICATION DATA:

FILING DATE: APPLICATION NUMBER:

17-JUN-1994

EP 94201743.5

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; TOPOLOGY: 11; MOLECULE TYPE: US-08-750-717-2
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Best Local (
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-883-534-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PATCH, ANDREW J.
REGISTRATION UNMBER: 32,925
REFERENCE/DOCKET NUMBER: BO 3
TELECOMMUNICATION INFORMATION:
TELEPHAN: 703-521-2297
TELEFAX: 703-685-0573
               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3262 HKMKTLCPGSSLGRHNDW 3279
                                                                            NAME: Billings, Lucy J. RECISTRATION NUMBER: 36,749 RECESTRATION NUMBER: PETELECOMMUNICATION INFORMATION: TELEPHONE: 415.855-555
                                                                                                                                                                                                                                                                              OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Bandman, Olga
APPLICANT: La1, Preeti
APPLICANT: Corley, Weil C.
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                 CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 3898 amino acids
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APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Palo Alto
STATE: CA
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                                                                 TELEFAX: 415-845-4166
                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                    FILING DATE:
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LENGTH:
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44.4%;
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                                                                                                                  PF-0332 US
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Pred. No.
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329 HKNGGKSYIYSGSHDG 344

1 HKNKGKK---NGKHNG 13

Matches

Best Local Similarity
Matches 8; Conserv

Conservative

Indels

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Gaps

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US-09-204-764-3
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US-09-204-764-3
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                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 606 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: NEUTGMT01
CLONE: 1221143
                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                          IMMEDIATE SOURCE:
LIBRARY: NEUTGMT01
CLONE: 1221143
                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/204,764
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Corley, Neil C.
TITLE OF INVENTION: TWO NEW WD-40 PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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                                                                                                                                        TOPOLOGY:
                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                TELEFAX: 415-845-4166
                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET:
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                                                                                                                                    linear
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50.0%;
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Score 38.5; DB 3;
Pred. No. 2.4e+02;
2; Mismatches 3;
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Pred. No. 2
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US-08-916-576B-4

Sequence 4,

, Application US/08916576B 6171816

Patent No.

GENERAL INFORMATION:

APPLICANT:

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; MOLECULE TYPE: protein US-08-916-576B-4
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US-09-203-716-2
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Best Local Similarity 43...
7; Conservative
                                                                                                                                                                                                   Sequence 2, Application US/09203716
Patent No. 6001653
GENERAL INFORMATION:
                             APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
EILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (202) 371-2540 INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/024,347
FILING DATE: 23-AUG-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 14
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1100 NEW CITY: WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: STEFFE, ERIC K. REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                27 HNGLGKGFGDHIHWRT 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDRESS, GREGORY A. IVENTION: NOVEL HUMAN GROWTH FACTORS
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DILLON, PATRICK J.
EBNER, REINHARD
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Pred. No. 84;
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                                                                                                       ; MOLECULE TYPE: protein US-08-183-214-12
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; Sequence 12, Appl
; Patent No. 571681
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US-09-203-716-2
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; LENGTH: 293
; TYPE: PRT
                               Matches
                                                            Query Match
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                                                                                                                                                                               TELEFAX: 415-543-5043 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                         FILING DATE: 22-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
REFERENCE/DOCKET NUMBER: 1520
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/183,214
                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                               FILING DATE: 14-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/888,231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
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                              Local Similarity
nes 7; Conserv
                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U:
ZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY:
                                                                                                                                                                  LENGTH:
1 HKNKGKKNGKHNGWK 15
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: CA
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                                                                                                                                                               345 amino acids
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                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nightingale, Maria S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stanley,
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                                            Score 38; I
Pred. No. 1.
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Pred. No. 1.4e+02;
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Search completed: July 6, 2001, 09:10:24 Job time: 190 sec

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Maximum Match 100%
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Maximum DB seq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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length: 2000000000
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## ALIGNMENTS

A; Mccession: S32422, MOLD: 3222334 A; Accession: S32422, MOLD: 3222334 A; Molecule type: mRNA A; Residues: 'ANSM',253-377 < AUE> A; Note: differences are due to known cloning artifacts R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985 A; Tittle: The amino acid sequence of the light chain of human high-molecular-mass kini A; Tittle: The amino acid sequence of the light chain sequence was not determined A; Reference number: A91153; MUID:86030270 A; Accession: A91153 A; Molecule type: protein A; Residues: 379-644 < LOT> A; Mueller type: protein A; Resilermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. A; Tittle: Completion of the primary structure of human high-molecular-mass kininogen. A; Residues: 'Z', 20-380 < KELL> A; Residues: 'Z', 20-380 < KELL> R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. A; Tittle: Anino acid sequence of the light chain of human high molecular mass kininoge A; Reference number: A27899 A; Accession: A27899 A; Accession: A27899	RESULT 1  KIGHUH1  KININGEN, HMW precursor [validated] - human  Kiningen, HMW precursor [validated] - human  Kiningen, HMW precursor [validated] - human  N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokiningen; prokiningen  N;Contains: bradykinin (kallidin I); HMW kiningen I; HMW kiningen II; low molecular  C;Species: Homo sapiens (man)  C;Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.  Biochemistry 23, 5691-5697, 1984  A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide

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A;Title: Purification from human plasma of a A;Reference number: S68059; MUID:96033974 A;Accession: S68059 Portein A;Residues: 431-434 <STR>
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; J. Biol. Chem. 260, 8610-8617, 1985
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A; Molecule type: protein
A; Residues: 1-19; 189-192; 310-314; 381-389
A; Residues: 1-19; 189-192; 310-314; 381-389
R; Kato, H.; Matsumura, Y.; Maeda, H.
A; Title: Structural organization of the human A; Reference number: A92545; MUID: 85234583 A; Contents: annotation; gene organization
                                                                                                                                                                                                                                         A; Molecule type: protein
A; Residues: 450-452, 'X', 454, 'X', 456 <LIT>
R; Straczek, J.; Maachi, F.; le Nguyen, D.;
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: protein
A:Residues: 264-359, 'N', 361-375 <LEN2>
R:Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A:Title: Human mast cell tryptase isoforms:
A:Reference number: S55239; MUID:95251593
A:Accession: S55239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lenarcic, B.; Krasovec, M.; Ritonja, A.;
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C
A;Reference number: S14303; MUID:91192133
A;Accession: S14447
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A; Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
R; Mindrolu, T.; Carretero, O.A.; Proud, D.; Walz, D.;
R; Mindrolu, T.; Carretero, D.; S19-526, 1986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Kato, H.; Matsumura, Y.; Maeda, H. FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues of bradykinin A;Reference number: A61495; MUID:88211869
A;Accession: A61495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Reference number: S02482; MUID:89076517
A;Accession: S02482
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A; Residues: 381-389 < MAE;
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A; Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 380-389 <KAT3>
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A; Residues: 381-389 < KAT2>
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A;Title: Human cathepsin B and cysteine proteinase inhibitors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein A; Residues: 380-389 <SAS>
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J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of
A;Reference number: A31905; MUID:89034061
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                                                                                                Takagaki,
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                                            kininogen
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                                                                                             Y.; Miyata,
                                              gene and a
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                                                                                             T.; Nakanishi,
                                              model for its evolut
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A;Accession: A91923 A;Molecule type: protein A;Residues: 376-391 <KAT

<KAT>

Iwanaga,

s.;

H3

A; Title: Studies on the structure of bovine kininogen: A; Reference number: A91923; MUID: 70180420

R; Kato, H.; Nagasawa, S.; Suzi J. Biochem. 67, 313-323, 1970

Suzuki,

GB:K01758; NID:g493; ki, T.

PIDN:CAA24736.1;

PID: 9494

cleavages

of.

disulfide

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N;Contains: bradykinin (Kallium,, ......)
N;Contains: bradykinin (Kallium,, ......)
C;Species: Bos primigenius taurus (cattle)
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Date: 14-Nov-1983 #text_ch
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F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F;431-434/Product: low molecular weight growth promoting factor #status experimental
F;19/Modified site: pyrrolidone carboxyllc acid (Gln) (in mature form) #status experi
F;28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond
F;28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond
F;28-910-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond
F;48/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;169,205,294/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;379-380/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;389-390/Cleavage site: 375-353,628/Binding site: carbohydrate (Thr) (covalent) #status
F;401,533,542,546,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status
A;Accession: A01282
A;Molecule type: mRNA
A;Residues: 1-619 <KIT>
A;Cross references: GB:V01492;
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F;19-131/Domain: cystatin homology <CYI>
F;142-253/Domain: cystatin homology <CYZ>
F;242-253/Domain: cystatin homology <CYZ>
F;264-375/Domain: cystatin homology <CYZ>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <BDY>
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F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>
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A; Contents: annotation; bradykinin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            kininogen,
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C; Comment:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               names: alpha-2-thiol proteinase inhibitor; preprokininogen
bradykinin (kallidin); kininogen I; kininogen II; prokinin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carbohydrate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 98; DE
Pred. No. 8.4
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (covalent)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                8.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DΒ
                                                                                                                                                                                                                                                                                                                                                                                                               T.; Nawa, H.; Nakanishi, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 644
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release of bradykinin.
                                                                                                                                                                                                                                                                                                         molecular weight kini
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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J. Biochem. 79, 1
A;Title: Primary
A;Reference numbe.
A;Accession: A919
A;Molecule type:
A;Residues: 387-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C/Superfamily: kininogen; Cystatin homology
C/Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F/1-18/Domain: signal sequence #status predicted <SIG>
F/19-619/Product: HMW kininogen II #status predicted <ANT>
F/19-310/Product: HMW kininogen II heavy chain #status experimental <HCH>
F/19-130/Domain: cystatin homology <CYI>
F/141-252/Domain: cystatin homology <CYI>
F/261-372/Domain: cystatin homology <CYI>
F/377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F/377-386/Product: bradykinin (kallidin II) #status experimental <CH>
F/378-386/Product: bradykinin (kallidin II) #status experimental <CH>
F/387-619/Product: bradykinin (kallidin II) #status experimental <CH>
F/387-619/Product: hMW kininogen II light chain #status experimental <CH>
F/388-619/Product: HMW kininogen II light chain #status experimental <CH>
F/389/Region: glycine/histidine/lysine-rich
F/37/S68/Region: glycine/histidine/lysine-rich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F:47/Binding site: carbohydrate (Asn) (covalent) #status absent
F:87,168,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F:197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F:376-377/Cleavage site: Met-Lys (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Note: article in Japanese C;Comment: The HMW kiningen precursor is produced from the same gene as the LMW form C;Comment: Kiningen is a cysteine proteinase inhibitor, takes part in initiation of C;Comment: The glycine/histidine/lysine-rich region of HMW kiningen light chain is im C;Comment: Bradykinin, released from kiningen by kallikrein, is a potent vasodilator, xyproline residue is present in the kiningen prior to the release of bradykinin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A:Molecule type: protein
A:Residues: 456-496 <HA2>
R:Sueyoshi, T.; Miyata T.; Hashimoto, N.; Kato,
J. Biol. Chem. 262, 2768-2779, 1987
A:Title: Bovine high molecular weight kininogen.
A:Reference number: A92627; MUID:87137530
A:Accession: B29559
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A;Title: Disulfide bonds in bovine HMW kininogens
DЬ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A94300
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A; Residues: 'Z', 20-104, 'E', 106-256, 'XX', 257-376
R; Lottspeich, F; Kellermann, J; Henschen, A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Contents: annotation; disulfide bonds
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                                                                                                                                                                                                                                                                                                                                  380/Modified site: 4-hydroxyproline (Pro) *status predicted (386-397/Cleavage site: Arg-Ser (Kallikrein) *status experimental (386-397/Cleavage site: arg-Ser (Kallikrein) *status experimental (396,400,404,510/Eninding site: carbohydrate (Ser) (covalent) *status experimental (397,398,518,522,534,546,551,568/Eninding site: carbohydrate (Thr) (covalent) *status experimental (496-497/Cleavage site: Arg-Thr (kallikrein) *status experimental
                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Accession: A91941
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J. Biochem. 152, 307-314, 1985
482
                                                                   1 HKNKGKKNGKHNGWKT 16
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HKNKGKNNGKHYDWRT
                                                                                                                                               l Similarity
12; Conser
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of bovine plasma high-molecular-weight kininogen. The MUID:76260155
                                                                                                                                                                                   .5%;
                                                                                                                                           Score 75; DB Pred. No. 0.001; Mismatches
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0.0019;
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                                                                                                                                                                                                                   Length 619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ₩.
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                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                                                          (covalent) #status
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Miyata,
                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       as the LMW form as n initiation of the light chain is imposed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T.;
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RESULT

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F;87,168,169,204/Binding site: carbohydrate (Asn.) (covalent) #status experimental F;136/Binding site: carbohydrate (Asn.) (covalent) #status experimental F;197/Binding site: carbohydrate (Thr.) (covalent) (partial) #status experimental F;197/Binding site: carbohydrate (Asn.) (covalent) (partial) #status experimental F;378-379/Cleavage site: Met-Lys (kallikrein) #status experimental F;382/Modified site: 4-hydroxyproline (Pro) #status experimental F;388-389/Cleavage site: Met-Lys (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                            F:141-252/Domain: cystatin homology <CY2>
F:263-374/Domain: cystatin homology <CY3>
F:263-384/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
F:389-621/Product: HMW kininogen I light chain #status experimental <LCH>
F:417-488/Region: glycine/histidine/lysine-rich
F:417-488/Region: glycine/histidine/lysine-rich
F:19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F:27-591.82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide
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C; Comment: The HMW kininogen precursor is produced from the same gene as the LMW form C; Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is i C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the kininogen prior to the release of bradykinin. C; Superfamily: kininogen; cystatin homology
C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d F; L-18, Domain: signal sequence #status predicted <SIG>
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A; Molecule type: protein
A; Residues: '2',20-123,'I',125-127,'I',129-378 <SUE>
R; Lottspeich, F; Kellermann, J; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
By J. Biochem. 152, 307
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;19-379/Product: HMW kininogen I heavy chain #status experimental F;19-130/Domain: cystatin homology <CY1>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Disulfide bonds in bovine HMW A; Reference number: A94300 A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Sueyoshi, T.; Miyata, T.; Kato, H.;
Seikagaku 56, 808, 1984
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J. Biochem. 77, 55-68,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: protein A; Residues: 378-393 < KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Accession: A91923
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A; Reference number: A91923;
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A; Residues: 1-621 <KIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Kato, H.; Nagasawa, S.; Suzuki, Biochem. 67, 313-323, 1970
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HMW prokininogen I #status predicted <MAT>
                                               4-hydroxyproline (Pro) #status predicted
ite: Arg-Ser (kallikrein) #status experimental
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S.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid sequence, positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hayashida,
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#text_change 21-Jan-2000

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Qy
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A; Reference number: Z21567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    probable integral membrane protein - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35064
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Map position: 1
A; Introns: 52/1; 77/3
C; Superfamily: Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               conserved hypothetical protein SPAC7D4.05 - fission yeast (Schizosaccharomyces C;Species: Schizosaccharomyces pombe C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 17-Mar-2000 C;Accession: T39083
R;Gentles, S.; Churcher, C.M.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
T39083
        RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data A; Reference number: Z21826 A; Accession: T39083
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                                                                                                                                                                                                                                                                                                A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-275 <SEE>
                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;EXperimental source: strain 972h-; cosmid c7D4
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A; Residues: 1-225 <GEN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                  Genetics:
Gene: SCOEDB:SC4G6.04c
                                                                                                                                                                       Query Match
Best Local
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7; Conser
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                                                                                                                                                   Conservative
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75.0%;
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                                                                                                                                                                                                                               RESULT
T49422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fraser, C.M.; Norris, S.J.; Weinstock, G.M.; White, O.; Sutton, G.G.; Dodson, Tson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Chidambaram, M.; Utterback, they, L.; Weidman, J.; Smith, H.O.; Penter, J.C. Science 281, 375-388, 1998
A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete
A;Status: preliminary A;Molecule type: DNA
                                         A; Reference number: 225022
A; Accession: T49422
                                                                                R;Schulte, U.; Aign, V.; submitted to the Protein
                                                                                                                                            RAD57 related protein [imported] - Neurospora N;Alternate names: protein B17C10.30 C;Species: Neurospora crassa C;Date: 02-Jun-2000 #sequence_revision 02-Jun-
                                                                                                                                                                                                                                                                                                                      Вþ
                                                                                                                                                                                                                                                                                                                                                        Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ribonuclease H (rnhA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 22-Jun-1999
C;Accession: G71333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Gene: FlyBase:Dhyd/mst101
A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mst101-1 protein - fruit fly (Drosophila hydei) C;Speckes: Drosophila hydei C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 C;Accession: S34153
                                                                                                                           C; Accession: T49422
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Superfamily: ribonuclease H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE001215; GB:AE000520; NID:g3322631; PIDN:AAC65340.1; PID:g332A;Experimental source: strain Nichols
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-169 <COL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Reference number: A71250; A; Accession: G71333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X73480; NID:g313199; PID:g313200
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Gene: TP0353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status:
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A; Residues: 1-344 <NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Reference number: S34153
A; Accession: S34153
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                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 7
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Matches 9; Conserv
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                                                                                                                                                                                                                                                                                                                      103 KHNGWKT 109
                                                                                                                                                                                                                                                                                                                                                           10 KHNGWKT 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                        Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann,
                                                                                                                                                                                                                                                                                                                                                                                               46.9%; ilarity 100.0%; Conservative
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                                                                                  Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence of Treponema pallidum, 50; MUID:98332770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.0%;
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Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                               %; Score 46; DB
%; Pred. No. 10;
0; Mismatches
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Pred. No.
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the syphilis spirochete

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May 2000

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Holland, R.;

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Gaps

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R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd A.; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E. Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

Nature 390, 249-256, 1997

N; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.

Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maucell, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A. Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serou akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Mipat, A.; Yamamoto, H.; Yamane, K.; Yata, K.; Yoshida, K.; Althors: Yoshikawa, H.; Danchin, A.

A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A. Accession. H6378
                                     C;Accession: T05352
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasewes, H.W.; Mayer, K.F.X.; Schueller, C.
submitted to the Protein Sequence Database, February 1999
                                                                                                                                              hypothetical protein F8B4.120 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
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Best Local Similarity
"~+~hes 9; Conserv
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A;Cross-references: EMBL:AL355926; GSPDB:GN00116; NCSP:B17C10.30
A;Experimental source: BAC clone B17C10; strain OR74A
C;Genetics:
                                                                                                                                                                                                                                                                                                                                    Вb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     F;9-269/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:Z99112; GB:AL009126; NID:g2633902; A;Experimental source: strain 168
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A; Residues: 1-648 < KUN>
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A; Reference number: A; Accession: T05352
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                                                                                                                                                                                                                                                            RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Superfamily: Bacillus subtilis probable protein kinase
;Keywords: ATP; phosphotransferase; protein kinase
;9-269/Domain: protein kinase homology <KIN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Species: Bacillus subtilis; Species: Bacillus subtilis; Species: Bacillus subtilis; Species: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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les 8; Conserv
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                          Z15409
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64.38;
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Pred. No.
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Mismatches
                                                                           Buysshaert, C.; Dasseville, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
34;
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A;Map position: II
C;Superfamily: globin; globin homology
C;Keywords: chromoprotein; heme; iron;
F;1-16/Domain: signal sequence #status
                                                                                                                                                                                                                                                                                                 hemoglobin V precursor - midge (Chironomus thummi piger)
C;Species: Chironomus thummi piger
C;Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Description: (EC 3.4.24.15) [validated C;Superfamily: oligoendopeptidase F C;Keywords: hydrolase; metalloproteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Characterization of PepB, a group B streptococcal oligopeptidase A;Reference number: Z25445; MUID:96333389
A;Accession: T51748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         thimet oligopeptidase (EC 3.4.24.15) PepB [validated] - Streptococcus agalactiae C;Speckes: Streptococcus agalactiae C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 15-Sep-2000 C;Accession: T51748
                                                                                  A; Gene: HbV
                                                                                                    C; Genetics:
                                                                                                                         A;Cross-references: EMBL:X56271; NID:g7069;
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-163 <HAN>
                                                                                                                                                                                submitted to the EMBL Data Library, September 1990 A;Description: Complete nucleotide sequence of a ha A;Reference number: S21627 A;Accession: S21633
                                                                                                                                                                                                                                                                R;Hankeln,
                                                                                                                                                                                                                                                                                   C; Accession: S21633
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Note: F8B4.120
C; Superfamily: cyclophilin homology
F; 6-162/Domain: cyclophilin homolog;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4
A; Introns: 26/3; 45/1; 74/3; 83/1; 122/2; 165/1; 270/2; 307/1; 731/2; 754/2
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A; Residues: 1-857 <BEV>
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Pred. No.
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A; Experimental : C; Genetics:
A; Gene: ftsX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-645 <BOND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Rod and cone photoreceptor cells express distinct genes for cGMP-gated channel A;Reference number: I50630; MUID:93264082 A;Accession: I50680
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alpha subunit of rod photoreceptor CNG-channel - chicken C; Species: Gallus gallus (chicken) C; Date: 13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change 13-Aug-1999 C; Date: 13-Sep-1996 *sequence_revision 13-Sep-1996 *text_change 13-Aug-1999 C; Date: 13-Sep-1996 *sequence_revision 13-Sep-1996 *sequence_r
RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C; Accession: I50680
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QΥ
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Best Local Similarity
"~+~hes 8; Conserv?
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F;19-162/Domain: globin homology <GLB>
F;76/Binding site: oxygen (His) (distal axial ligand) *status predicted
F;711/Binding site: heme iron (His) (proximal axial ligand) *status predicted
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A; Residues: 1-298 <STO>
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Nucleic Acids Res. 28, 4317-4331,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ъ
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                                                                                                         HKNKDKKKGK 99
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Res. 28, 4317-4331, 2000
Hete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
Imber: A83650; MUID:20263314
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34;
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                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein yljD [imported] - Lactococcus lactis subsp. lactis (strain II140 c;Species: Lactococcus lactis subsp. lactis C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 23-Mar-2001 C;Accession: A86772 R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Eh Genome Res. in press, 2001 Genome Res. in press, 2001 A;Title: The complete genome sequence of the lactic acid bacterium.
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                                                                                                                                                                                       A; Gene: yljD
                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-81 <STO>
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A; Accession: A86772
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Best Local S
Matches 8
                                                                            Local Similarity hes 8; Conserv
35
                        2 KNKGKKNGKHN 12
KKNGKKNMKHN 45
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72.78;
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Pred. No.
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Search completed: July 6, 2001, 09:18:03 Job time: 649 sec

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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 ,
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Copyright (c) 1993 - 2000
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14.581 Million cell updates/sec
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MEDITINE=90255622; PubMed=4952632;

Pierce J.V.;

"Structural features of plasma kinins and kininogens.";
Fed. Proc. 27:52-57(1968).

DISULFIDE BONDS.
Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
"Disulfide bonds in bovine HMW kininogens.";

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                                                                                                                                                                                                       Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; Thiol protease
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MIM; 228960;
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SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
TISSUB SPECIFICITY: PLASMA.
TISSUB SPECIFICITY: PLASMA.
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       MEDLINE=87137530;
                          Kitamura N., Takagaki Y., Furuto S., Tanaka T., "A single gene for bovine high molecular weight weight kininogens.";
Nature 305:545-549(1983).
                                                                                Eukaryota; Metazoa;
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Kato H.,
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                                                                                                                INHIBITOR) (CONTAINS:
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Hayashida H.,
                                        and
                                              Nawa
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(POTENTIAL).
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                                         low molecular
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                                              H., Nakanishi
                                                                                       Bovoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HMW-KININOGEN LAYS AN INHIBITORS OF THIOL PROTEASES; (2)
HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRINGESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIDOROTICCTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACCTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han Y.N., Komiya M., Iwanaga S., Suzuki T.; Studles on the primary structure of bovine high-molecular-weight wininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
                                                          InterPro; IPR000010; -.
InterPro; IPR002395; -.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
                                                                                                                                                                        EMBL; V01492; CAA24736.1; -.

EMBL; V01492; CAA24737.1; ALT_SEQ.

PIR; A01282; KGB042.

PIR; B29559; B29559.

HSSP; P04129; IAFI.
               Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Han Y.N., Kato H., Iwanaga S., Suzuki T.;
"Primary structure of bovine plasma high-molecular-weight kininogen.
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus of the bradykinin moiety.";
J. Blochem. 79:1201-1222(1976).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=70180420; PubMed=4986212; Kato H., Nagasawa S., Suzuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 456-496 MEDLINE-75170265; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=76260155; PubMed=956151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ACTION).

SUBCELLULAR LOCATION: EXTRACELLULAR.

SUBCELLULAR LOCATION: EXTRACELLULAR.

ALTERNATIVE PRODUCTS: HAW II AND LAW II KININOGEN PRECURSORS PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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response
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RESULT 3

KNH1_BNH1_B

AC P01044

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Best Local S
Matches 12
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Nature 305:545-549/19
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P01044;
21-JUL-1986 (Rel. 0
21-JUL-1986 (Rel. 0
01-JUN-1994 (Rel. 0
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CARBOHYD
                                                               SEQUENCE OF 19-378.
SEQUENCE OF 19-378.
MEDLINE-87137530; PubMed-3546295;
Sueyoshi T., Miyata T., Hashimoto
Miyata T., Iwanaga S.;
                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=84014106; PubMed=6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T.,
"A single gene for bovine high molecular weight
                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebra
Mammalia; Eutheria; Cetartiodactyla; Ruminantia;
Bovidae; Bovinae; Bos.
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CHAIN
                                                 "Bovine high molecular weight kininogen. positions of carbohydrate chains and dis
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SEQUENCE OF 378-393
MEDLINE=70180420; Po
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                                       portion.'
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                               Chem.
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                              262:2768-2779(1987)
                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                . 01, Created)
. 01, Last sequence update)
. 29, Last annotation update)
PRECURSOR (THIOL PROTEINASE
 PubMed=4986212;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       68710
                                                                                                                                                                                                                                                                                                                                                                                                       76.5%;
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CYSTATIN-LIKE 1.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 3.

PYRROLIDONE CARBOXYLIC A

N-LINKED (GLCNAC. . . ).
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Pred. No.
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N-LINKED (GLCNAC.
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-> V.
-> K.
F04320A8EB0EE0DA CRC64;
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                                                                              Z
                                                  disulfide
                                                                              Kato H., Hayashida
                                                                                                                                                                                                                                                                                                                                                                                                     DB 1; 1
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minantia; Pecora;
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                                                  bridges in the heavy
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and low molecular
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                                                            sequence,
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HAW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREALLIKERIN AND FACTOR XI USET
TO FACTOR XII; (3) HAW-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOUTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HAW-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIDOROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACCTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
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J. Blochem. 77:55-68(1975).
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PROSITE; PS00287; CYSTATIN; 2.
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PIR; A29559; A29559.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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ALTERNATIVE PRODUCTS: HMW I AND LMW I KININGGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININGGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collab
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  Suzuki T.;
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Q08695;
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use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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- FUNCTION: POSSIBLE STRUCTURAL ROLE IN TASSOCIATED WITH AXONEMAL STRUCTURES.

- I - SUBCELLULAR LOCATION: CYTOPLASMIC (BY SOCIETY OF THE PROPERTY OF THE PROPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   repetitive, axoneme-associated protein with differential abundance Y chromosomal deletion mutant flies.";

Dev. Biol. 162:414-475.7674.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1995
01-OCT-2000
                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPERMATID BUNDLES.
-!- DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL
-!- POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MST101(1
                                                                                                                                                                                                                                                                   EMBL;
                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                             between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=94200512; PubMed=8150205;
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                                                                                                                                                                                                                     PIR; S34153; S34153.
HSSP; P01032; 1C5A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neesen J., Buenemann H., Heinlein
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                                                                                                                                                                                                                                                                                                                                                                                                                      SWISS-PROT entry is copyright. It is produced through a ceen the Swiss Institute of Bioinformatics and the EMBL
                                                                                                                                                                                                                                                                 X73480; CAA51875.1;
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12; Conser
                    Similarity
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epeat; Multigene family.
58 337 19 x 16
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228
263
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(Rel. 31, Last sequence update)
(Rel. 40, Last annotation update)
CIATED PROTEIN MST101(1).
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247
266
339
369
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                    48.0%;
69.2%;
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                                                                                                           MW;
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                    Score 47; Pred. No.
                                                                                                                              19 x 16 AA APPROXIMATE TANDEM REPEATS K-K-C-X-E-X-A-[KQ]-K-X-X-E-X-A-X.
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                                                                                                           24C65D2510387E2A
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                                                                                                                                                                                                                                                                                                                                 noved. Usage by and for commercial
  (See http://www.isb-sib.ch/announce/
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                         ω
                    DB 1;
3.1;
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                                         Length 344;
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                                                                                                                                                                                                                                                                                                                                                                                                    restrictions
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SAFFE
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                                                                    PEPB_STRAG
                                                                                    RESULT
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Best Local Similarity
PEPB_STRAG
Q53778;
15-JUL-1999
15-JUL-1999
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083372;
                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=9833770; PubMed=965876;
Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
Dodson R., Gwinn M., Hickey E.K., Clayron R., Ketchum K.A.,
Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Petterson J.,
Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                               METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- FUNCTION: THIS ENZYME IS AN ENDONUCLEASE THE
RNA-DNA HYBRIDS SPECIFICALLY (BY SIMILARITY)
-!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of Treponema pallidum, spirochete.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=NICHOLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Treponema pallidum.
Bacteria; Spirochaetales; Spirochaetaceae; Treponema
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RIBONUCLEASE H (EC RNHA OR TP0353.
                                                                                                                                                                                                                                                    SEQUENCE
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METAL
                                                                                                                                                                                                                                                                                                                                                                          EMBL; AE001215; AAC65340.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Science 281:375-388(1998).
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                                                                                                                          103 KHNGWKT 109
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE RNASE H FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MONOESTER.
                                                                                                                                                    KHNGWKT 16
                                                                                                                                                                                                                                                                                                                                    PF00075; rnaseH;
                                                                                                                                                                                                                                                                                                                                                               TP0353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       the Swiss Institute of Bioinformatics
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                                                                                                                                                                                                                                                 Nuclease; Endonuclease; Magnesium.

12 12 MAGNESIUM (BY SIMILARITY).
63 63 MAGNESIUM (BY SIMILARITY).
87 87 MAGNESIUM (BY SIMILARITY).
151 151 MAGNESIUM (BY SIMILARITY).
169 AA; 18184 MW; 164311053632B047 CRC64;
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169
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(Rel.
(Rel.
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
H (EC 3.1.26.4) (RNASE H).
                                                                                                                                                                                 Conservative
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                                                       STANDARD;
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38, Created)
38, Last sequence update)
38, Last annotation update)
                                                                                                                                                                                            46.9%;
100.0%;
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                                                                                                                                                                                            Score 46;
Pred. No.
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RESULT 7
GLBV_CHITP
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Matches
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                                                                                                                                                                                                                                         GLBV_CHITP
P29243;
01-DEC-1992
01-DEC-1992
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COLIGAN J.E., Egan M.L., Pritchard D.G.;

COLIGAN J.E., Egan M.L., Pritchard D.G.;

Characterization of PepB, a group B streptococcal oligopeptidase.";

Infect. Immun. 64:3401-3406(1996).

Infect. Immun. 64:340
                                                                                                        Chironomus thummi piger (Midge).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Nematocera;

Chironomoidea; Chironomidae; Chironominae; Chironomus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
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      Metalloprotease;
      Hydrolase;
      Zinc

      METAL
      386
      386

      ACT_SITE
      387
      387
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      METAL
      390
      390
      ZINC

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                                                                                   NCBI_TaxID=7156;
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MEROPS; M03.008;
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                    Hankeln T.,
                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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FE; PS00142; ZINC_PROTEASE; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 53. 7; Conservative
1 (SEP-1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR000130; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             email to license@isb-sib.ch).
                                                                                                                                                                                                                  (Rel. 24, Created)
(Rel. 24, Last sequence update)
(Rel. 35, Last annotation updat
v PRECURSOR (HBV).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC44215.1;
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                                                                                                                                                                                                                                                                                                                               STANDARD;
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                      P.,
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Schmidt E.R.,
the EMBL/GenB
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  EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (EC
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
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                                                                                          Diptera; Nemaccominae; Chironomus.
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                                                                                                                                                                                                                                                                                                                               163
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                      Broecker M.
                                                                                                                                                                                                                                         update)
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RESULT 8
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01-NOV-1997 (Rel. 35, Last sequence up
01-NOV-1997 (Rel. 35, Last annotation
CYCLIC NUCLEOTIDE GATED CHANNEL, ROD F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
01-NOV-1997 (Rel.
                                           between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (CNG CHANNEL 3) (CNG-3) (CNG3). Gallus gallus (Chicken).
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use by non-profit institutions as lomodified and this statement is not remo
                                                                                                                                                                                                                                                                                                              Boenigk W., Altenhofen W., Mueller F., Dose A., Illing M. Molday R.S., Kaupp U.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNG3_CHICK
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HSSP; P02229; 1ECO.
                                                                                                                                                                                                                                                       Neuron 10:865-877(1993).
                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=93264082; PubMed=7684234;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Archosauria; Aves;
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PRINTS; PR00611; ERYTHCRU
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InterPro; IPR002336; -.
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                       European Bioinformatics Institute.
                                                                                                                                                                      FUNCTION: VISUAL SIGNAL TRANSDUCTION IS MEDIATED BY A G-PROTEIN COUPLED CASCADE USING CGMP AS SECOND MESSENGER. THIS PROTEIN CAN BE ACTIVATED BY CYCLIC GMP WHICH LEADS TO A OPENING OF THE CATION CHANNEL AND THEREBY CAUSING A DEPOLARIZATION OF ROD
                                                                                                                SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN. SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE-GATED CATION CHANNEL
                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                              PHOTORECEPTORS
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a; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
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CHLOROPLAST
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NCBI_TaxID=2787;
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                modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                        between the Swiss Institute of Bioinformatics and the Ethe European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content
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P51298;
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PROSITE; PS00889; CNMP_BINDING_2; 1.
PROSITE; PS0082; CNMP_BINDING_3; 1.
Ionic channel; Ion transport; CAMP-binding; Transmembrane; Vision;
                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                               Plant Mol. Biol. Rep. 13:333-335(1995).
                                                                                                                                                                                                                          genome
                                                                                                                                                                                                                                                                STRAIN-AVONPORT;
Reith M.E., Munholland
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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P09790;
01-MAR-1989
01-MAR-1989
01-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
15-JUL-1998 (Rel. 36,
HYPOTHETICAL 43.4 KDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00333; Ribosomal_S5; 1. PROSITE; PS00585; RIBOSOMAL_S5; 1. Ribosomal protein; Chloroplast. SEQUENCE 174 AA; 18294 MW; 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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NCBI_TaxID=4896;
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Neisseria gonorrhoeae.
                                            PROTEASE).
                                                                    IGA-SPECIFIC
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(Rel. 10, Last sequence update)
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C SERINE ENDOPEPTIDASE PRECURSOR
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Best Local
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                                      GARP_PLAFF STANDARD; PRT; 678 AA. P13816; P13816; O1-JAN-1990 (Rel. 13, Created) O1-JAN-1990 (Rel. 13, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) GLUTAMIC ACID-RICH PROTEIN PRECURSOR.
                            GARP.
                                                                                                                                                                                                                                                                                                                                                     PROPEP
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EW the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entities requires a license agreement (See http://www.isb-s
Plasmodium falciparum (isolate FC27 Eukaryota; Alveolata; Apicomplexa; I
                                                                                                                                                                                                                                                                                                               SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bachovchin W.W., Plaut A.G., Flentke G.R., Lynch M., Kettner C.A.;
"Inhibition of IgAl proteinases from Neisseria gonorrhoeae and Hemophilus influenzae by percentage of the profile boronic acids.";
J. Biol. Chem. 265:3738-3743(1990).
-!- FUNCTION: THIS PROTEASE IS SPECIFIC FOR IMMUNOGLOBULIN A.
-!- CATALYTIC ACTIVITY: CLEAVAGE OF IMMUNOGLOBULIN A MOLECULES AT CERTAIN PRO-|-XAA BONDS IN THE HINGE REGION. NO SMALL MOLECULE SUBSTRATES ARE KNOWN.
-!- SUBCELLUIAR LOCATION: SECRETED.
-!- DOMAIN: THE SIGNAL PEPTIDE GUIDE THE PRECURSOR TO THE PERIPLASMIC
                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            Fransmembrane;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria; beta subdivision;
                                                                                                                                                                          326
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN. THE HELPER DOMAIN IS THEN RELEASED BY AUTOPROTEOLYSIS. SIMILARITY: BELONGS TO PERTIDASE FAMILY S6 (SERINE PROTEASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SPACE, AND THE CARBOXY-TERMINAL HELPER DOMAIN ASSOCIATES WI' OUTER MEMBRANE TO FORM A PORE FOR EXCRETION OF THE PROTEASE
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                                                                                                                                                                          HDNAGTVKGNGEHH-WKT
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(isolate FC27 / Papua New Guinea)
Apicomplexa; Haemosporida; Plasmo
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CLEAVAGE (AUTO-).
CLEAVAGE (AUTO-).
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  Plasmodium
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Q9ZJC3;
                                                                                                                                                                                                                                             gastric pathogen Helicobacter pylori.";
Nature 397:176-180(1999).
-i- FUNCTION: THE NATURAL SUBSTRATE FOR
TRNAS WHICH DROP OFF THE RIBOSOME DU
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30-MAY-2000 (Rel. 39, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29) (PTH).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               the European Bioinformatics Institute. use by non-profit institutions as 10 modified and this statement is not rem
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Helicobacter pylori J99 (Campylobacter pylori J99).
Bacteria; Proteobacteria; epsilon subdivision; Helicobacter group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PTH OR JHP1390.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=89040048; PubMed=2903445; Triglia T., Stahl H.-D., Crewther
                                                                                                                                                                                               Genomic sequence comparison of two unrelated isolates pathogen Helicobacter pylori.";
                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=85963;
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                    SUBCELLULAR LOCATION: CYTOPLASMI
                                                                CATALYTIC ACTIVITY: N-SUBSTITUTED AMINOACYL-TRNA + H(2)O N-SUBSTITUTED AMINO ACID + TRNA.
                                                                                                                 (BY SIMILARITY).
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                       CYTOPLASMIC (BY SIMILARITY)
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PROTEIN SYNTHESIS
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Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
-!- COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
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PROSITE; PS01195; PEPT_TRNA_HYDROL_1;
PROSITE; PS01196; PEPT_TRNA_HYDROL_2;
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                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z99110; CAB13011.1; -. SubtiList; BG13136; yjbG.
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Bacillus/Staphylococcus
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       SEQUENCE
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42; ZINC_PROTEASE; 1.
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396
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           MW.
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ZINC (CATALYTIC) (BY SIMILARITY)
ZINC (CATALYTIC) (BY SIMILARITY)
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tation update)
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MBL outstation -
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RESULT 15
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A Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

A McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., White O.,

Balzberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

A Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from

"Evidence sequence of Thermotoga maritima.";

L Nature 399:323-329(1999).

L Nature 399:323-329(1999).

C -I DDNA. IT IS PROTEIN HAS A WEAK ATPASE ACTIVITY.

C -I SIMILARITY: BELONGS TO THE DNA MISMATCH REPAIR MUTS FAMILY.
Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best Local Similarity 50.0
Matches 6; Conservative
                                                                            PROSITE; PSO
DNA repair;
NP_BIND
CONFLICT
CONFLICT
CONFLICT
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                            EMBL; U71155; AA
EMBL; AE001811;
TIGR; TM1719; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P74926;
15-JUL-1998
30-MAY-2000
30-MAY-2000
                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN-MSB8 / DSM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Wetmur J.G., Rosenfeld A., Wong D.M.; "Hyperthermophilic MutS proteins: isolation, characterization and enhancement of PCR specificity."; submitted (OCT-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                               Pfam; PF00488; MutS_C; 1. Pfam; PF01624; MutS_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. Wetmur J.G., Rosen
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NCBI_TaxID=2336;
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358 YENKGKRNGAYS 369
                                                                                                                                                                                              PS00486; DNA_MISMATCH_REPAIR_2; 1.
                                                                                             ATP-binding;
589 596
233 233
262 262
287 287
506 506
                                                                                   793
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(Rel. 39, Last sequence update)
(Rel. 39, Last annotation update)
 Conservative
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1; AAD36785.1;
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                                                                                 91065 MW;
                41.8%;
72.7%;
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A -> G (IN REF. 1).

L -> W (IN REF. 1).

L -> G (IN REF. 1).

K -> T (IN REF. 1).
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5; Mismatches
                                                                                 1BCB2342E4F9B1BD CRC64;
 Mismatches
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772
      2 KNKGKKNGKHN 12
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Search completed: July Job time: 971 sec 2001, 09:26:40

OLSD) SAVING SINI

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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1: sp_archea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate
6: sp_mammal:*
7: sp_mbc:*
8: sp_organelle:*
9: sp_phage:*
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Gapop 10.0 , Gapext 0.5
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98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HKNKGKKNGKHNGWKT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                  sp_organelle:*
                                                                                                                                                      sp_invertebrate: *
sp_unclassified:*
sp_vertebrate:*
sp_virus:*
                                                   sp_rodent:*
                                                                 sp_plant:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	_C	4	·	2	دسز	Result No.
43	43	43	43	44	44	45	46	46	46	46	46	46	46	46	47	47	49	50	Score
43.9	43.9	43.9	43.9	44.9	44.9	45.9	46.9	46.9	46.9	46.9	46.9	46.9	46.9	46.9	48.0	48.0	50.0	51.0	Query Match Length
915	808	504	171	806	298	1251	2254	2187	1388	1372	857	648	516	95	275	225	3898	581	Length I
5	10	G	w	10	2	5	4	4	4	4	10	2	w	۲	N	w	14	10	DB
Q9GNU7	023052	097467	Q9UTT3	Q9FIM2	Q9K6X3	016637	Q9HCYO	Q9Н197	Q9HAW2	Q9HAW1	Q9SUV0	034507	Q9P6E6	Q9HL50	Q9S2U7	014262	Q68965	Q9SEL2	ID
Q9gnu7 plasmodium	023052 arabidopsis	O97467 plasmodium	Q9utt3 schizosacch	Q9fim2 arabidopsis	Q9k6x3 bacillus ha	016637 caenorhabdi		Q9h197 homo sapien		Q9haw1 homo sapien	Q9suv0 arabidopsis	034507 bacillus su	Q9p6e6 neurospora		Q9s2u7 streptomyce	014262 schizosacch	Q68965 classical s	Q9sel2 vitis vinif	Description

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O92304 CLASSICAL S			Q9i8x6 xiphophorus	Q9szy0 arabidopsis	O08764 rattus norv	5 aral	homo	Q9hdd2 homo sapien			Q17768 caenorhabdi	O49546 arabidopsis		016789 caenorhabdi		Q9u0n1 plasmodium	Q9y521 homo sapien	Q23780 chironomus		Q9w2p6 drosophila	Q23783 chironomus	Q9rlc7 mus musculu	drosc	homo	Q9nwu9 homo sapien	Q9p0q2 homo sapien

### ALIGNMENTS

of O;	01-MAY-2000 (TrEMBLrel. 13, Created) 01-MAY-2000 (TrEMBLrel. 13, Last sequence update) 01-MAY-2000 (TrEMBLrel. 16, Last annotation update) GAG-POL POLYPROTEIN. Vitis vinifera (Grape). EUNARYOTE; VIIIdlplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; endicotyledons; core eudicots; Vitaceae; Vitis. NCBI_TAXID=29760; [1] SEQUENCE FROM N.A. STRAIN-CV. DANUTA; TISSUE=YOUNG LEAVES; Verries C., Bes C., Tesniere C.; VLNE 1: a long terminal repeat element integrated in an Adh gene of v. Danuta and dispersed in this Vitis vinifera genome. "; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases. InterPro; IPR001284; InterPro; IPR001284; InterPro; IPR001284; InterPro; IPR001286; PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1. PROSITE; PS00136; SUBTILASE_ASP; UNKNOWN_1. SMART; SM00343; ZnF_C2HC; 1. POLYPROTEIN. SMART; SM00343; ZnF_C2HC; 1. POLYPROTEIN. SMART; SM00343; ZnF_C2HC; 1. POLYPROTEIN. SEQUENCE 581 AA; 66488 MW; A908822FFB09B41D CRC64; SEQUENCE 581 AA; 66488 MW; A908822FFB09B41D CRC64; SEQUENCE 581 AA; 66488 MW; A90882FFB09B41D CRC64; SCORE 50; DB 10; Length 581; t Local Similarity 62.5%; Pred. No. 5.3; ches 10; Conservative 1; Mismatches 5; Indels 0; Gaps 1 HKNAGKKNGKHNGWKT 16 [11] [   1   1   1   1   1   1   1   1   1	13, Created) 13, Last sequence update) 16, Last annotation update) 16, Last annotation update) 16, Last annotation update) 16, Last annotation update) 18, Embryophyta; Tracheophyta 29dons; core eudicots; Vitac 29dons; core eudicots; Vitac 20dons; core eudicots; Vitac 20dons; core eudicots; Vitac 21 this Vitis vinifera gen 21 this Vitis vinifera gen 22 the EMBL/GenBank/DDBJ datab 23 the EMBL/GenBank/DDBJ datab 24 the EMBL/GenBank/DDBJ datab 25 the EMBL/GenBank/DDBJ datab 21; 1. 20dons; Core 50; DB 10; Len 20dons; Score 50; DB 10; Len	3, Created) 3, Last seq 6, Last ann embryophyt dons; core eyoung Leav ere C.; repeat elem in this Vit he EMBL/Gen 1;	Lrel. 1: Lrel. 1: Lrel. 1: Lrel. 1: N. ape) lantae; icotylee icoty	01-MAY-2000 (TrEMBLrel GAG-POL POLYPROTEIN. Vitis vinifera (Grape) Eukaryota; Viridiplant Magnoliophyta; eudicot NCBLTAXID-29760; [1] SEQUENCE FROM N. A. STRAIN=CV DANUTA; TIS Verries C., Bes C., Teg "VINE 1: a long termin cv. Danuta and dispers Submitted (DEC-1998) t EMBL; AF116598; AAF202 InterPro; IPR001584; InterPro; IPR001584; InterPro; IPR001584; InterPro; IPR00136; SUBJ SMART; SM00343; ZnF_CZ POLYPOTENI. SEQUENCE 581 AA; 66 ches 10; Conservati 1 HKNAGKKNGKHNGWKT 1                     1	Ol-MAY-2000 (T. Ol-MAY-200 (T. Ol-MAY-2000 (T. Ol-MAY-2000 (T. Ol-MAY-2000 (T.	DT OO
		581 AA	PRT;	PRELIMINARY;	PREL	RESULT 1.1. Q9SEL2 ID Q9SEL2	RESULT Q9SEL2 ID Q

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RESULT 014262 1D 201 AC 01 DT 01 DT 01 DT 01 DT 01 DT 01 DT 02 SC OC SC 
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  Query Match
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InterPro; 1PR001550; ...
Pfam; pF00271; helicase_C; 1.
PRINTS; PR00729; CDVENDOPTASE.
PROSITE: PS00037; MYB_1; UNKNOWN_1.
PROSITE: PS00531; RNASE_T_22; UNKNOWN_1.
SMART; SM00490; HELICC; 1.
SMART; SM00490; Helicase; Polyprotein.
ATP-binding; Helicase; Polyprotein.
ATP-binding; Helicase; Polyprotein.
ATP-binding; Helicase; Polyprotein.
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01-JAN-1998 ()
01-MAY-1999 ()
01-MAR-2001 ()
HYPOTHETICAL
                                                                                                                                             Gentles S., Churcher C.M., Wood V., Barrell B.G., Submitted (SEP-1997) to the EMBL/GenBank/DDBJ dat: -!- SIMILARITY: TO YEAST YMR130W.
EMBL; 299532; CAB16722.2; -.
InterPro; IPR001454; -.
                                                                     Hypothetical p
SEQUENCE 225
                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces.
NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                     Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Muramatsu M., Yamada A.;
"Comparison of the entire nucleotide and "Comparison of the entire nucleotide and comparison of the entire nucleotide standard hog cholera vaccine str
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                                                                                                                                                                                                                                                              STRAIN-972;
                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=95390794; PubMed=7661692; Ishikawa K., Nagal H., Katayama K., Takeuchi K., Hishiyama M., Saitoh A., Muramatsu M., Yamada A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      014262
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-!- SIMILARITY: TO HELICASE C-TERMINAL DOMAIN.
EMBL; D49533; BAA08477.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Classical swine fever virus.
Viruses; ssRNA positive-strand viruses,
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InterPro; IPR001005;
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IPR001568;
                                                                                                                                           IPR001454;
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AL 26.6 KDA PROTEIN C
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25 AA; 26299
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., Takagi M., Gotoh K.,
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Q9HL50;
Q1-MAR-2001
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01-MAR-2001
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Q9S2U7;
Q1-MAY-2000
01-MAY-2000
01-MAY-2000
SEQUENCE FROM N.A.
STRAIN=DSM 1728;
MEDLINE=20479972; PubMed=11029001;
Ruepp A., Graml W., Santos-Martinez M.-L., Koretke Mewes H.-W., Frishman D., Stocker S., Lupas A.N., B Mewes H.-W., Frishman D., Stocker S., Lupas A.N., B
                                                                                                                                                                             Thermoplasma
Archaea; Eury
                                                                                                                                                                                                                      TA0381
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria;
Actinomycetales; Streptomycineae; Stre
                                                                                                                                                             Thermoplasma
                                                                                                                                                                                                                                      HYPOTHETICAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=97000351; PubMed=8843436; Redenbach M., Kieser H.M., Denapa Kinashi H., Hopwood D.A.;
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                                                                                                                                       NCBI_TaxID=2303;
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8 Mb Streptomyces coelicolor A3(2) ch

Microbiol. 21:77-96(1996).

AL096884; CAB51427.1; -.
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                                                                                                                                                                         Euryarchaeota;
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(JUL-1999)
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1 (TrEMBLrel. 16,
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AL PROTEIN TA0381.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
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Last annotation update)
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EMBL/GenBank/DDBJ database
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annotation update)
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                    Baumeister W.;
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submitted (MAY-2000) to the EI
EMBL; AL355926; CAB91223.1; -
InterPro; IPR001553; -
InterPro; IPR003593; -
SMART; SM00382; AAA; 1.
STRAIN-168;
MEDLINE-98044033; PubMed-9384377;
Kunst F., Ogasawara N., Moszer I., A
Azevedo V., Bertero M.G., Bessieres
                                                                                                                                                                                                                                                      01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                             Bacillus subtilis
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Nyakatura G., Mewes I
Submitted (MAY-2000)
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01-MAR-2001 (TremBLrel.
RAD57 RELATED PROTEIN.
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EMBL; AL445064; CAC11525.1; Hypothetical protein.
SEQUENCE 95 AA; 11025 MW;
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Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.

NCBI_TaxID=5141;
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                                                                                            SEQUENCE FROM N.A.
                                                                                                                                  Bacteria; Firmicutes; Bacillus/Staphylococcus NCBI_TaxID=1423;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                486
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                                                                                                                                                                                                                                       PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 60. 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 516 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genome project;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86
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                                                                                                                                                     Bacillus/Clostridium us group; Bacillus.
                                                                                                                                                                                                                                                          05,
16,
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15,
16,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MW;
                                                                                                                                                                                                                                                        Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                Created)
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Last sequence update)
Last annotation update)
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Pred. No. 3.8;
0; Mismatches
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Pred.
                                                                                                                                                                                                                                                                                                                                          PRT;
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                               Albertini A.M., Alloni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 46;
No.
                                                                                                                                                                                                                                                                                                                                          648
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A Glimsppi G., Guy B.J., Haga K., Haiech J., Harwood C.R., Henaut A.,
A Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L.,
A Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
A Kobayashi Y., Koetter P., Koningstein G., Krogh S., Kumano M.,
A Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
A Kurita K., Lapidus A., Liu H., Masuda S., Mauel C., Medigue C.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
A Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
A Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
A Persean E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
A Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Scoffone F.,
A Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
A Sato T., Scanlan E., Takagi T., Takahashi H., Takamaru K.,
A Sorokin A., Tacconi E., Takagi T., Takahashi H., Takamaru K.,
A Tosato V., Uchiyama S., Vandenbbl M., Vannier F., Vassarotti A.,
A Vanier A. Wamhitt P. Wedler H. Weitzenerger T.
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Best Local
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Q9SUVO PRELIMINARY; PRT; 857
Q9SUVO;
O1-MAY-2000 (TrEMBLrel. 13, Created)
O1-MAY-2000 (TrEMBLrel. 16, Last sequence
O1-MAR-2001 (TrEMBLrel. 16, Last annotation of the control of the cont
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Submitted
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InterPro; IPR0007290; -.
Pfam; PF00069; pkinas; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; UNKNOWN_1.
PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.
PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
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Submitted (AUG-1997) to the EMBL/GenBs
-i-SIMILARITY: TO THE SER/THR FAMILY
EMBL; 299112; CAB13450.1; -
EMBL; X13937; CAA7/267.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Viari A., Wambutt R., Wedler E., Wedler H., Weitzenegger T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Ya Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchi "The complete genome sequence of the gram-positive bacterium subtilis.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATP-binding; Serine 648 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   317
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 KNKGKKNGKHNGW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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48 AA; 71866 MW; 9653AB5CFBAA7900 CRC64;
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61.5%;
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SER/THR FAMILY OF PROTEIN KINASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yoshikawa H., Danchin A.;
the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
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Pred. No. 25;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             i G.,
., Henaut A.,
<sup>Tones L.</sup>,
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Tracheophyta;

Spermatophyta;

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RESULT OPHAMI ID AC QX AC QX DT 0 0 DT 0 
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Best Local s
Matches 8
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Best Local :
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Q9HAW1;
Q1-MAR-2001
Q1-MAR-2001
Q1-MAR-2001
                                                                                                                                                                                                 "Different human TFIIIB activities direct RNA pol
transcription from TATA-containing and TATA-less
Genes Dev. 14:2650-2663(2000).
                                                                                                                                                                                       EMBL; AF298152; AAG30221.1;
                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. MEDLINE=20496900; PubMed=11040218;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Terryn N., Ardiles W., Buysshaert
De Keyser A., Neyt P., Rouze P., V
Gielen J., Van Montagu M., Mewes H
Submitted (MAR-2000) to the EMBL/G
                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RNA POLYMERASE III TRANSCRIPTION INITIATION FACTOR B''
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EU Arabidopsis sequencing projections the EMBL; AL161581; CAB7959.1; --
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                                                                                                                                                                Initiation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam: PF00160; pro_isomerase; 2.
PRINTS; PR00153; CSAPPISMRASE.
Probom: PD001861; -; 1.
PROSITE; PS50072; CSA_PPIASE_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HSSP; P05092; 1CWL.
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1372 AA
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n Den Daele H.
W., Lemcke K.,
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Best Local S
Matches 8
Survival motor neuron gene.",
Submitted (DEC-1999) to the EN
EMBL; AJZ79120; CAC21448.1; JC
EMBL; AJZ79122; CAC21448.1; JC
EMBL; AJZ79123; CAC21448.1; JC
EMBL; AJZ79123; CAC21448.1; JC
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EMBL; AJZ79127; CAC21448.1; JC
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Kelter A.R., Herch
"Transcription fac
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MEDLINE-20496900; PubMed-11040218;
SChramm L. Pendergrast P.S., Sun Y.,

"Different human TFIIIB activities dir

"ranscription from TATA-containing and
Genes Dev. 14:2650-2663,2000).

EMBL: AF298151; AAG30220.1;
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Eukaryota; Metazoa; C
Mammalia; Eutheria; P
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RNA POLYMERASE III TRANSCRIPTION INITIATION FACTOR B''.
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Eukaryota; Metazoa; Chordata;
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Matches 8; Conserv
                                       016637; PRELIMINARY;
016637; O1-JAN-1998 (TrEMBLrel. 0
01-MAY-2000 (TrEMBLrel. 1
01-JUN-2000 (TrEMBLrel. 1
W09G10.4 PROTEIN.
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01-MAR-2001
01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Wirth B.;
Kelter A.R., Herchenbach J., Wirth B.;
Wirth B.;
The transcription factor like nuclear regulator (TFNR) contains novel 55-amino acid motif repeated 9 times and maps closely to SM submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ238520; CAC04245.1; -
EMBL; AJ238520; CAC04245.1; -
EMBL; BJ50E96F53F04CFE CRC64;
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SEQUENCE
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EMBL;
EMBL;
EMBL;
EMBL;
EMBL;
   Eukaryota; Metazoa;
                     Caenorhabditis elegans
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Mammalia;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE
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AJ279149;
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001 (TrEMBLrel. 16, Last sequence update)
001 (TrEMBLrel. 16, Last annotation update)
001 (TrEMBLrel. 16, Last annotation update)
TRANSCRIPTION FACTOR-LIKE NUCLEAR REGULATOR.
                                                                                                                                                                                                                                                                                                                           Conservative
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CAC21448.1;
CAC21448.1;
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57.1%;
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Pred. No.
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 Chromadorea; Rhabditida; Rhabditoidea;
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O9K6X3;
O1-OCT-2000 (TrEMBLrel. 1
O1-OCT-2000 (TrEMBLrel. 1
O1-OCT-2000 (TrEMBLrel. 1
                                                                                                                                                         SEQUENCE FROM N.A.

STRAIN-C-125 / JCM 9153;

Takami H., Nakasone K., Takaki Y.;

Takami H. (MAR-2000) to the EMBL/GenBank/DDBJ

EMBL; AP001519; BAB07320.1; -

SEQUENCE 298 AA; 33374 MW; 5F86FB72EC1B62B
                                                                                                                                                                                                                                                                                                                                     Bacillus halodurans.
Bacteria; Firmicutes; Bacillus/Clostridium
Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AF016671; AAB66112.2; -... IPR000408; -... IPR0002553; -... IPR002553; -... Pfam; PF01602; Adaptin_N; 1... PF05TITE; PS00626; RCC1_2; UNKNOWN_1... C3BOB18DAEF1AA38 CRC64; SEQUENCE 1251 AA; 139949 MW; C3BOB18DAEF1AA38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     CELL-DIVISION
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Bentley D., Goela D., Holmes
"The sequence of C. elegans
Submitted (AUG-1997) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=86665;
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  HKNKGKKNGKHNGWKT
                                               Similarity 50.8; Conservative
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9; Conservative
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50.0%;
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                                            Score 44; DB Pred. No. 24; 1; Mismatches
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Last sequence update)
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Pred. No.
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24;
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RESULT 15

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Database
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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A_Geneseq_0601:*

1: /SIDS8/gcgdata/geneseq/geneseqp/AA1980.DAT:*
2: /SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:*
3: /SIDS8/gcgdata/geneseq/geneseqp/AA1982.DAT:*
4: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
5: /SIDS8/gcgdata/geneseq/geneseqp/AA1983.DAT:*
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Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HGHEQQHGLGHG 12
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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11	10	9	000	7	o	U	4	· (u)	2		No.	Poen I+
75	75	75	75	75	75	75	75	75	75	75	Score	
100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	Match	*
255	186	131	94	83	63	62	55	. 28	17	12	Length DB	
21	21	16	21	21	16	21	21	21	17	21	DB	
AAY93342	AAY93349	AAR75181	AAY93351	AAY93347	AAR75186	AAY93348	AAY93346	AAY81996	AAW07627	AAY81992	ID	CORPORATE
Light chain of hum	Light chain of hum	Partial peptide of	Light chain of hum	Light chain of hum	Partial peptide of	Light chain of hum	Light chain of hum	Human high molecul	Human high polymer	Human high molecul	Description	

A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis

WPI; 2000-376483/32.

İS	AAG13901	21	396	58.7	44	45
is thal	AAG22954	21	389		44	44
İS	AAG06064	21	389		44	43
is thal	AAG49725	21	388		44	42
is thal	AAG13902	21	388		44	41
is thali	AAG13903	21	384		44	40
0	AAY37637	20	356	Ψ,	44	39
	AAG22955	21	309		44	38
s	AAG06065	21	309		44	37
ē	AAB87345	22	831		45	36
ω.	AAW74581	19	564		45	35
Murine transcripti	AAY96405	21	421	.0	45	34
-	AAW96263	20	421		45	ω ω
	AAY73840	20	165		45	32
ococcus a	AAW98038	20	121	.0	45	31
ept	AAR75182	16	88		46	30
	AAG46905	21	179	N	47	29
dopšis thali	AAG24334	21	179	N	47	28
high	AAY81997	21	28	2	47	27
high mole	AAY81994	21	12	N	47	26
of h	AAY93352	21	11	5	. 49	25
	AAG43478	21	398	68.0	51	24
	AAG22263	21	398	8	51	23
	AAG43479	21	344	8	51	22
	AAG22264	21	344	8	51	21
idopsis	AAG43480	21	330	8	51	20
idopsis thali		21	330	œ	51	19
additive p		13	85	9	52	18
chain of	AAY93353	21	179	ω	55	17
t chain of hu		21	47	ω	55	16
peptide		16	110	0	68	15
al peptide		16	41	0	68	14
chain of	9334	21	186	2	69	13
Light chain of hum	AAY93350	21	16	Ν	69	12

#### ALIGNMENTS

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AAY81992
                                                                                                                                                                                                                                                                                                            RESULT
                                                                                                                                                                                   Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                            05-NOV-1999;
                                                              (MCCR/) MCCRAE R K.
                                                                                       10-NOV-1998;
                                                                                                                               18-MAY-2000.
                                                                                                                                                WO200027866-A1.
                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                  Human high molecular weight kininogen domain 5 fragment #1.
                                                                                                                                                                                                                                                    16-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                         AAY81992;
                                                                                                                                                                                                                                                                                        AAY81992 standard; peptide; 12 AA.
                                                                                                                                                                                                                                                                                                            -
                                                                                         98US-0107833
                                                                                                            99WO-US26419.
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Claim

5

Page 27-28; 52pp; English.

The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kalikrein. It kan or a synthetic compound comprising part or all of the present sequence may be used in a pharmaceutical composition for inhibiting anylogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit and cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides.

밁 Qy

**...** 

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1 HGHEQQHGLGHG 12

Human high polymer quininogen L-chain derived peptide.

Human; high polymer; quininogen; L-chain

04-FEB-1997

(first entry)

AAW07627;

AAW07627 standard; peptide; 17 AA

Matches Query Match Best Local

Similarity

100.0%;

Score 75; Pred. No.

1.5e-05; DB 21; 0;

Length 12;

Conservative

0;

Mismatches

Indels

0;

Gaps

0;

Sequence

12

AA;

phase synthesis methods.

0;

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Query Match
Best Local Similarity
                                                         The present peptide is derived from residues 402-498 of the human high polymer quininogen L-chain. It was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                                                   Cell adhesion inhibiting peptide(s), used as cancer metastasis inhibitor - comprises partial amino acid sequence of human high polymer quininogen {\bf L} chain
                                      Sequence
                                                                                                Example; Page 8; 14pp; Japanese
                                                                                                                                                            WPI; 1996-421988/42
                                                                                                                                                                                                   28-SEP-1994;
                                                                                                                                                                                                                      28-SEP-1995;
                                                                                                                                                                                                                                                           JP08208692-A.
                                                                                                                                                                                                                                                                                Homo sapiens.
                                                                                                                                                                              (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                                          13-AUG-1996
                                        17
                                        A,
                                                                                                                                                                                                  94JP-0259451
                                                                                                                                                                                                                     95JP-0276418
 100.0%;
 Score
Pred.
 No.
 DB 17;
2.1e-05;
         Length 17,
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J)

밁 Ωy

hgheqqhg1ghg

Matches

12;

Conservative

0;

Mismatches

0;

Indels

0;

Gaps

0

 $\vdash$ 

HGHEQQHGLGHG 12

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RESULT
AAY81996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PD XXX XXX
                                                                     YY XY PA
                                                                                                                 The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kb glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HK) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                            A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO200027866-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
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                                                                                                                                                                                                                                                                                                                                                                               Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2000-376483/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    05-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human high molecular weight kininogen domain 5 fragment #5
                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McCrae RK;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                            8; Page 28; 52pp;
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                                                                     28 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98US-0107833.
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100.0%; Score 75; DB 21; 100.0%; Pred. No. 3.5e-05;
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RESULT
AAY93348
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AAY93346
                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                        Matches
Light chain of human high molecular weight kininogen analogue
                            04-SEP-2000
                                                        AAY93348
                                                                                 AAY93348 standard; peptide;
                                                                                                                                                                                                                                                                                             The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Colman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (NOUS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1998;
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                                                                                                                                                                                                       Local Similarity
hes 12; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ) DUPONT PHARM CO.
) COLMAN W R.
) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Page 36;
                                                                                                                                                                                                                                                                         55
                                                                                                                                                                                                       Conservative
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                            (first entry)
                                                                                                                                                                                                                                                                        AA;
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                                                                                                                                                                                                                  100.0%;
                                                                                 62
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                                                                                                                                                                                                                  Score 75; DB 21
Pred. No. 7e-05;
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                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                             21;
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28-MAR-1995 JP07082172-A Homo sapiens

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RESULT
AAR75186
В
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                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also k used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting
                                                                                     high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
                                                                                                                                  Partial peptide of human HMW kininogen fragment
                                                                                                                                                                   05-DEC-1995
                                                                                                                                                                                                  AAR75186;
                                                                                                                                                                                                                             AAR75186 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 37; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \boldsymbol{\cdot}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman WR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UTEM ) UNIV TEMPLE (DUPO ) DUPONT PHARE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10-NOV-1998;
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les 12; Conserv
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COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                               100.0%;
ilarity 100.0%;
Conservative 0
                                                                                                                                                                  (first entry)
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                                                                                                                                                                                                                               peptide;
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                                                                                                                                                                                                                                                                                                                                                                 Score 75; DB Z1,
Pred. No. 7.9e-05;
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                                                                                                                                                                                                                                                                                                                                                                                               Length 62;
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be used to
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0;
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17-SEP-1993;

93JP-0230616

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CCX SS X PTTT X P P P A X P R X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T X P T 
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Best Local
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                                             Claim 5;
                                                                                          Method for inhibiting endothelial cell proliferation, that inhibit endothelial cell migration
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                                                                                                                                                                   WPI; 2000-376306/32
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                                                                                                                                                                                                                Colman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY93347 standard;
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                                                                                                                                                                                                                                                                                       (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R
                                                                                                                                                                                                                                                                                                                                                                                         10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                (MOUS/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            wound treating agent contg. a partial peptide of kininogen ave growth promotion activity of fibroblasts.
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6 hgheqqhglghg 17
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                                                                                                                                                                                                                WR,
                                                                                                                                                                                                                                                           ) DUPONT PHARM CO.
) COLMAN W R.
) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high
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                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 AA;
                                                                                                                                                                                                              Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecular weight kininogen;
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                                               37;
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                                             41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide; 83
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Pred. No.
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                                                                                                                 using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            endothelial
                                                                                                                 compound
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The

present sequence represents an analogue of the light chain

of.

human

inhibiting

endothelial cell

proliferation.

compounds

can also

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RESULT
AAY93351
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Best Local
          The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for the invention of the invention of the method containing high molecular weight kininogen analogues. The method and the compounds can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell prolliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell prolliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                    WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
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(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                          10-NOV-1998;
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                                                                                                                                                                                                                   od for inhibiting endothelial cell proliferation, using compound inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                     2000-376306/32.
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                                                                                                                                                                                  8; Page 39; 41pp;
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                                                                                                                                                                                                                                                                                                                                      MOUSA A S.
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Pred.
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No.
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0.00011;
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RESULT 1
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                                                                                                                                Query Match
Best Local Similarity
Matches 12; Conser
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                                                                                                                                                                                                             AAR75181 is a partial peptide corresponding to human kininogen fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compons. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
  04-SEP-2000
                     AAY93349;
                                        AAY93349 standard; peptide; 186 AA
                                                                                                                                                                                 Sequence
                                                                                                                                                                                                     on
                                                                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                                                                           A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                            WPI; 1995-158909/21
                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      used for inhibiting angiogenesis. The compounds can also be inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                               (FARH ) HOECHST JAPAN KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              high molecular weight; kininogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR75181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR75181 standard; peptide; 131 AA
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                                                                                                                                                                                                     fibroblasts.
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                                                                                       9
                                                                                                                                                                                                                                                                         Page
                                                                                                                                                                                 131 AA;
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                                                                                                                               Conservative
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  (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA,
                                                                                                                                                                                                                                                                         7; 8pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weight; kininogen; fragment; 1.2; 1; 2; partial; agent; human; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                  93JP-0230616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 of human HMW kininogen
                                                                                                            12
                                                                                           85
                                                                                                                                          100.0%;
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Pred. No. 0.00012;
                                                                                                                                Score 75; DB 16;
Pred. No. 0.00017;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 fragment
                                                                                                                                                                                                               growth promotion activity
                                                                                                                                                   Length 131;
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                              The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
Sequence
                                                                                                                                                                                                                                                                           Claim
                                                                                                                                                                                                                                                                                                               Method for inhibiting endothelial cell proliferation, using that inhibit endothelial cell migration \,
                                                                                                                                                                                                                                                                                                                                                                      WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                        Colman WR,
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(DUPO ) DUPONT PHARN
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-NOV-1998;
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COLMAN W R.
MOUSA A S.
                                                                                                                                                                                                                                                                           Page 38; 41pp; English
 186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                        Mousa AS
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hgheqqhglghg 16
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                               Mismatches
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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.

Homo sapiens

Light chain of human high molecular weight kininogen.

AAY93342; 04-SEP-2000

(first entry)

AAY93342 standard;

protein;

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                                                                                                                                                                          Synthetic
                                                                                                                                                                                                  Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                 Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                  04-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376306/32
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
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                                                                                                                                                                                                                                                                                                 (first entry)
                                98US-0107844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of endothelial cells to vitronectin.
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Best Local S
Matches 11
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                                                                                                                                                                                                                                                                                                        Human; high molecular weight kininogen; glycoprotéin; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also used for inhibiting angiogenesis. The compounds can also be used to
                                                     (UTEM ) UNIV TEMPLE.
                                                                                                                           09-NOV-1999;
                                                                                                                                                                                  WO200027415-A2
                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93343 standard; peptide; 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       endothelial cell proliferation. The method comprises contacting
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                                          (COLM/)
                                                                                               10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376306/32.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inhibit migration of endothelial cells to vitronectin.
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                          COLMAN W
MOUSA A S
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COLMAN W R.
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                           AS.
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                                                                                               98US-0107844
                                                                                                                           99WO-US26377.
                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                            /note= "Xaa are unspecified amino acids"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   41pp;
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Pred. No.
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WPI; 2000-376306/32

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Best Local Similarity
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                                          AAR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 45c-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                               on fibroblasts.
                                                                                                                                        Claim 6;
                                                                                                                                                                                                                     WPI; 1995-158909/21
                                                                                                                                                                                                                                                                                    17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                   17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                  28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                 Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                              high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Partial peptide of HMW kininogen fragment 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      171
                                                                                                                                                                    wound treating agent contg. a partial peptide of kininogen ave growth promotion activity of fibroblasts.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             agent; bovine; growth promotion;
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                                            because they have growth promotion activity
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Pred. No.
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                                                                                                                           AAR75178 is a partial peptide corresponding to bovine kininogen fragment 1.2, amino acids 387-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compons. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                              Sequence
                                                                                                                                                                                            Claim 4;
                                                                                                                                                                                                                A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                WPI; 1995-158909/21.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    high molecular weight; kininogen; fragment; 1.2; wound treating agent; bovine; growth promotion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Partial peptide of HMW kininogen fragment 1.2
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                                          Local Similarity les 10; Conserv
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hghqkqhglghg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     standard;
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                                          Conservative
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fibroblast.
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length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/Dackfiles1.pep:*
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US-08-23-3
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RESULT 1 US-08-450-945-67 Sequence 67, Application US/08450945 Patent No. 5783383 GENERAL INFORMATION: APPLICANT: KONDO, KAZUhITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: WOCATSAI, Edward S. Jr. TITLE OF INVENTION: OF CYTOMEGALOVI NUMBER OF SEQUENCES: 75 CORRESPONDENCE ADDRESS: ADDRESSE: Dehlinger & Associates STREET: S30 Cambridge Avenue, Sui CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IMP C Compatible OPERATION TYPE: PODS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION NOMBER: US/08/450,945 FILING DATE: 23-MAY-1995 CLASSIFICATION NUMBER: US/08/450,945 FRIEDROME CHARACTERISTICS: REGISTRATION INFORMATION: TELEPANORE: (415) 324-0880 TELEPANORE: (415) 324-0860 INFORMATION FOR SEQ ID NO: 67: SEQUENCE CHARACTERISTICS: LEUGTH: 154 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-450-945-67	. ALIGN	28 36 48.0 1075 5 PCT-US94-0. 29 36 48.0 1250 1 US-08-441- 30 35 46.7 64 1 US-08-200- 31 35 46.7 114 1 US-08-385- 32 35 46.7 347 1 US-07-637- 33 35 46.7 348 1 US-07-637- 34 35 46.7 348 1 US-07-637- 35 46.7 387 1 US-07-637- 36 35 46.7 387 1 US-07-637- 37 38 46.7 387 1 US-07-637- 38 35 46.7 387 1 US-07-637- 40 35 46.7 387 1 US-07-637- 40 35 46.7 388 1 US-07-637- 41 35 46.7 388 1 US-07-637- 42 35 46.7 388 1 US-07-637- 43 35 46.7 388 1 US-07-637- 43 35 46.7 388 1 US-07-637- 44 35 46.7 388 1 US-07-637- 45 35 46.7 388 1 US-07-637- 46 35 46.7 388 1 US-07-637- 47 38 35 46.7 388 1 US-07-640- 48 35 46.7 388 1 US-07-640-
PTS AND PROMOTERS RUS  te 250  Version #1.30	MENTS	4-07297-41 Sequence 41-139-9 Sequence 00-016-6 Sequence 87-272A-8 Sequence 85-241-3 Sequence 87-870-5 Sequence 87-399-8 Sequence 97-399-8 Sequence 12-703-8 Sequence 12-703-9 Sequence 12-703-9 Sequence 40-476-12 Sequence 12-703-7 Sequence 12-703-7 Sequence 37-899-7 Sequence
		ence 41, Applience 9, Applience 6, Applience 3, Applience 10, Applience 8, Applience 8, Applience 8, Applience 9, Applience 12, Applience 12, Applience 12, Applience 7, Applience 11, Applience
	SULT 1 -08-450-945-67 Sequence 67, Application US/08450945 Patent No. 578383 GENERAL INFORMATION: APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: KONDO, KAZUHITO APPLICANT: MOCGATSKI, EDWARD S. Jr. APPLICANT: MOCGATSKI, EDWARD S. Jr. TITLE OF INVENTION: OF CYTOMEGALOVIRUS NUMBER OF SEQUENCES: 75 CORRESPONDENCE ADDRESS: ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: ISM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOCTWARE: PAPLICATION DATA: SOCTWARE: PAPLICATION DATA: SOCTWARE: PAPLICATION DATA: APPLICATION UNMBER: US/8/450,945 FILING DATE: 23-MAY-1995 CLASSIFICATION: 424 ATTORNEY/AGENT INFORMATION: REFERENCE/DOCKET NUMBER: 38,615 REFERENCE/DOCKET NUMBER: 38600-0157 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OF SEQ ID NO: 67: SEQUENCE CHARACTERISTICS: LENGTH: 154 amino acids TYPE: amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: protein	ALIGNMENTS SULT 1 -08-450-945-67 Sequence 67, Application US/08450945 Patent No. 5783383 GENERAL INFORMATION: APPLICANT: KONGO, Kazuhiro APPLICANT: KONGO, Kazuhiro APPLICANT: MOCGAISKI, Edward S. Jr. APPLICANT: MOCGAISKI, Edward S. Jr. TITLE OF INVENTION: OF CYTOMEGALOVIRUS NUMBER OF SEQUENCES: 75 CORRESPONUENCE ADDRESS: ADDRESSEE: Dehlinger & Associates STREET: 350 Cambridge Avenue, Suite 250 CITY: Palo Alto STATE: CA COUNTRY: USA ZIP: 94306 ZIP: 94306 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version CURRATION UNMBER: US/8/450,945 FILING DATE: 23-MAY-1995 CLASSIFICATION UNMBER: 38.615 REFERENCE/DOCKET NUMBER: 38.600-0157 TELECOMMUNICATION INFORMATION: REFERENCE/DOCKET NUMBER: 38.600-0157 TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION OF SEQ ID NO: 67: SEQUENCE CHARACTERISTICS: LENGTH: 154 amino acids TYPE: amino acids TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: amino acid TYPE: Amino acid TYPE: Amino acid TYPE: Amino acid TYPE: Amino acid TYPE: Amino acid TYPE: Amino acid TYPE: Amino acid

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Best Local Similarity
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APPLICANT: Kondo, Kazuhiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960
INFORMATION FOR SEQ ID NO: 67
                                                                                                                                              APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
TITLE OF INVENTION: EPIMERASE
NUMBER OF SEQUENCES: 9
COMPUTER READABLE FORM
                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: KONGO, NGAULLA APPLICANT: MOGATSKI, Edward S. Jr.
APPLICANT: MOGATSKI, LATENT TRANSCRIPTS AND PROMOTERS
TITLE OF INVENTION: OF CYTOMEGALOVIRUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 154 amino acids
TYPE: amino acid
TOPOLOGY: linear
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MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: FLOPP Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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NAME: Sholtz, Charles K.
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APPLICATION NUMBER:
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ADDRESSEE: Dehlinger & Associates
                                    COUNTRY:
                                                                                      ADDRESSEE: Knobbe, Martens, Olson & Bear STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Sholtz, Charles K.
REGISTRATION NUMBER: 38,615
REFERENCE/DOCKET NUMBER: 8600-0157
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CITY: Palo Alto
STATE: CA
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                                                                     Newport Beach
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                                    U.S.A.
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Pred. No.
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Best Local Similarity
             PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/553,703
FILING DATE: 30.NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
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                                                                                                                                                                             OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                               COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
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REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714,760-0404
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
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CURRENT APPLICATION DATA:
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TITLE OF INVENTION: EPIMERASE
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ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                              STREET: 620 Newport Center Drive CITY: Newport Beach STATE: CA
                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 92660
                                                                                                                               CLASSIFICATION:
                                                                                                                                                              APPLICATION NUMBER: US/09/006,021
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                                                                                                                                                                                                                                                 Diskette
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                              16th Floor
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; MOLECULE TYPE:
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US-09-006-021-2
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Conservative
Query Match
Best Local Similarity
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                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                        TOPOLOGY: lir
MOLECULE TYPE:
FRAGMENT TYPE:
                                                                                                                                                                                                                        NAME: Altman, Daniel E
REGISTATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/553,703A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Knobbe, Martens, Olson & Bear
STREET: 620 Newport Center Drive 16th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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TITLE OF INVENTION: EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Newport Beach
STATE: CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 417 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                          TELEPHONE: 714-760-04
TELEFAX: 714-760-9502
                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM:
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TELEFAX: 714-760-9502
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                                                                                                                              : 419 amino acids amino acid
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OHTA, YASUHIRO
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N-terminal
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N-terminal
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Score 39;
Pred. No.
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 DB 1;
95;
               Length 419;
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US-08-845-998-8
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                                                                         Sequence 8, Application US/08845998 Patent No. 5879892
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                                                              GENERAL
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APPLICATION NUMBER: 08/553,703
FILING DATE: 30-NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Altman, Daniel E
REGISTRATION NUMBER: 34,115
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 714-760-0404
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APPLICANT: MARU, ISAFUMI
APPLICANT: OHTA, YASUHIRO
APPLICANT: TSUKADA, YOJI
APPLICANT: TNUENTION: EPIMERASE
                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 419 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/006,021
                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: peptide FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 92660
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                               APPLICANT:
                                              APPLICANT:
   APPLICANT:
                 APPLICANT:
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CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS: sir
TOPOLOGY: linear
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TELEFAX: 714-760-9502
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                                                              INFORMATION:
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Van Baren, Nicolas
Coulie, Pierre G.
De Smet, Charles
Lucas, Sophie
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620 Newport Center Drive 16th Floor
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62.5%;
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APPLICANT: Van Ba
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                                                                                                                                                                                                                                                                                                                                                                                                                     tent No.
                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: PatenLIn Release #1.0, Version #1.25
                                                CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COmpatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845,998
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TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                               TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES NUMBER OF SEQUENCES: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: (617)720-3500
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             FILING DATE:
CLASSIFICATION:
                                                                                                                                                                 COUNTRY: US
ZIP: 02210
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ZIP: 02210
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CLASSIFICATION: 435
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APPLICATION DATA
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Boon, Thierry
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De Smet, Charles
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54.5%;
                                                us/09/206,537
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95;
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US-08-918-727-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                         OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/918,727
FILING DATE: Herewith
CLASSIFICATION 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                       INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Corley, Neil C.
APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN S100 PROTEINS
NUMBER OF SEQUENCES: 7
                                                                                                                        REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                            FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 420 amino acid
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NAME: Van Amsterdam, John R.
REGISTRATION NUMBER: 40,212
REFERENCE/DOCKET NUMBER: L04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION: TELEPHONE: (617)720-3500
                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
ZIP: 943
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STREET:
                STRANDEDNESS:
                                                                                                                                                                                    NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Incyte Pharmaceuticals, Inc STREET: 3174 Porter Drive
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Local Similarity 54.5%;
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                                                    CENGTH:
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                                               113 amino acids
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linear
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; CLONE: 488157
US-09-205-680A-7
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US-09-205-680A-7
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Best Local :
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                                                                                                                                                                                                                                                                   NAME: Colette C. Muenzen
REGISTRATION NUMBER: 39,784
REFERENCE/DOCKET NUMBER: PF-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
TELEFAX: 650-845-4166
                                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 113 amino acid
                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION UNMBER: US/09/205,680A FILING DATE: Herewith CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Lal, Pr
APPLICANT: Shah, P
TITLE OF INVENTION:
                                                                                                                                                            IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
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102 GHDHRHGKGCG 112
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OPERATING SYSTEM:
                                                    Local Similarity
les 6; Conserv
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                       2 GHEQQHGLGHG 12
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3174 Porter Drive
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Corley, Neil C.
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Pred. No.
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36;
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36;
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; SEQ ID NO 1
; LEWGTH: 286
; TYPE: PRT
; ORCANISM: Homo sapiens
US-09-203-716-1
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US-09-203-716-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application Patent No. 5780040
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                                                                      TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
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CURRENT FILING DATE: 1998-12-02
                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                   SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
                                                                                                                            TELEPHONE: (617) 542-5070
                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Plaut, Andrew G
APPLICANT: Gilbert-Rothste
APPLICANT: Wright, Andrew
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                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/08/255,457 FILING DATE:
                                                                                                                                                                                                                                             CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Boston
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                                 ENGTH:
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amino acid
3Y: linear
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                                                                                                         (617) 542-8906
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85.7%;
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Pred. No.
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91;
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RESULT 14
PCT-US95-05772-1
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Best Local Similarity
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Sequence 1, Application PC/TUS9505772 GENERAL INFORMATION:
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Patent No. 5972348
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                                                                                                                                                                                                                                                                                                                         TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2IP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/115,032
                                                                                                                                                                                                                                                                                                                                                     NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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APPLICANT: Wright, Andrew
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CITY: E
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                                                                                        3 HEQQHGLGH 11
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4 HEEQHG-GH 11
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77.8%;
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Pred. No. 2:
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US-07-945-283-2
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino array
                                                                                                                                                                                                                                                                                                                                                                       Sequence 2, Application US/07945283 Patent No. 5352596
                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION UNMBER: 30,162
REFERENCE/DOCKET NUMBER: 0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/07/945,283
FILING DATE: 19920911
                                                                                                                                                                                                                                                                                 APPLICANT: Cheung, Andrew K.
APPLICANT: Wesley, Ronald D.
TITLE OF INVENTION: Pseudoral
TITLE OF INVENTION: Involving
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: 1:
MOLECULE TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Wright, Andrew TITLE OF INVENTION: HELICO TITLE OF INVENTION: BINDIN
                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                  COUNTRY: U
                                                                                                                                                                                               STREET: 1815
CITY: Peoria
                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 225 I
                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
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1815 No. 5352596th University Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              225 Franklin Street
                                                                                                                                                                  USA
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Gilbert-Rothstein, Joanne V.
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                                                                                                                                                                                                                                                                                   Involving
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                                                                                                                                                                                                                                                                                     Pseudorabies Virus Deletion Mutants Involving The EPO and LLT Genes
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Pred. No. 23;
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CLASSIFICATION: 424

ATTORREY/AGENT INFORMATION:
NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976

TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 309-685-4011 ext.513
TELEPHONE: 309-685-4011 ext.513

TELEPHONE: 309-685-4011 ext.513

TELEPHONE: 309-685-4011 ext.513

TELEPHONE: 309-685-4011 ext.513

TELEPHONE: 309-685-4011 ext.513

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-945-283-2

Query Match
Best Local Similarity 63.6%; Pred. No. 1e+03;
Matches 7; Conservative 1; Mismatches 0; Indels 3; Gaps

Oy 1 HGHEQOHGLGH 11

Db 135 HG---EHGLCH 142

Search completed: July 6, 2001, 09:10:20

Job time: 186 sec
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GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd

Result No. Minimum DB Maximum DB Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries Total number of hits satisfying chosen parameters: Database Scoring table: Perfect score: Title: OM protein -Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Score 46.5 50.5 50 50 49 49 seq protein search, using sw model length: 0 length: 2000000000 Query Match Length PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* 900.0 900.0 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 900.7 Gapop 10.0 , Gapext 0.5 BLOSUM62 US-09-437-912-1 75 219241 seqs, 76174552 residues July HGHEQQHGLGHG 12 6, 2001, 09:07:14; Search time 73.59 Seconds (without alignments) 12.421 Million cell updates/sec DВ T45059 A43742 S58327 E83992 T07618 A45969 T02681 Ħ SUMMARIES 219241 hypothetical hypothetical gene gene ATP/GTP-binding pr cold stress protei hypothetical prote hypothetical hypothetical hypothetical prote hemolymph antifung major acute phase K-kininogen, hypothetical hypothetical hypothetical probable zinc tran peptidyl-prolyl ci kininogen, HMW I K-kininogen, kininogen, kininogen, Description nypothetical prote pipsqueak pro pipsqueak pro [ C-8 protein etical prote sterile hom accumulatio MMH prote prote prote prote LMW prote prote

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42	42	43	43	43	43	43.5	43.5	44	44	44	44	44	44	45	45
56.0	56.0	57.3	57.3	57.3	57.3	58.0	58.0	58.7	58.7	58.7	58.7	58.7	58.7	60.0	60.0
177	102	507	335	203	18	410	136	697	690	389	378	356	208	529	507
Ν	N	N	N	N	2	N	N	N	N	N	N	Ν	N	N	N
S65780	T30119	D64575	D38532	T36240	B32473	T26757	JQ2266	T03834	н69268	в96635	T49164	н71496	T07732	T08684	S54303
glycine/proline-ri	hypothetical prote	hypothetical prote	hypB protein - Rho	hypothetical prote	histidine-rich pro	hypothetical prote	cold acclimation p	nuclear distributi	copper-transportin	hypothetical prote	zinc transporter-l	probable aminopept	tuberisation-relat	hypothetical prote	zinc transport pro

## ALIGNMENTS

# kininogen, HMW precursor [validated] - human RyAlternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen NyContains: bradykinin (kallidin 1); HMW kininogen I; HMW kininogen II; low molecular C; Species: Homo sapiens (man) C; Species: Homo sapiens (man) C; Date: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000 C; Date: 28-May-1986 #sequence_revision 28-May-1989; A27899; A27699; A31905; A34030; R; Ohkubo, I; Kurachi, K; Takasawa, T; Shiokawa, H; Sasaki, M. Biochemistry 23, 5691-5697, 1984 A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its A;Reference number: A90490; MUID:85122621 A;Accession: A01279 R.Takagaki, Y.; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 A.; Hitle: Cloning and sequence analysis of cDNAs for A.; Reference number: A92544; MUID:85234582 A;Cross-references: GB:K02566; NID:g177889 R;Takagaki, Y.; Kitamura, N.; Nakanishi, S A; Molecule type: mRNA A; Residues: 1-389 < OHK>

molecular

A;Molecule type: mRNA
A;Residues: 1-592,'I',594-644 <TAK>.
A;Residues: 1-592,'I',594-647, NID:g186751; PIDN:AAB59550.1; PID:g186852
A;Cross-references: (B:M11437; NID:g186751; PIDN:AAB59550.1; PID:g186852
R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain A;Title: Clumber: S32422; MUID:93223854
A;Accession: S32422; MUID:93223854

A; Accession: A25276

human high

molecular weight

and

A; Molecule type: mRNA A; Residues: 'ANSM', 253-377 <AUE>

A;Note: differences are due to known cloning artifacts
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini
A;Reference number: A91153; MUID:86030270
A;Accession: A91153

R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. Eur. J. Blochem. 154, 471-478, 1986
A;Tille: Completion of the primary structure of human high-molecular-mass kininogen. A;Reference number: A24871; MUID:86108361 A; Accession A; Accession A; Aolecule type: protein A; Rosidues: 379-644 <LOT>
A; Note: the bradykinin sequence preceding A; Note: the bradykinin sequence preceding A; Note: Lottspeich, F;; Henscher receding the light chain sequence Henschen, A.; Mueller-Esterl, W. was not determined

A; Accession: A24871

A; Molecule type: protein A; Residues: 'Z', 20-380 <KEL1>

R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New A;Title: Amino acid sequence of the light chain of human high molecular mass kininoge A;Reference number: A27899

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A; Molecule type: protein
A; Residues: 450-452, 'X', 454, 'X', 456 <LIT>
R; Straczek, J.; Maachi, F.; le Nguyen, D.;
FBBS Lett. 373, 207-211, 1995
A; Title: Purification from human plasma o
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A; Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli,
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin molety in human plasma kininogens.
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein
A; Residues: 264-359, 'N', 361-375 <LEN2>
R; Little; S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A; Title: Human mast cell tryptase isoforms:
A; Reference number: S55239; MUID:95251593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Lenarcic, B.; Krasovec, M.; Ritonja, A.;
FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C &
A;Reference number: S14303; MUID:91192133
A;Accession: S14447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A:Residues: 1-19;189-192;310-314;381-389 <LEN1>
R:Kato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 184
A;Title: Isolation and identification of hydroxyproline analogues of bradykinin A;Reference number: A61495; MUID:88211869
A;Accession: A61495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors A;Reference number: S02482; MUID:89076517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K. Biochem. Biophys. Res. Commun. 150, 511-516, 1988 A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released A;Reference number: A34030; MUID:88106632 A;Accession: A34030
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: A31905; A; Accession: A31905
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                                                                       R;Kitamura, N.; Kitagawa, H.; Fukushima, D.;
J. Biol. Chem. 260, 8610-8617, 1985
                                                                                                                           A; Molecule type: protein A; Residues: 431-434 <STR>
                                                                                                                                                                               A; Reference number: A; Accession: S68059
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A; Residues: 381-389 < KAT2>
A; Experimental source: urine
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A; Residues: 380-389 < KAT1>
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Molecule type: protein
;Residues: 1-19;189-192;310-314;381-389 <LEN1>
                Structural organization of the human nce number: A92545; MUID:85234583
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Chem. 263, 16051-16054, 1988
Purification and identification of [hydroxyprolyl(3)]bradykinin in ascitic flu-
nce number: A31905; MUID:89034061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              381-389 <MAE>
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gene organization
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; MUID:96033974
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                                                                                                  Takagaki, Y.; Miyata,
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                                                 kininogen
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                                                 a model for its evolut
                                                                                                  T.; Nakanishi,
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F;142-253/Domain: cystatin homology <CV2>
F;264-375/Domain: cystatin homology <CV2>
F;264-375/Domain: cystatin homology <CV2>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
F;381-389/Product: bradykinin (kallidin I) #status experimental <CCH>
F;381-389/Product: low molecular weight growth promoting factor #status experimental F;431-434/Product: low molecular weight growth promoting factor #status experimental F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi F;28-614,83-94,107-126,142-145,066-218,229-248,264-267,328-340,351-370/Disulfide bond F;28-614,83-94,107-126,142-145,066-218,229-248,264-267,328-340,351-370/Disulfide bond F;28-614,83-94,107-126,142-145,066-218,229-248,264-267,328-340,351-370/Disulfide bond F;48/Binding site: carbohydrate (Asn) (covalent) #status experimental F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F;389-390/Cleavage site: Arg-Ser (kallikr
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C;Comment: The HMW kininogen precursor and the LMW form are produced from the same ge
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is i
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the kininogen prior to the release of bradykinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kininogen, HMW II precursor - bovine

Kininogen, HMW II precursor - bovine

Kilternate names: alpha-2-thiol proteinase inhibitor; preprokininogen

N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen

C;Species: Bos primigenius taurus (cattle)

C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999

C;Accession: A01282; A91923; A91941; A91938; B29559

R;Kitamura, N: Takagaki, Y:; Furuto, S:; Tanaka, T:; Nawa, H.; Nakanishi, S

Nature 305, 545-549, 1983
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F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>
F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-31/Domain: cystatin homology <CYI>
;19-31/Domain: Cystatin homology <CYI
F;19-31/Domain: Cystatin homology <CYI
F;19-31/Domain: Cystatin homology <CYI
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A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor;
A; Molecule type: protein A; Residues: 376-391 < KAT
                                                                                                                                    A; Accession: A91923
                                                                                                                                                                                                                                                                        A; Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds
                                                                                                                                                                                                                                                                                                                                           R; Kato, H.; Nagasawa, S.; Suzu
J. Biochem. 67, 313-323, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-619 <KIT>
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<KAT>
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Pred. No. 0.0
0; Mismatches
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Iwanaga,

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F;387-619/Product: HMW kininogen ii iiyn.
F;418-488/Region: glycine/histidine/lysine-rich
F;418-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
F;47/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;136/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;376-377/Cleavage site: Met-Lys (kallikrein) #status experimental
F;380/Modified site: 4-hydroxyproline (Pro) #status experimental
F;380/Modified site: Arg-Ger (kallikrein) #status experimental
F;396,400,404,510/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;397,398,518,522,534,544,551,568/Binding site: carbohydrate (Thr) (covalent) #status experimental
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A;Title: Primary s
A;Title: Primary s
A;Reference number
A;Accession: A9194
A;Molecule type: p
A;Residues: 387-45
A;Note: 398-Pro, 4
R;Han, Y.N.; Komiy
J. Biochem. 77, 55
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A;Title: Disulfide bonds in bovine HMW kininogens
A;Reference number: A94300
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A; Residues: 456-496 < HA2>;
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, J. Biol. Chem. 262, 2768-2779, 1987
A; Title: Bovine high molecular weight kininogen.
A; Reference number: A92627; MUID:87137530
A; Accession: B29559
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Residues: 'Z',20-104,'E',106-256,'XX',257-376
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Best Local
                                                                                                                                                          Matches
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Biochem. 77, 55-68, 1
461
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                                                                         1 HGHEQQHGLGHG 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398-Pro, 401-Val,
HGHQKQHGLGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387-455 <HAN>
                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      structure
                                                                                                                                                  Conservative
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152, 307-314, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A91941;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and 455-Lys were also Iwanaga, S.; Suzuki, T.
                                                                                                                                                                                           90.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
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                                                                                                                                                  2;
                                                                                                                                                                                           Score 68;
Pred. No.
                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of bovine high-molecular-weight kininogen.
                                                                                                                                                                                       DB 1;
0.0026;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The amino acid sequence, positions of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         H.; Hayashida, H.; Miyata, T.;
                                                                                                                                                  0;
                                                                                                                                                                                                                                Length 619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B.; Muller-Esterl,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             proteinase inhibitor; dup.
                                                                                                                                                  0;
                                                                                                                                                  Gaps
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RESULT

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F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-621/Product: HMW prokininogen I heavy chain #status experimental <HCH>
F;19-79/Product: HMW prokininogen I heavy chain #status experimental <HCH>
F;19-130/Domain: cystatin homology <CY1>
F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY2>
F;363-388/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;389-388/Product: bradykinin (kallidin I) #status experimental <KBDY>
F;380-388/Product: bradykinin (kallidin I) #status experimental <CH>
F;380-388/Product: hysyl-bradykinin | i #status experimental <CH>
F;380-388/Product: bradykinin (kallidin I) #status experimental <CH>
F;380-388/Product: hysyl-bradykinin | i #status experimental <CH>
F;380-389/Classine: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond F;87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental F;380-79/Cleavage site: Met-Lys (kallikrein) #status experimental F;382/Modified site: 4-hydroxyproline (Pro) #status experimental F;382/Modified site: 4-hydroxyproline (Pro) #status experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experimental experime
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A;Contents: annotation; bovine cleavage sites; bovine carbohy R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S. Seikagaku 56, 808, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 378-393 <KAT>
R; Han, Y.N.; Komiya, M.; Iwanaga,
J. Biochem. 77, 55-68, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Studies on the stra
A; Reference number: A91923;
A; Accession: A91923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokinin C;Species: Bos primigenius taurus (cattle) C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun C;Accession: A01281; A91923; A91938; A29559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               c;comment: BradyKinin, released from kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the kininogen prior to the release of bradykinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in init C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent v
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Comment: The HMW kininogen precursor is produced from the same gene as the LMW form
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A; Residues: '2',20-123,'I',125-127,'I',129-378 <SUE>
R:Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch,
Eur. J. Blochem. 152, 307-314, 1985
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: protein A; Residues: 378-393 < KAT>
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A: Reference number: A93317;
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                                                F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Note: article in Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Contents: annotation; disulfide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A94300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Disulfide bonds in bovine HMW kininogens
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    512/Binding site:
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1317; MUID:84014106
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carbohydrate
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    (Ser)
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    (covalent)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The amino acid sequence, positions o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cysteine
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       carbohydrate binding sites
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    #Status
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experimental
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N;Contains bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C;Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene 1
A;Reference number: A92625; MUID:87137443
A;Accession: A25486
A;Molecula type: mRNA
A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for residue 347 as Asn
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <MAIN-
F;19-639/Product: kininogen, HMW I #status predicted <MAIN-
F;19-131/Domain: cystatin homology <CY1>
F;264-375/Domain: cystatin homology <CY3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: C25486

R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.

J. Biol. Chem. 262, 2190-2198, 1987

A;Title: Differing expression patterns and evolution of the rat kininogen gene family. A;Reference number: A92625; MUID:87137443

A;Recession: C25486
A;Molecule type: DNA
A;Residues: 1-264 <KIT>
A;Residues: 1-264 <KIT>
  RESULT
                                                                                             QΥ
                                                                                                                  Query Match
Best Local Similarity
Thehes 9; Conserv
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C;Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 30-Sep-1993
C;Accession: C25486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 kininogen, HMW I precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C25486
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
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Best Local
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|||::||||||
463 HGHQKQHGLGHG 474
                                                           450
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nes 9; Conserv
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nes 10; Conserv
                                                                                             1 HGHEQQHGLGHG 12
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  6
                                                           HGHQKPHGLGHG 461
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                                                                                                                                      Conservative
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   rat
                                                                                                                                    2;
                                                                                                                                                      Score 62; DB 2; Pred. No. 0.024;
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Pred. No. 0.0098;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 68; DB 1;
Pred. No. 0.0026;
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                                                                                                                                    Mismatches
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                R; Fung, W.P.; Schreiber, G.
J. Biol. Chem. 262, 9298-9308, 1987
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A; Title:
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C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31
C;Accession: A27115
                                                                                                                     major acute phase alpha-1 protein 1 - rat (fragments)
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Best Local Similarity
~+~hes 8; Conserv
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R;Kageyama, R; Kitamura, N.; Ohkubo, H.; Nakanishi, J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcr: A;Reference number: A25488; MUID:87137465
A;Accession: A25488
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J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the genes
A;Reference number: A92653; MUID:87250580
A;Accession: C27115
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
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C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989
C;Accession: C27115; A25488
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A;Residues: 1-189 <PAR>
A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72599.1;
A;Experimental source: serotype O2, strain NCTC 11168
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A;Molecule type: DNA
A;Residues: 1-48 <KAG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:J02662; NID:g205071; C;Superfamily: kininogen; cystatin homology
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Pred. No.
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                                        31-Mar-1989 #text_change 16-Jul-1999
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and expression of the

genes for major acute phase alpha-1-protein

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09:48:00 2001

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A; Reference number: A92653; M
A; Accession: A27115
A; Status: not compared with c
A; Molecule type: DNA
A; Residues: 1-315 <FUN>
C; Genetics:
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A;Residues: 1-85 <IIJ>
A;Cross-references: GB:D13797; NID:g391903; PID:d1003460; PID:g391904
                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;I1jima, R.; Kurata, S.; Natori, S.
J. Biol. Chem. 268, 12055-12061, 1933
A;Title: Purification, characterization, char
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hemolymph antifungal protein precursor - flesh fly (Sarcophaga peregrina) C;Species: Sarcophaga peregrina C;Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Sep-1997
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Best Local Similarity
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A; Molecule type: DNA
A; Residues: 1-314 <SEE>
A; Cross-references: EMBL:AL031515; PIDN:CAA20646.1; GSPDB:GN00070; SCOEDB:SC5C7.34
A:Fynerimental source: strain A3(2)
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A; Accession: T35241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 05-Nov-1999
C;Accession: T35241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   밁
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F;19-65/Domain: cystatin homology (fragment) <CYS>
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C; Superfamil
                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; Accession: A45969
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 73.3%;
Best Local Similarity 66.7%;
Matches 8; Conservative
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148 NGHQKPHGLGHG 159
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8; Conser
                                                                                                                                                                   Conservative
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75.0%;
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66.7%;
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                                                                                                                                                                                                  Score 52; DB 2
Pred. No. 0.12;
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Pred. No. 0.
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A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT TO 2681
                                                                                                                                                                                                                                                                                      A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-409 <STO>
                                                                                                                                                                                                                                                                                                                                                     Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20263314
A;Accession: E83992
                                                                                                                                                                                                                                                                                                                                                                                                                                           probable zinc transporter At2g46800 [imported] - Arabidopsis thaliana N;Alternate names: hypothetical protein F19D11.8 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02681; D84907
                                                                                                                                                                                                   C;Genetics:
A;Gene: BH2741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84907
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A;Description: Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence A;Reference number: Z14698
                                                                                                                                                                                                                                            A;Cross-references: GB:AP001516; GB:BA000004; NID:g10175192; PIDN:BAB06460.1; GSPDB:GA;Experimental source: strain C-125
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A; Residues: 1-398 <STO>
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A; Residues: 1-398 < ROU>
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Best Local
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Best Local
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  242 HSHDKQKGIGHG
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                                                                                                        Score 51; DB 2
Pred. No. 0.87;
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Pred. No. 0.
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                                                                                        Mismatches
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A;Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up for A;Reference number: S66148; MUID:96134923
A;Accession: S66148
                                                                                                                                                                      C;Accession: S66148
R;Weber, U.; Siegel, V.; Mlodzik, M.
EMBO J. 14, 6247-6257, 1995
                                                                                                                                                                                                                                           gene pipsqueak protein A short form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Map position: 3
A; Introns: 163/2
A; Note: T20010.200
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A;Residues: 1-199 <OBE>
A;Cross-references: EMBL:AL163816
A;Experimental source: cultivar Columbia; BAC clone T20010
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein T20010.200 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C;Accession: T48099
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                       A; Molecule type: DNA
A; Residues: 1-535 <WEB>
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A;Experimental source: cv. Taichung 9
C;Comment: This protein is cold-induced.
C;Superfamily: cold stress protein COR19
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A;Accession: T07618
A;Status: translated from GB/EMBL/DDBJ
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Bot. Bull. Acad. Sin. 39, 9-15, 1998
A;Title: Characterization of a pea gene responsive to low temperature.
A; Cross-references:
                                                                          A;Status: preliminary
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A; Accession: T48099
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A; Residues: 1-110 < KUN>
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Best Local S
Matches 8
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Best Local Similarity 42.9%;
Matches 9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                       92 HGHGRGHGHGHG 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               33 HGHEHGHGAEYKGEEHGFGHG 53
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EMBL: X90986; NID: g1149498; PIDN: CAA62473.1; PID: g1149499
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66.7%;
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Pred. No. 0.
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C;Superfamily: POZ domain homology
F;21-123/Domain: POZ domain homology <POZ>
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""" 8; Conservative
332 HEHEHNHGHGHG 343
                      1 HGHEQQHGLGHG 12
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66.7%;
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Pred. No. 1.6;
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Search completed: July Job time: 643 sec

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Result
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Listing first 45 summaries
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Copyright (c) 1993 - 2000 Compugen Ltd.
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CH38_DROME
CH36_DROME
KE4_BRARE
CSUP_DROME
YML3_ARATH
PRSG_ECOL1
PIX1_DROME
                                                                     HYPB_RHOCA
SLYD_AERHY
DHN3_PEA
BOX5_NOTVI
SR68_DROME
SR68_HUMAN
SR68_CAEEL
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KE4L_CAEEL
KE4_HUMAN
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ANTF_SARPE
S109_RABIT
VG50_HSVI1
FSH_DROME
                                                                                                                           KE4_PIG
BR3A_MOUSE
ZNT1_MOUSE
ZNT1_RAT
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P17208
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P01044 bos taurus
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								P51606 homo sapien			P22239 craterostig	P23792 drosophila

## ALIGNMENTS

R R R R R R R R R R R R R R R R R R R	R R R R R	RRR	RT	RP	RRT	R R X	R R R	R R	RA RX	R R R	RT RT	R RX	7 R R	20000		RESI KNG ID
[6] DISULFIDE BONDS. Sueyoshi T., Miyata T., Kato H., Iwanaga S.; "Disulfide bonds in bovine HMW kininogens.";		Eur. J. Biochem. 152:307-314(1985). [5] SEOHENCE OF 381-380	W.; d sequence m.	SEQUENCE OF 379-644. MEDLINE=86030270; PubMed=4054110; Lottspeich F., Kellermann J., Henschen A., Foertsch B.,	ht kininogen.";	85122621; ., Kurachi on of a hu	J. BIOI. Chem. 260:8610-8617(1985). [3] SEQUENCE OF 1-401 FROM N.A.	ructural org	=298 , Fu	J. Biol. Chem. 260:8601-8609(1985). [2] GENE STRUCTURE.	ning and sequence analysis of conting and low molecular weight prehuman prekininogens.";	TISSUE=LIVEI; MEDLINE=85234582; PubMed=2989293; Takagaki Y., Kitamura N., Nakanishi S.;	SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW).	Homo sapiens (Human).  Homo sapiens (Human).  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  NCBI_TaxID=9806;	21-JUL-1986 (Rel. 01, Created) 01-FEB-1986 (Rel. 33, Last sequence update) 01-OCT-2000 (Rel. 40, Last annotation update) KININGEN PRECURSOR (ALPHA-2-THIOL PROTEINASE INHIBITOR) [CONTAINS: BRADYKININ].	RESULT 1  KNG_HUMAN STANDARD; PRT; 644 AA.

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THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TEXT OF THE TE
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PIR; A25276; A3
PIR; A01280; KC
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PIR; S02482; SC
SWISS-2DPAGE; I
                               CHAIN
CHAIN
                                                                                          SIGNAL
                                                                                                                                               Glycoprotein; Plas
Bradykinin; Blood
                                                                                                                                                                                                          PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN;
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Pfam; PF00031;
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11. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2).

11. FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2).

12. HAMP-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HAMP-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-INUGED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HAMP-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTRALANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION); (5) LAMP-KININOGEN IN HIBBITS THE AGGREGATION OF THROMBOCYTES; (6) LAMP-KININOGEN IS IN CONTRAST TO HAMP-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restitute European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                    InterPro; IPR000010; -.
InterPro; IPR002395; -.
                                                                                                                                                                                                                                                                                                                                                                   MIM; 228960;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; HWW (SHOWN PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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M11437;
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                                                                                                                                            287; CYSTATIN; 2.
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P01045;

21-JUL-1986 (Rel C

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KININOGEN, HMW II F

BRADYKININ)
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                SEQUENCE OF 19-376.
MEDLINE=87137530; PubMed=3546295;
                                                             weight kininogens.";
Nature 305:545-549(1983).
                                                                               "A single gene for weight kininogens."
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                                                                                                           Takagaki Y.,
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PRECURSOR (THIOL PROTEINASE
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Pred. No. 0.0001;
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Kato H.,
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(GLCNAC.
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 Hayashida
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Miyata

Iwanaga S.;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biol.
[3]
            Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
                                                   InterPro; IPRO00010; -.
InterPro; IPRO02395; -.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
                                                                                                                                                       EMBL; V01492; CAA24736.1; -.
EMBL; V01492; CAA24737.1; ALT_SEQ.
PIR; A01282; KGBOH2.
PIR; B29559; B29559.
HSSP; P04129; 1AFI.
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HELPING TO POSITION OPTIMALLY PREKALLIKESIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine high-molecular-weight
kininogen. Amino acid sequence of a fragment ('histidine-rich
peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
-i- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
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MEDLINE-70180420; PubMed-4986212;
Kato H., Nagasawa S., Suzuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 456-496
MEDLINE=75170265; Po
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Han Y.N., Kato H., Iwanaga S., Suzuki T.;
"Primary structure of bovine plasma high-molecular-weight kininogen.
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus of the bradykinin moiety.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       positions of carbohydrate chains and chain portion.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=76260155; PubMed=956151;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: EXTRACELLULAR.

ALTERNATIVE PRODUCTS: HAW II AND LAW II KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TO RESIDUE 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ACTION)
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                        positions of carbohydrate
chain portion.";
                                                                                                                           Bovidae; Bovinae; Bos.
NCBI_TaxID=9913;
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21-JUL-1986 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                        BOVIN
KNH1_BOVIN
SEQUENCE OF 378-393.
MEDLINE=70180420; PubMed=4986212;
                                            Sueyoshi T., Miyata T., Hashimoto N., Kato H., Miyata T., Iwanaga S.;
                                                           MEDLINE=87137530;
                                                                 SEQUENCE OF 19-378
                                                                               weight kininogens.";
Nature 305:545-549(1983).
                                                                                            "A single gene for
                                                                                                         MEDLINE=84014106; PubMed=6571699;
                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Peo
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                   J. Biol.
                                       "Bovine high molecular weight kininogen.
                                                                                                   Kitamura N., Takagaki Y.,
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bovine high molecular weight
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83.3%;
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(THIOL PROTEINASE INHIBITOR) (CONTAINS)
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PRINTS; PRO034; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing;
Glycoprotein; Plasma; Bradvkinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HAW-KININGEN ARE INHIBITORS OF THIOL PROTEASES; (2)
HAW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMW-KININGEN INHIBITS THE THROMEIN- AND
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(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIDOROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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PIR; A29559; A29559.
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J. Biochem. 77:55-68(1975).
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                                                                                                                                                                                                                                                                                                                                                                                            SIGNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=75170265; PubMed=1169237;
Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
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                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory response;
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SUBCELLULAR LOCATION: EXTRACELLULAR.

SUBCELLULAR LOCATION: EXTRACELLULAR.

ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PTM: BRADYKININ IS RELEASED FROM KININOGEN BY SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE SPECIFICITY: PLASMA.
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on the structure of bov
d of methionyl bonds in
em. 67:313-323(1970).
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
PYRROLIDONE CARBOXYLIC ACID.
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N-LINKED (GLCNAC. . .).
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                                                                                                  **Rageyama R., Kitamura N., Ohkubo H., Nakanishi S.;

**Differing utilization of home transcription initiation sites of rat K and T kininogen genes under inflammation condition.";

J. Biol. Chem. 262:2345-2351(1987).

-i- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

-HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND PACTOR XI NEXT TO PACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF THROMBOCYTES; (3) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF THE ACTIVE PROTECTION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF THE ACTIVE PER PROTECTION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF THE ACTIVE PER PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE PROTECTION OF THE 
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Structure and expression of the genes protein (thiostatin) and kiningen in t J. Biol. Chem. 262:9298-9308(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Primary structures of the mRNAs encoding the rat precursors bradykinin and T-kinin. Structural relationship of kininogens bradykinin and T-kinin and alpha 1-cysteine proteinase
                                                                                                                                                                                                                                                                                                                            STRAIN=WISTAR; TISSUE=Liver; MEDLINE=87137465; PubMed=3818598;
                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 1-41 FROM N.A.
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Mammalia; Eutheria; Rodentia;
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P08934; P08933;
01-NOV-1988 (Re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=86008264;
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                PHYSTOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
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pfam; pF00031; cystatin; 3.
prints; pR00334; KININOGEN.
pROSITE; pS00287; CYSTATIN; 2.
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININGEN BY PLASMA
MISCELLANEOUS: RAT EXPRESS FOUR TYPES OF KININGENS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 European
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HMW/LMW
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CC -!- FUNCTION: (1) KININGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

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CC -!- FUNCTOR XII, INDICATE OF THE OFFICE                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed. entitles requires a license agreement (See or send an email to license@isb-s.b.ch).
                                                                                                                                                    Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN; 1.
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                                                                                                Glycoprotein; Plasma; Repeat; T
Bradykinin; Blood coagulation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Takano M., Kondoh J., Yayama K., Okamoto H. "Molecular cloning of cDNAs for mouse low-
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Mammalia; Eutheria; Rodentia;
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ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
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BRADYKININ IS RELEASED FROM KININOGEN
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RESULT 6
CAUP_DROME
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Best Local
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                                                                                                                                               Ferres Marco D., Modolell J.;

"Araucan and caupolican, two members of the encode homeoproteins that control proneural Cell 85:95-110(1996).
                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VARSPLIC
SEQUENCE
                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CARBOHYD
                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=96180722; PubMed=8620542;
                                                                                                                                                                                                                                           NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                   Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                               460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
       ween the Swiss Institute of Bioinformatics and the EMBL outstati
European Bioinformatics Institute. There are no restrictions on
by non-profit institutions as long as its content is in no
lified and this statement is not removed. Usage by and for comment
ities requires a license agreement (See http://www.isb-sib.ch/annou
                                                                             TRANSCRIPTION INITIATION.
SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
SIMILARITY: BELONGS TO THE TALE/IRO FAMILY OF HOMEOBOX PROTEINS.
                                                                                                                       FUNCTION: CONTROLS PRONEURAL AND VEIN FORMING GENES. POSITIVE TRANSCRIPTIONAL CONTROLER OF AC-SC (ACHAETE-SCUTE). MAY ACT A ACTIVATOR THAT INTERACTS WITH THE TRANSCRIPTIONAL COMPLEX
                                                                                                               ASSEMBLED ON THE AC AND SC PROMOTERS AND
                                                SWISS-PROT entry is copyright. It is produced through en the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                             DROME
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an
email to license@isb-sib.ch)
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661 AA;
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73102 MW;
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75.0%;
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KININOGEN LIGHT C
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

N-LINKED (GLCNAC...) (POTENTIAL).

VSPPYIAREQEERDAETEQGPTHGHGWLHEKQ ->
CEYKGRLSKAGAEPAPERQAESSQVKQ (IN ISO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 62; DB 1;
Pred. No. 0.012;
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and vein-forming
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RESULT 7
ANTF_SARPE
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Best Local
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                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                    J. Biol. Chem. 268:12055-12061(1993).
                                                        Fungicide;
                                                                     EMBL; D13797; BAA02954.1; PIR; A45969; A45969.
                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                               +++
                                                                                                                                                                                                                                                                                                                                      MEDILING P., Kurata S., Natori S.;
Iijina R., Kurata S., Natori S.;
"Purification, characterization, and cDNA cloning of an antifungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Oestroidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sarcophaga peregrina (Flesh fly) (Boettcherisca peregrina).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-MAY-2000 (Rel. 39, Last annotation ANTIFUNGAL PROTEIN PRECURSOR (AFP).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X95178; CAA64485.1; -
HSSP; P02833; 1SAN.
FlyBase; FBgn0015919; caup.
InterPro; IPR001356; -.
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                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=93280179; PubMed=8505329;
                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=7386;
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                                                                                                                                                                                                                            SUBUNIT: HOMODIMER.
TISSUE SPECIFICITY: HEMOLYMPH.
PTM: THE N-TERMINUS IS BLOCKED.
                                                                                                                                                                                                                                                                    FUNCTION: THIS PROTEIN INHIBITS THE GROWTH OF A VARIETY FUNGAL SPECIES. THE ANTIFUNGAL ACTIVITY OF THIS PROTEIN ENHANCED BY THE PRESENCE OF SARCOTOXIN IA.
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31, Last sequence
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75.08;
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POTENTIAL.
ANTIFUNGAL PROTEIN.
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POLY-SER.
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Pred. No. 0.11;
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CA_BIND 9
CA_BIND 53
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P50117;
01-OCT-1996
15-JUL-1999
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SEQUENCE
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                  REPEAT
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PROSITE; PS00018; EF_HAND;
PROSITE; PS00303; S100_CABI
                                                                                                                                                                              Pfam; PF01023; S_100; 1. Pfam; PF00036; efhand; 1
                                                                                                                                                                                                                                                           EMBL; AF091849; AAC61771.1; -. EMBL; D17404; BAA04227.1; -.
                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mori S., Goto K., Goto F., Mutakami K., Ohkawara S., Yoshinaga M.; "Dynamic changes in mRNA expression of neutrophils during the cour of acute inflammation in rabbits.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-NEW ZEALAND WHITE; MEDLINE-94198229; PubMed-8148323;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-calgranulin C when incubated with inorganic [35S]sulfate."; C. Biol. Chem. 271:19802-19809(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-NEW ZEALAND WHITE: TISSUE-Neutrophils; MEDLINE-96355278; PubMed-8702688;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Cı
Mammalia; Eutheria; Lagomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S100A9 OR MKr-14.
Oryctolagus cuniculus (Rabbit).
Vertebrata;
Oryctolagus cuniculus (Rabbit).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (MRP-14) (FRAGMENT).
S100A9 OR MRP-14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-CCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN
                                                  DOMAIN
                                                                                                                                                                                                              InterPro; IPR002048; -.
InterPro; IPR002395; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Underwood
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                                                                                                                                                                                                                                                InterPro; IPR001751; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      . Immunol. 6:149-156(1994).
SIMILARITY: BELONGS TO THE S-100 FAMILY.
SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Z., de Veer M.J., Gardiner E.E.,
rwood J.R., Robinson H.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGGQDQHGYGHG
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                                                                                                          Repeat.
                                                                                                                              EF_HAND; 1.
S100_CABP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33
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9018
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64
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Pred. No. 0.05
1; Mismatches
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SITE II ()
2 X 8 AA '
G-H-S-H.
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E381779F923FB69B CRC64;
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                                                              I (LOW AFFINITY) (POTENTIAL)
II (HIGH AFFINITY) (POTENTIA
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                                                 TANDEM
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0.057;
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the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Viruses; dsDNA viruses, no unclassified Herpesviridae.
                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                           EMBL; M75136; AAA88153.1;
                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Channel catfish virus:
Virology 186:9-14(1992).
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Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
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EMBL; M23221; AAA28541.1; ALT_TERM.
EMBL; M23222; AAA28541.1; -
EMBL; M15762; AAA70422.1; -
EMBL; M15763; AAA70423.1; -
EMBL; M15763; AAA70422.1; -
EMBL; M15742; A43742
PIR; A43742; A43742
PIS; P04002; 1MFA.
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Dev. Biol. 134:246-257(1989).
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                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF00439; bromodomain;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
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Best Local
           TRANSMEM
TRANSMEM
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SEQUENCE FROM N.A.
MEDLINE-92375034; PubMed-1508175;
MCMaster J.A., Cubbertson M.R.,
Conklin D.S., McMaster J.A. Cubertson M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COT1_YEAST
P32798;
01-OCT-1993
                                                                                                          EMBL; M88252; AAA74884.1; -. EMBL; X90565; CAA62171.1; -. EMBL; Z75224; CAA99636.1; -.
                                                                                                                                                                                 use by non-profit institutions as long modified and this statement is not removed entities requires a license agreement (See
                                                     InterPro; IPR002524; -.
Pfam; PF01545; Cation_efflux;
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                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                      Yeast 12:1021-1031(1996).

-i- FUNCTION: PROBABLY RESPONSIBLE FOR THE UPTAKE OF COBALT IONS. APPEARS TO ACT IN A DOSAGE-DEPENDENT MANNER TO COUNTERACT THE ADVERSE EFFECTS OF COBALT IONS ON CELLS. IT MAY PARTICIPATE IN THE REGULATION OF COBALT LEVELS UNDER KORMAL PHYSIOLOGICAL CONDITIONS AND MAY BE IMPORTANT IN THE SUPPLY OF METALLOENZYME OR COFACTOR SYNTHESIS. IT REDUCES TOXICITY OF COBALT AND RHODIUM IONS. OTHER COMPONENTS RESPONSI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COBALT UPTAKE PROTEIN COT1.
COT1 OR YOR316C OR O6131.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1993 (Rel.
01-OCT-1996 (Rel.
30-MAY-2000 (Rel.
                                       Transport;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schweizer M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97051589; PubMed=8896266;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 HGHEQQHGLGHG 12
                                                                                                                                                                                                                                                                             FOR COBALT TRANSPORT EXIST.
SUBCELLULAR LOCATION: MITOCHONDRIAL MEMBRANE. ANOTHER POSSIBILITY
EXISTS THAT IT IS ASSOCIATED WITH ANOTHER UNIDENTIFIED MEMBRANE
THAT HAS BEEN ENRICHED IN THE MITOCHONDRIAL MEMBRANE FRACTIONS.
SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.
                                                                               S31302; S31302.
S0005843; COT1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       нснснснснс 607
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8; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 g of a 35.71 kb DNA segment on the right arm of XV reveals regions of similarity to chromosomes
                                       Cobalt; Mitochondrion;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. 12:3678-3688(1992).
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34, Last sequence up
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66.7%;
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Pred. No.
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                                       Transmembrane.
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in Saccharomyces
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Perfect score:
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 spTREMBL_16:*
1: sp_archea:*
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4: sp_inverteb:
6: sp_mammal:*
5: sp_mac:*
7: sp_mhc:*
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11: sp_rodent:
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Gapop 10.0 , Gapext 0.5
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sp_bacteria:*
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sp_virus:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

19	18	17	16	15	14	13	12	11	10	9	8	7	6	ر ت	4	ω	2	_	Result
50	50	50	50.5	51	51	51	51	51	51	51	51	51	54	54	54	55	56	62	Score
66.7	66.7	66.7	67.3	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	68.0	72.0	72.0	72.0	73.3	74.7	82.7	Query Match 1
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Q9V5N1	Q9GTN0	Q9LYB2	064396	Q9W2S4	077280	Q9W4I6	Q9K9A8	081036	Q9W2X1	Q9ZRC7	022671	Q9M435	Q9VXG3	086731	Q9VYP3	Q9PJ12	Q9VU00	009016	ID
Q9v5n1 drosophila	Q9gtn0 drosophila	Q9lyb2 arabidopsis	064396 pisum sativ	Q9w2s4 drosophila	077280 drosophila	Q9w4i6 drosophila	Q9k9a8 bacillus ha	O81036 arabidopsis	Q9w2x1 drosophila	Q9zrc7 alnus gluti	022671 alnus gluti	Q9m435 quercus rob	Q9vxg3 drosophila	O86731 streptomyce	Q9vyp3 drosophila	Q9pj12 campylobact	Q9vu00 drosophila	009016 rattus norv	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20
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60.0	60.0	60.0	60.0	60.0	61.3	61.3	61.3	61.3	62.0	62.7	62.7	62.7	62.7	64.0	64.0	65.3	65.3	65.3	65.3	65.3	65.3	65.3	65.3	66.0	66.7
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Q9vex1 drosophila	Q9grw9 drosophila	Q9jkn2 mus musculu	Q9qvz9 mus sp. brn	005673 mycobacteri		_	Q9nnv9 plasmodium	Q9vwm5 drosophila	Q18401 caenorhabdi	Q9x9w6 streptomyce	049678 arabidopsis	Q9m0l8 arabidopsis	Q43520 lycopersico	Q9w0q4 drosophila	Q9y0e4 drosophila	Q9w3l3 drosophila	Q9nes7 caenorhabdi	Q9vws0 drosophila	Q9w4c1 drosophila	Q26227 rhynchoscia	_	Ģ	Q9gtn1 drosophila	Q9v3p9 drosophila	Q24455 drosophila

## ALIGNMENTS

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LT 2 00 29 <b>v</b> u00	1 HGHEQQHGLGHG 	Query Match Best Local Sim Matches 9;	KININGEN (FRAGMEN KINGK. Rattus norvegicus (R Eukaryota; Metazoa; ( Eukaryota; Metazoa; ( Mammalia; Eutheria; NCBI_TaxID=10116; [1] NCBI_TaxID=10116; [1] SEQUENCE FROM N.A. STRALN=DONRYU; MEDLINE=97468288; Pul Harris E.L., Grigor J Jacob H.J.; "Strain-specific dell kininogen genes allo Mamm. Genome 8:791-77. EMBL; AFO03562; AACO Interpro; IPR002395; PRINTS; PR00334; KIN NON_TER NON_TER 126 AA;	ILT 1 116 009016 009016; 01-JUL-1997 01-JUL-1997
PRELIMINARY;	HGLGHG 12         HGLGHG 49	n 82.7%; Similarity 75.0%; 9; Conservative	RAGMENT).  RAGMENT).  azoa; Chordal eria; Rodent. 16;  N.A.  N.A.  N.A.  PubMed=9: rigor M.R.;  ic deletions is allow mapp: 791-792(1997). AAC09070.1. 02395; AAC09070.1. 4; KININGGEN 4; KININGGEN AA; 14092	PRELIMINARY; (Tremblrel 04, (Tremblrel 04,
PRT;		Score 6 Pred. N 2; Mism	ia; Craniata; ia; Sciurogna ia; Sciurogna 221484; [Innes B.A., H in exon 10 o ing of both g )). ;	PRT; Created) Last seq
693 AA.		re 62; DB 11; Length 126; d. No. 0.0067; Mismatches 1; Indels 0; Gaps 0	Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Rattus.  84; 8 B.A., Harrap S.B., Koike G., exon 10 of rat K-kininogen and T1- of both genes to rat chromosome 11.";  9 CCDF8751DA49C88 CRC64;	r; 126 AA. Led) Sequence update)
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                                                                                                                                                                         RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Mogres Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Brandon R.C., Mogres Y.-H.C., Blazej R.G., Champe M., Pfeliffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Hehman T.J., Wei M.-H., Ibeyaum C.,
RA Harris N.L., Harvey D., Hehman T.J., Wei M.-H., Ibeyaum C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kull D., Lai Z.,
Lai X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Remington K., Stangeon M., Skupski M.P., Smith T.,
RA Reinert K., Remington K., Stangeon M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
"The genome sequence of Drosophila melanogaster.";

C. --- Subcelling R.N., Zhong W., Zhong S., Zhu X., Smith H.O.,
RA Jane G., Sheng S., Jane M., Shith H.O.,
RA Jane G., Sheng S., Jane M., Shith H.O.,
RA Jane G., Sheng S., J
                                                                                            Query Match
Best Local
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: TO OTHER HOMEOBOX DOMAINS. EMBL; AE003540; AAF49895.1; -.
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Amanatides P.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                          FlyBase; FBgn0015919; caup.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ephydroidea;
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656 HGHGHGHGLGHG
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                                                                                                                                                                                                                                                                                            nterPro;
                                                                                          Local
                                  1 HGHEQQHGLGHG
                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY)
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
                                                                          Conservative
                                                                                                                                                                       Homeobox; Nuclear protein.
93 AA; 73667 MW; FBEB1616493F7EC9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              coptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Drosophilidae; Drosophila.
667
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                                                                                          74.7%;
75.0%;
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"The genome sequence of the food-borne pathogen Campylobacter je reveals hypervariable sequences.";
Nature 403:665-668(2000).
                                                                                                                                         MEDLINE-20196006; PubMed-10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Ananatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Rogers M., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Baldwin D.,
Brandon R.G., Baldwin D.,
Brandon R.G., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
Brandon R.G., Baldwin R.G., Baldwin D.,
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Brandon R.G., Baldwin R.G., Baldwin R.G., Baldwin R.G.,
Brandon R.G., Baldwin R.G., Bal
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Q9YVP3;
01-MAY-2000 (TrEMBLrel 13;
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01-MAR-2001 (TrEMBLrel 16;
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Q9PJ12;
01-OCT-2000
01-OCT-2000
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S., Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P., de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
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STRAIN-NCTC 11168;
MEDLINE-20150912; PubMed-10688204;
Parkhill J., Wren B.W., Mungall K.,
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Bacteria; Proteobacteria;
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01-CCT-2000 (TrEMBLrel. 15, Last sec
01-MAR-2001 (TrEMBLrel. 16, Last and
PEPTIDYL-PROLYL CIS-TRANS ISOMERASE.
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Last annotation update)
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47B5F5D047549D7F CRC64;
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a; Brachycera; Musc
                                            Center A., Chandra I.,
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RA Durbin K.J., Evangelista C.C., Ferriara S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J. Li Z., Liang-Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
DR EMBL; AE003488; AAF48149.1:
DR F19Base; FBgn0030378; CG15733.
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                         Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical map
                                                                                                                                                                STRAIN-A3(2);
Parkhill J.,
                                                                                                                                                                                                                                                              STRAIN-A3(2);
                                                                                                                                                                                                                                                                                                                               Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
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01-NOV-1998 (TrEMBLrel. 08, La
01-JUN-2000 (TrEMBLrel. 14, La
HYPOTHETICAL 33.6 KDA PROTEIN.
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01-NOV-1998
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                                                                         MEDLINE=97000351; PubMed=8843436;
                                                                                                              SEQUENCE FROM
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nes 8; Conserv
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Mb Streptomyces coelicolor A3(2) chromosome.";
Microbiol 21:77-96(1996).
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e EMBL/GenBank/DDBJ databases
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RA Becson K.Y., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Becson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Derrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
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RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.M., Li J., Li Z., Liang Y., Lin X.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Mount S.M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Paeleb J.M.,
RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Rhine R. C. Siden Kimmos T. Sinnson M. Skinski M. D. Smith T.
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Best Local
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               Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T. Spler E., Spradling A.C., Stapleton M., Strong R., Sun E., Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Wooddage T., Worley K.C., Wu D., Yang S., Yao Q. Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zhe Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smi Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., "The genome sequence of Drosphila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q9VXG3;
Q9VXG3;
01-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
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SIGNAL
SEQUENCE
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01-NOV-1998 (TrEMBLrel.
AG164 PROTEIN PRECURSOR
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TISSUE-IN VITRO SHOOT CULTURES;
Gil B., Pastoriza E.M., Ballester A., Sanchez C
"Identification of a phase-change related mRNA
derived from basal sprouts and crown branches."
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ d
EMBL; AJ271778; CAB72442.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Owercus robur (English oak).
Eukaryota; Viridiplantae; Embry
Magnoliophyta; eudicotyledons;
Fagales; Fagaceae; Owercus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00191; annexin; 4.

PRINTS; PR00196; ANNEXIN.

PRINTS; PR00334; KININOGEN.

PRINTS; PR01217; PRICHEXTENSN.

PROSITE; PR00223; ANNEXIN; 3.

PROSITE; PS00142; ZINC_PROTEASE; UNKNOWN_1.

Annexin; Calcium/phospholipid-binding; Repeat.

Annexin; Calcium/phospholipid-binding; Repeat.

SEQUENCE 511 AA; 56214 MW; 74712A8F1C54283B
   Alnus
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HSSP; P79134; 1AVC.
FlyBase; FBgn0030749; Anxb11.
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InterPro; IPR001464;
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lons; core eudicots; Rosidae; eurosids I;
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Pred. No. 0.53
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TISSUE-ROOT NODULES;
Dobritsa S.V., Mullin B.C.;
"In vitro expression of actinorhizal nodulin AgNOD-GHRP and demonstration of its toxicity of Escherichia coli.";
(In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);
the Biology of Plant Microbe Interactions:
Proceedings of the 8th International Symposium on Molecular - The Advance Interactions, pp.1-1, Unknown Publisher (1996)
   PRINTS; F
SEQUENCE
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01-MAY-1999
01-MAY-1999
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ACTINORIZAL
                                                                                   actinorhizal nodule development. Submitted (SEP-1996) to the EMBL EMBL; U69156; AAD00171.1; -.
                                                                                                                                                                                 Pawlowski K., Twigg P.G., Dobritsa S.V., (
"A nodule-specific gene family from Alnus
and histidine-rich proteins expressed in t
                                                                                                                                                                                                                                                                                                                                                                               protein from Alnus
Thesis (1993), The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Embry
Magnoliophyta; eudicotyledons;
Fagales; Betulaceae; Alnus.
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                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                     "Isolation of a nodule-specific cDNA encoding protein from Alnus glutinosa."; Thesis (1993), The University of Tennessee, Kr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Twigg P.G.;
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Alnus glutinosa
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NCBI_TaxID=3517;
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   2ACBE4D57C070E83 CRC64;
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
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RA Dodson K., Doup F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Rainert K., Remington K.A., Sinpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
RA Shue B.C., Siden-Kiamos I., Sinpson M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
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RA Yel J., Yeh R., -F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
RA Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Zheng X.H., Schols S., Pollard J., Puri S., Zhu X., Smith H.O.,
RA Zheng S., Shan M., Woodage T., Wonley K.C., Wu D., Yang S., Yao Q.A.,
Ra Zheng X.H., Zhong W., Zhou X., Zhu X., Smith H.O.,
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Q9W2X1;
01-MAY-2000
01-MAY-2000
01-JUN-2000
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                                                                                                           FlyBase; FBgn0030187; CG2961.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20196006; PubMed=10731132;
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Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota;
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                                                                        InterPro;
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8; Conservative
                                          PR00334;
                                                                            IPR002395;
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KININOGEN.
A; 33212 M
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Last sequence update)
Last annotation update)
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   8DB719D2AEB8B374 CRC64;
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081036;
01-NOV-1998
                                                                                               Pfam; PF(
SEQUENCE
                                                                                                                                                                                                                                                                                           01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation updat
ATP/GTP-BINDING PROTEIN (IMPB/MUCB/SAMB FAMILY).
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01-MAY-2000 (TrEMBLrel. 13
PUTATIVE ZINC TRANSPORTER.
                                                                                                                                       STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Taka
Submitted (MAR-2000) to the
EMBL; AP001516; BAB06460.1;
                                                                                                                                                                                                                                                                                                                                       Q9K9A8;
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., M
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Ven
"Arabidopsis thaliana chromosome II BAC F19D11 genomic s
submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AC005310; AAC33498.1; -.
InterPro; IPR002524; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillus/Staphylococcus
                                                                                                                                                                                                                                                                     Bacillus halodurans.
                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                          NCBI_TaxID=86665;
                                                                                                                                                                                                                                                                                    BH2741
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                                                                                                           InterPro; IPR001126; Pfam; PF00817; IMS;
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1 HGHEQQHGLGHG 12
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NCE 398 AA; 43827 MW;
                          7; Conser
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8; Conser
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8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PREMALE 1. 08, C1 (TREMBLIE 1. 08, L) (TREMBLIE 1. 08, L) (TREMBLIE 1. 08, L)
                           Conservative
                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Brassicaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N.A.
                                                                                               IMS;
                                                                                                                                                                                                                                                                                                                                                                                                                                           195
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                                                                                                46251 MW;
                                         68.0%;
58.3%;
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                                                                                                                                                                                                                                         Bacillus/Clostridium group; us group; Bacillus.
                                                                                                                                                                      Takaki Y.
                                                                                                                                                                                                                                        group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis.
                                                                                                                                                     EMBL/GenBank/DDBJ databases
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                                         Score 51; I
Pred. No. 1
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Pred. No. 1.
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L; Mismatches
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7E20E0B29237BB23 CRC64;
                                                                                                5721AC1D8FDD3722 CRC64;
                           Mismatches
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                                      DB
1.3;
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1.2;
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Db

242 HSHDKQKGIGHG

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RA Addams N.D., Celniker S.E., Hilt R.A., Evans C.A., Golayne J.D.,
RA Addams N.D., Celniker S.E., Hilt R.A., Sabburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burtis K.C., Basua A., Baxendale J., Beyzakrarglu L., Bessley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Beyzakrarglu L., Bessley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Bortova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bortova D., Botchen A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K.C., Dauber A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Colory J.M., Cawley S., Dahlke C., Davenport L.B., Davkes P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrica S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gunn P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lii X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Reinert K., Semington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Syler E., Syradling A.C., Stapleton M., Strong R., Sun E.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Hoston C., Year J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Hoston C., Stapleton M., Strong R., Sun E.,
Schence 287:2185-2195(2000).
                                                                        Matches
                                                                                                                                                               EMBL; AE003431; AAF45965.1; -. FlyBase; FBgn0025613; EG:84H4.4 SEQUENCE 457 AA; 48919 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W4I6;
01-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EG:84H4.4 PROTEIN.
EG:84H4.4 OR CG3081.
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341 НСИННЕНСИСНО
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                           Local
                      1 HGHEQQHGLGHG 12
                                                                      Similarity
8; Conserv
                                                                      Conservative
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 352
                                                                                       68.0%;
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13,
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Last annotation update)
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                                                                                       Score 51; DB
Pred. No. 1.4;
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                                                                      Mismatches
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077280
                 Query Match
Best Local Similarity
Matches 8; Conserv
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Q9W2S4;
01-MAY-2000 (TrE
01-MAY-2000 (TrE
01-JUN-2000 (TrE
CG9732 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             077280
                                                                                                                                                                                                    STRAIN-BERKELEY;
                                                                                                                                                                                                                                             Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                          MEDLINE=20196006;
                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                             CG9732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases EMBL; AL031766; CAA21135.1; -FlyBase; FB990025613; EG:84H4.4. SEQUENCE 605 AA; 64947 MW; B06C84AC4D7D2C84 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;
Ferraz C. Vidal S., Brun C., Bucheton A., Demaille J.G.;
Sequencing the distal X chromosome of Drosophila melanogaster.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1998 (TremBLrel.
01-MAR-2001 (TremBLrel.
EG:84H4.4 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Benos
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                                                                                                                                                                                                                                                                                                                                                                                                                  341 НСНИНСИСИСИ 352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14
                                                                                                                                                                                                                                                                                                                                                                                                                                     1 HGHEQQHGLGHG 12
Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 13, ) (TrEMBLrel. 13, ) (TrEMBLrel. 14,
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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                                                                                                                                                                                        PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      68.0%;
66.7%;
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 51;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
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1.9;
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                                                                                                                                                                                                                                                          Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 605
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KE4_PIG
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Best Local S
Matches 7
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Best Local
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NON_TER
SEQUENCE
                                                                                                                                                                                                  TRANSMEM
DOMAIN
DOMAIN
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2029175; 09XT01;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-Belgian Landrace; Chardon P., Rogel-Gaillard C., Peelman L.J., Yerle M., Renard C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Winteroe A.K., Fredholm M., Davies "Evaluation and characterization of Ilbrary: analysis of 839 clones."; Mamm. Genome 7:509-517(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HKE4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                          EMBL; AF146397; AAD44801.1;
                                                                                                                                                                                                                                                                                           EMBL; F14787; CAA23256.1; +.
                                                                                                                                                                                                                                                                                                                        or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                   This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           class II region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 125-155 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sus scrofa (Pig)
                                                                                                                                                                                                                                                             Transmembrane.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Small
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 1-124 FROM
                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96327607; PubMed=8672129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Physical organization of the swine major histocompatibility complex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /aiman M.;
                   49
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                   HGHSHGHGHAHG
                                              HGHEQQHGLGHG
                                                                                                                                                                                                                                                                                                                                                                                                SWISS-PROT entry is copyright. It is produced through a collaboration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        НGHSHAHGHGH 66
                                                                            Similarity 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 7; Conserv
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19
49
81
124
155
                                                                              Conservative
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39
59
86
125
                                                                                                                                                     16840 MW;
                                                                                         60.0%;
58.3%;
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63
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Pred.
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HIS-RICH.
POLY-GLU.
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Pred.
                                                                                                                                                       56354DE3CAAE4524 CRC64;
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                                                                              Mismatches
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                                                                                         No. 1.3;
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Cytogenet. Cell Genet. 66:267-271(1994).
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
NCBI_TaxID=10090;
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01-OCT-2000 (Rel. 40, Last annotation update)
BRAIN-SPECIFIC HOMEOBOX/POU DOMAIN PROTEIN 3A
POU4F1 OR BRN3A OR BRN3 OR BRN-3.
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Theil T., Zechner U., Klett C., Adolph S., "Chromosomal localization and sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUBCELLULAR LOCATION: NUCLEAR.
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL KE4-LIKE PROTEIN H13N05.5 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
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EMBL; AF117221; AAD12305.1;
EMBL; AL031228; CAA20238.1;
                                                                                                                                                                                                                                                                                                                                                                                              Tubby B.;
Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ando A., Kikuti Y.Y., Shigenari A., Kawata H., Okamoto N., Shii Chen L., Ikemura T., Abe K., Kimura M., Inoko H.; "cDNA cloning of the human homologues of the mouse Ke4 and Ke6 at the centromeric end of the human MHC region.";
                                                                                                                             TRANSMEM
                                                                                                                                                                                       Transmembrane;
                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                 modified
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MEDLINE=97001166;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
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INTEGRAL MEMBRANE PROTEIN (PR
N-LINKED (GLCNAC. . .) (POTENTIAL).
A -> G (IN REF. 1 AND 2).
E -> G (IN REF. 1 AND 2).
S -> T (IN REF. 1 AND 2).
CALLTEGGAVGSEIAGGAGPGWYLFTAGGFIYVATVSYLP
ELLREASPLQSLLEVLGLLGGVIMMVLIAHLE -> VPFSL
KEEQMTYKLOVYGYLAGSCHLLQVALST (IN REF. 1
AND 2).
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HIS-RICH.
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PLACENTA, LUNG, KID
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RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Haslin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Retchum K.A.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Sylrskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z. Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong W., Zhou X., Zhu X., Smith H.O.,
RA Clubs R.A., Myers E.W., Rubin G.M., Venter T.C.,
RA Clubs R.A., Myers E.W., Rubin G.M., Venter J.C.,
RA Pathurs, PRO0334; KININOGEN,
SO SEDUENCE 989 AA; 98851 MW; 642726D9EDADECB4 CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 3.1;
Matches 8; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Mismatches 8; Completed: 0; Mismatches 4; Indels 0; Gaps 0;
Job Lime: 988 sec
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Maximum DB seq
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      length:
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    AAY81993
AAW07628
AAW07628
AAY93346
AAY93346
AAY93348
AAR75186
AAR933317
AAX93351
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Human high molecul
Human high polymer
Human high molecul
Light chain of hum
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partial peptide of
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Partial peptide of
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Partial peptide of
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## ALIGNMENTS

RESULT AAY81993

1

AAY81993 standard; peptide; 12

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AC AAY81993;

XX

DT 16-OCT-2000 (first entry)

XX

DE Human high molecular weight kininogen domain 5 fragment #2.

XX

KW Human; high molecular weight kininogen; HK;

KW two-chain high molecular weight kininogen; HKa;

KW angiogenesis inhibition; tumour; cancer; ocular disorder;

KW angiogenesis inhibition; tumour; cancer; ocular disorder;

XX

XX

NS

Homo sapiens.

XX

PD

18-MAY-2000.

XX

PD

18-MAY-2000.

XX

PF

05-NOV-1999; 99WO-US26419.

XX

PF

(UTEM ) UNIV TEMPLE.

PA

(MCCR/) MCCRAE R K.

XX

DR

WPI; 2000-376483/32.
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A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis

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RESULT
AAW07628
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        weight kiningen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kiningen (HKa) by plasma kallikrein. HKa or a synthetic compound comprising part or all of the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by analowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis methods
                                                                             The present peptide is derived from residues 402-498 of the human high polymer quininogen L-chain. It was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                       Sequence
                                                                                                                                                                 Cell adhesion inhibiting peptide(s), used as cancer metastasis inhibitor - comprises partial amino acid sequence of human high polymer quininogen L chain
                                                                                                                                                                                                                          WPI; 1996-421988/42
                                                                                                                                                                                                                                                                                 28-SEP-1994;
                                                                                                                                                                                                                                                                                                                                                                      JP08208692-A.
                                                                                                                                                                                                                                                                                                                                                                                                                         Human; high polymer; quininogen; L-chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human high polymer quininogen L-chain derived peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAW07628;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW07628 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 5;
                                                                                                                                      Example; Page 8; 14pp; Japanese
                                                                                                                                                                                                                                                      (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                                                                                                             28-SEP-1995;
                                                                                                                                                                                                                                                                                                                                          13-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  phase synthesis methods.
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mes 12; Conserv
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                                                       20 AA;
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100.0%;
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Score
Pred.
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Pred. No.
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No.
DB 17;
1.8e-05;
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           Length 20;
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Best Local Similarity Matches 12; Conserv

Conservative

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Mismatches

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RESULT
AAY81996
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                                                                                                                                                   The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell proliferation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             two-chain high molecular weight kininogen; HKa; angiogenesis inhibition; tumour; cancer; ocular disorder; rheumatoid arthritis; endothelial cell apoptosis.
                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 28; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                               A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                              methods.
                                                                                                            chemically
                                                                                                                        peptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-376483/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human high molecular weight kininogen domain 5 fragment #5
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(MCCR/) MCCRAE R K.
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                                                                                                           apoptosis. Peptides used in the compostion may be recombinant ides, natural peptides, or synthetic peptides. They may also bically synthesised, using, for example, solid phase synthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LDDDLEHQGGHV 12
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                                                             28 AA;
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100.0%;
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 Score 68; DB 21;
Pred. No. 2.6e-05;
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              Length 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                             Best Loc
Matches
                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                               The present sequence represents a fragment of the light chain of huma high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UTEM )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
           04-SEP-2000
                                   AAY93346;
                                                           AAY93346
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3; Page 36; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Method for inhibiting endothelial cell proliferation, using that inhibit endothelial cell migration \,\cdot\,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman WR, Mousa AS
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                                                                                                                                                   1 LDDDLEHQGGHV 12
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12; Conserv
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DUPONT PHARM CO
COLMAN W R.
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                                                           standard;
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                                                                                                                                                                                                                                           47
                                                                                                                                                                             Conservative
          (first entry)
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                                                                                                                                                                                                                                           ΑA,
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                                                          peptide;
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100.0%; P
ative 0;
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                                                             55
                                                                                                                                                                           Score 68; DB 21;
Pred. No. 4.7e-05;
; Mismatches 0;
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                                                                                                                                                                                                   Length 47;
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RESULT
AAY93348
ID AAY9
XX AAY9
XX AAY9
XX Ligh
DT 04-5
DT Ligh
XX Ligh
XX Huma
KW Huma
KW Plas
KW endc
XX Synthom
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Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells; where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                        Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                   04-SEP-2000
                                                                                                                                                                               AAY93348;
                                                                                                                                                                                                          AAY93348 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colman WR, Mousa AS
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                                                                                                                     Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                                                                                                 Local Similarity
nes 12; Conserv
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                                                                                                                                                                                                                                                                                                                   1 LDDDLEHQGGHV
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                                                                                                                                                                                                                                                                                     4; Page
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cell migration
                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                             Score 68; DB 21;
Pred. No. 5.6e-05;
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                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                            Length 55;
                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                 0
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0

Synthetic. Homo sapie

sapiens

WO200027415-A2

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RESULT
AAR75186
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be inhibiting endothelial cell proliferation. The compounds can also be
WPI;
                         (FARH ) HOECHST JAPAN KK
                                                 17-SEP-1993;
                                                                         17-SEP-1993;
                                                                                                                           JP07082172-A
                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                           Partial peptide of human HMW kininogen fragment
                                                                                                                                                                                                                                     05-DEC-1995
                                                                                                                                                                                                                                                                                    AAR75186 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        kininogen analogues. The method and the compounds can be used to inhibiting endothelial cell proliferation. The compounds can also used for inhibiting angiogenesis. The compounds can also be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 6; Page 37;
                                                                                                                                                                           wound
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les 12; Conserv
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 1995-158909/21
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) DUPONT PHARM CO.
) COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                            100.0%; ilarity 100.0%; Conservative
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                                                  93JP~0230616
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                endothelial cells to vitronectin.
                                                                                                                                                                          bovine;
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bovine; growth
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                   fragment;
                                                                                                                                                                          promotion;
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. 6.4e-05;
ches 0;
                                                                                                                                                                                    1.2;
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Best Local Similarity
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The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for
                                                                                                                                                                                                                                                                       (UTEM )
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(COLM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   agent compsns. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                       Claim
                                                                                                                                                                            Method for inhibiting
                                                                                                                                                                                                                                   Colman WR,
                                                                                                                                                                                                                                                                                                                                                      09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cell proliferation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high molecular weight kininogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 8; Page 8; 8pp; Japanese.
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                                                                                                                                                                                                                                                                     DUPONT PHARM CO-
COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
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                                                                                                                                                                                                                                   Mousa AS
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ilarity 100.0%;
Conservative (
                                                                                                                                                              nhibiting endothelial cell proliferation, using compound endothelial cell migration
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                                                                                                                                       37;
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Pred. No.
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of fibroblasts.
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6.5e-05;
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The fragments are
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Query Match
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                                                                  The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting anglogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
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                                                                                                                                                                                                                          Claim
                                                                                                                                                                                                                                               Method for inhibiting endothelial cell proliferation, using that inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                                  WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                         Colman WR, Mousa AS,
                                                                                                                                                                                                                                                                                                                                                                                                                  09-NOV-1999;
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DUPONT PHARM CO
COLMAN W R.
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 Score 68;
Pred. No.
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Pred. No. 8.8e-05;
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cell migration; vitronectin.
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          Length 94;
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                                                                                                         AAY93353;
Synthetic
                     endothelial
                               Human; high molecular weight kininogen; glycoprotein; endothelial cell;
plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                              Light chain
                                                                                     04-SEP-2000
                                                                                                                             AAY93353 standard;
                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                          on fibroblasts
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                                                                                                                                                                                                                                                                                                                                                                                                         A wound treating agent contg. a have growth promotion activity of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Partial peptide of human HMW kininogen fragment 1.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-DEC-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17-SEP-1993;
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                                                                                                                                                                                                                                                                                    131 AA;
                                                               of human high molecular weight kininogen analogue
                    cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    weight;
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                                                                                                                                                                                                                                                                                                                                                                                   8pp;
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                                                                                                                            peptide; 179
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                                                                                                                                                                                                                                       100.0%;
                                                                                                                                                                                                                                                                                                                                                                                   Japanese.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          growth promotion;
                                                                                                                                                                                                                                       Score 68; DB 16
Pred. No. 0.0001
                                                                                                                                                                                                                                                                                                                                                                                                         a partial peptide of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           B
                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    fragment;
                                                                                                                                                                                                                                                                                                                    growth promotion activity
                                                                                                                                                                                                                          16;
0015;
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1.2; 1; 2; partial;
on; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                             The fragments are
                                                                                                                                                                                                                                                                                                                                                                                                                   of kininogen
                                                                                                                                                                                                                                                 Length 131;
                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                             0;
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                                                                                                                                                                                                                                                                                                                                                    and
                                                                                                                                                                                                                              Gaps
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AAY93349
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Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                           09-NOV-1999;
                                                                                WO200027415-A2
                                                                                                                        Synthetic.
                                                                                                                                                   endothelial
                                                                                                                                                              Human; high molecular weight kininogen; glycoprotein; endothelial cell;
plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                     Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                   04-SEP-2000
                                                                                                                                                                                                                                                              AAY93349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 11; Page 40-41; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Colman WR, Mousa AS
 10-NOV-1998;
                                                    18-MAY-2000
                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                        AAY93349 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                     1 LDDDLEHQGGHV 12
                                                                                                                                                                                                                                                                                                                                                         ldddlehqgghv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
12; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNIV TEMPLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DUPONT PHARM CO
COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 179
                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                 (first entry)
 98US-0107844.
                         99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98US-0107844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99WO-US26377.
                                                                                                                                                proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                           25
                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                          100.
                                                                                                                                                                                                                                                                                                                                                                                                                          0.0%;
                                                                                                                                                                                                                                                                                        186
                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 68; DB 21;
Pred. No. 0.00021;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 179;
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RESULT
AAY93342
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Matches 12; Conserv
                                                                                     (UTEM )
(DUPO )
(COLM/)
                                                                                                                                                                                                                                                                                                      Human; high molecular weight kininogen; glycoprotein; endoth plasma kallikrein; heavy chain; light chain; analogue; angic endothelial cell proliferation; endothelial cell migration;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Where it is cleaved by plasma kallikrein into heavy and light chains.
                                                                                                                                                                                 09-NOV-1999;
                                                                                                                                                                                                               18-MAY-2000
                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                   Light chain of human high molecular weight kininogen.
                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY93342 standard; protein; 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 9; Page 38; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Colman WR,
                                                                                                                                                  10-NOV-1998;
                                                                                                                                                                                                                                            WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for inhibiting endothelial cell that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Nous/)
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                                                                                   UNIV TEMPLE.
DUPONT PHARM CO
COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               186 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                  98US-0107844
                                                                                                                                                                                 99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 68; DB Pred. No. 0.0 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proliferation, using compound
                                                                                                                                                                                                                                                                                                                      glycoprotein; endothelial cell;
hain; analogue; anglogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  00022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                         vitronectin.
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WPI; 2000-376306/32

Colman WR,

Mousa AS

MOUSA A S.

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells. HW or a synthetic compound comprising the present sequence may be
                                                                                                                                     A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                       two-chain high molecular weight kininogen; HKa; angiogenesis inhibition; tumour; cancer; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAY81998 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               8661
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that
                                                                                           Claim 9;
                                                                                                                                                                                   WPI; 2000-376483/32
                                                                                                                                                                                                                McCrae
                                                                                                                                                                                                                                                                                                                      05-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                    18-MAY-2000.
                                                                                                                                                                                                                                                                                                                                                                                 WO200027866-A1
                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                            rheumatoid arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human two-chain high molecular weight kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 16-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method
                                                                                                                                                                                                                                             (UTEM ) UNIV TEMPLE (MCCR/) MCCRAE R'K.
                                                                                                                                                                                                                                                                                         10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    od for inhibiting endothelial cell proliferation, using compound inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high molecular weight kininogen;
                                                                                         Page 28; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence represents the light chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                                                                         98US-0107833.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                         endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 68; DB 21;
Pred. No. 0.00031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        high molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   fragment #7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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AAG01773
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Best Local
                                         The present sequence is a polypeptide encoded by one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed CNNA libraries. Such ESTs are not well suited for isolating CNNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain occular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis methods.
                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                    Claim 13; SEQ ID 5854; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500381/45.
N-PSDB; AAC01779.
                                                                                                                                                                                                                                                                                                                                                                                                                     Dumas Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAG01773 standard;
                               regulatory sequences
                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-FEB-1999;
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nes 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6 ldddiehgggh 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chromosome mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expressed sequence tag; secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                               and to design expression and secretion vectors
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQ ID NO: 5854
                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
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Sequence

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Ouery Match
Best Local Similarity 54.5%; Pred. No. 1.9;
Matches 6; Conservetive 3; Mismatches 2; Indels 0; Gaps 0;

Oy 2 DDLERGOGRY 12
Db 1::||1||;
Db 40 dhelengaphm 50

Search completed: July 6, 2001, 09:09:17

Job time: 123 sec
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Result
No.
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Perfect score:
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seq length: 2000000000
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Match
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/PCTUS_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*
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      GenCore version (c) 1993 - 2000
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US-08-409-3017-817-14
US-08-409-731A-2
US-08-470-298B-2
US-08-470-298B-2
US-08-820-825-2
US-08-820-825-2
US-08-468-577B-12
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US-08-33-485-67
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Length :		
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US-09-307-817-14

Sequence 14,

4, Application US/09307817 6232291

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Sequence 2, Approximately No. 5658758
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Best Local Similarity
Matches 6; Conserv
                                                                                                                           GENERAL INFORMATION:
                                                                   APPLICANT:
APPLICANT:
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NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 106 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
                          CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                            APPLICANT:
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                                       TITLE OF INVENTION: CYTOSTATIN I
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 STREET:
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                ADDRESSEE:
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9410 KEY WEST AVENUE
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                                                                  Gentz, Reiner
Rosen, Craig A.
                                                                                           Ni, Jian
Yu, Guo-Liang
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YU, GUO-LIANG
GENTZ, REINER L.
                                                                                                                                                                                                                                                                                 Conservative
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PatentIn Release #1.0, Version #1.30
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54.5%;
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Pred. No.
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RESULT 4
US-08-470-298B-2
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                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/470,298B
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ALLAN A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: 9F175D1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-309-8504
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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NFORMATION FOR SEQ ID NO:
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APPLICANT: GENTZ, RE:
APPLICANT: YU, GUO-L:
APPLICANT: ROSEN, CRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/409,731A
FILING DATE: 24-MAR-1995
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 107 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ITLE OF INVENTION:
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40 DKEIEHQGNHM 50
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ZIP: 20850
                                                                                                                                                                                                                                                                                                                                                  STATE:
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REGISTRATION NUMBER: 3
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ROSEN, CRAIG A.
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                   301-309-8512
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54.5%;
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Pred. No. 2
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RESULT 6
US-08-820-825-2
; Sequence 2, Application US/08820825
; Patent No. 5945309
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Best Local Similarity
%** 6; Conserva
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Patent No. 5977309
Patent INFORMATION:
                                                                                                                                               Matches
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                 MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: 301-610-5772
                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/09/023,073A
FILING DATE: 13-FEB-1998
CLASSIFICATION: 424
ATTORNEY/ACENT INFORMATION:
NAME: Wales, Michele M.
REGISTRATION NUMBER: P-43,975
REGISTRATION NUMBER: P-43,975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Ni, Jian
APPLICANT: Gentz, Re
APPLICANT: Yu, Guo-1
APPLICANT: Rosen, C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
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LENGTH: 107 amino acids
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TYPE: a
                                                                                     40 DKEIEHQGNHM 50
                                                                                                                                               Local Similarity
les 6; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                      TOPOLOGY:
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                                                                                                                  2 DDDLEHQGGHV 12
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                                                                                                                                                                                                                                                                               107 amino acids
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                                                                                                                                               Conservative
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Pred. No. 2
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2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Ve
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,825
FILING DATE: 19-MAR-1997
CLASSIFICATION: 435
ATTORNEY/AGRAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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APPLICANT: YU, GUO-LIANG
APPLICANT: GENTZ, REINER L.
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOSTATIN III
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
COMPOTER: IBM COMPACTION
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
CONTROL OF TO ATTON NUMBER: US/08/899,031
                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                           APPLICANT: Bandman, Olga
APPLICANT: Guegler, Karl J.
APPLICANT: Shah, Purvu
                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                           TITLE OF INVENTION: HUMAN RETINOID BINDING PROTEIN NUMBER OF SEQUENCES: 4
                                                                                                                                                                                 STREET: 3174 PO:
CITY: Palo Alto
STATE: CA
                                                                                                                                               COUNTRY: U
ZIP: 94304
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ZIP: 20850
                                                                                                                                                                                                                     ADDRESSEE: Incyte Pharmaceuticals, Inc. STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity les 6; Conserv
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                                                                                                              Diskette
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309-8512
NO: 2:
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54.5%;
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Pred. No. 3;
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CLASSIFICATION: 530 PRIOR APPLICATION DATA:

APPLICATION NUMBER:

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RESULT 8
US-09-307-817-2
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2,
                                                        ATTORNEY/AGENT INFORMATION:
NAME: BROOKES, ANDERS A.
REGISTRATION NUMBER: 36,373
REFERENCE/DOCKET NUMBER: PF22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 135 amino acid
                                TELEFAX: (301) 309-85: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: APPLICANT:
                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                  CLASSIFICATION:
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: GENTZ, REINEK L
APPLICANT: DILLON, PATRICK
TITLE OF INVENTION: CYTOST'
                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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LIBRARY: Sin...
TONE: 367304
                                                                                                                                                     FILING DATE:
                                                                                                                                                                  APPLICATION NUMBER:
                                                                                                                                                                                                               FILING DATE:
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REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: HUMAN GENOME SCIENCES, INC STREET: 9410 KEY WEST AVENUE
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135 amino acids
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YU, GUO-LIANG
GENTZ, REINER L.
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54.5%;
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Pred. No.
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Best Local Similarity
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                                                        TELEFAX: (914) 332-18
INFORMATION FOR SEQ ID NO:
                                                                                                        REFERENCE/DOCKET NUMBER: MD TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                APPLICATION NUMBER: US 07/441,703 FILING DATE: 04-DEC-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                     FILING DATE: 05-MAY-1994

PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 07/872,646

FILING DATE: 08-JUN-1992

PRIOR APPLICATION UNMBER: US 07/715 101

PRIOR APPLICATION UNMBER: US 07/715 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: Syst
SOFTWARE: WordPerfect
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Diskette, 3.50 inch, 1.4 Mb storage
                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                            APPLICATION NUMBER: US 0: FILING DATE: 17-FEB-1989
ATTORNEY/AGENT INFORMATION: NAME: Kurt G. Briscoe
                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 07/715,181 FILING DATE: 14-JUN-1991 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: PANCREATIC ISLET CELL ANTIGENS TITLE OF INVENTION: OBTAINED BY MOLECULAR CLONING
                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA: US 08/239,276
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: OF CLASSIFICATION:
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Tarrytown STATE: New York
                                                                                         TELEPHONE:
                                                                                                                                              REGISTRATION NUMBER: 33,141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: Apple Macintosh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 10591-5144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE:
                    ENGTH:
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o. 5955345
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                  604 amino acids
                                                                       (914)
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                                                                                           (914)
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                                                                     332-1844
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                                                                                         332-1700
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                                                                                                                                                                                                                     US 07/312,543
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                                                                                                                           MDI 251.7-KGB
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Pred. No.
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Query Match 52.9%; Best Local Similarity 66.7%; Matches 6; Conservative

Score 36; DB 2; Le Pred. No. 1.6e+02; 0; Mismatches 3;

Length 604;

Indels

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Gaps

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DDLEHOGGH 11

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US-08-468-577B-12 ; Sequence 12, Application US/08468577B
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                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US 08/239,276
FILING DATE: 05-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/872,646
FILING DATE: 08-JUN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: U
FILING DATE: 14-JUN-
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                                                                              351 DTFEHGGGH 359
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                                                                                                                                           Local Similarity
nes 6; Conserv
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REFERENCE/DOCKET NUMBER: MDI 251.5-KGB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: FILING DATE: 04-DEC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: Apple Macintosh
OPERATING SYSTEM: System
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Tarrytown STATE: New York
                                                                                                                                                                                                                                                         TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                      TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/312,543 FILING DATE: 17-FEB-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
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                                                                                                             3 DDLEHQGGH 11
                                                                                                                                                                                                                                     amino acid
OGY: linear
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                                                                                                                                                                                                                                                                       604 amino acids
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                                                                                                                                                                                                                                                                                                                       (914)
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                                                                                                                                                                                                                                                                                                                     332-1844
                                                                                                                                                          52.9%;
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                                                                                                                                                          Score 36; DB 2;
Pred. No. 1.6e+02;
                                                                                                                                           Mismatches
                                                                                                                                                                         Length 604;
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US-08-476-008-67; Sequence 67, Appli; Patent No. 5627061
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Matches 6
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GENERAL INFORMATION:
                                  GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
APPLICANT: Stallings, William C.
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          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER: US 07/715,181
FILING DATE: 14-UN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                       Local Similarity
les 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kurt G. Briscoe
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
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STATE: New York
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                                                                                                                                        Application US/08476008
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Glyphosate Tolerant
5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                                                                                        52.9%;
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Pred. No. 1.6e+02;
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                                                                                                                                                                                                                                                                                                                     Length 604;
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CORRESPONDENCE ADDRESS:

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Best Local Similarity
"hes 7; Conserv."
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Sequence 67, Approx
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TELECOMMUNICATION INFORMATION:
TELLEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 67:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: . PC-DOS/MS-DOS
SOETWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US//8/476,008
FILING DATE: 07-JUN-1997
CLASSTEF
       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
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TOPOLOGY: line

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PRIOR APPLICATION NUMBER: US 08
APPLICATION NUMBER: US 08
FILING DATE: 13-SEP-194
                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: 61yphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
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                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     383 DDGLEIQGG 391
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                                                                                                                        COUNTRY: U
ZIP: 63198
                                                                                                                                                                                                                                  CITY: St.
                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                                                                                                                                                ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 DDDLEHQGG 10
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                                                                                                                                                                                           Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Application US/08306063
                                                                                                                                                                                                                                                                     E: Dennis R. Hoerner, Jr., Monsa
700 Chesterfield Village Parkway
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700 Chesterfield Village Parkway
                                                                                                                                                               USA
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                                                                                                                                                                                                                                      Louis
E: Floppy disk
IBM PC compatible
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77.8%;
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; Pred. No. 2.5e
0; Mismatches
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US-08-833-485-67; Sequence 67, Application US/08833485; Patent No. 5804425
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INFORMATION FOR SEQ ID NO: 67
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
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Best Local :
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FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/ACENT INFORMATION:
NAME: UCCTOT TO TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE TOTAL TO THE 
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                             PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
                                                                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsa
STREET: 700 Chesterfield Village Parkway
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APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
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APPLICANT: Kishore, Ganesh M.
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEPEAX: (314)537-6047
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SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                       PRIOR APPLICATION DATA:
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CLASSIFICATION: 435
                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/833,485 FILING DATE: 07-APR-1997
                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: St. Louis
STATE: Missouri
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63198
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In Release #1.0; Version #1.25
US 07/749,611
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Pred. No. 2.
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537

FILING DATE: 28-AUG-1991 CLASSIFICATION: 435

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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/647,484

FILING DATE: 14-MAY-1996

CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/430,033

FILING DATE: 27-APR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Gaylo, Paul J.
REGISTRATION NUMBER: 36,808
REFERENCE/DOCKET NUMBER: X-10006
TELECOMMUNICATION: NIMBER: X-10006
TELECOMMUNICATION: X-10006
TELECOMUNICATION: X-10006
TELECOMMUNICATION: X-10006
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REFERENCE/DOCKET NUMBER: 38-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6049
TELEPAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 amino acids
TYPE: amino acid
TOPOLOGY: linear
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Best Local Similarity
Matches 7; Conserva
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APPLICANT: Ni, Binhui
APPLICANT: Paul, Stev
                               SEQUENCE CHARACTERISTICS:
LENGTH: 560 amino acids
TYPE: amino acid
TOPOLOGY: linear
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FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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STATE: Indiana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Eli Lilly and Company STREET: Lilly Corporate Center
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                                                                                US-08-647-484-2
                    Query Match
Best Local Similarity 41.,
---hes 5; Conservative
91 VNNSTTHRGGHV 102
                1 LDDDLEHQGGHV 12
                                           50.0%;
41.7%;
                                    4; Mismatches
                                           Score 34; E
Pred. No. 3.
                          3.2e+02;
                                                   Length 560;
                                    0;
                                   Gaps
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0

Search completed: July 6, 2001, 09:10:20 Job time: 186 sec

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Copyright GenCore version (c) 1993 - 2000 4.5 Compugen Ltd

OM protein - protein search, using sw model

Run on: July 6, 2001, 09:17:57; Search time 73.59 Seconds

(without alignments)
12.421 Million cell updates/sec

Perfect score: US-09-437-912-2

1 LDDDLEHQGGHV 12

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

Maximum Minimum DB seq length: 0 seq length: 2000000000

Post-processing:

Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database PIR_68:* pir1:*
pir2:*
pir3:*
pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	% Query Match	Length	B	ID	Description
о Р	68	100.0	544	υμ	KGHUH1	, HMW
ω κ	44		174	<i>ر</i> د	T34850	hvnothetical prote
4	43		683	N	S01433	_
ъ	42	61.8	3282	N	E82750	nin-l
6	42		3442	N	E82589	hemagglutinin-like
7	42	•	3455	N	B82519	hemagglutinin-like
œ	41		538	ب	O4CKA4	cytochrome P450 52
9	40.5		536	N	T27668	1 prot
10	40		1025	N	S69790	fibronectin-bindin
11	40	•	1733	N	S27939	tensin – chicken
12	40		1744	Ν	A54970	'n
13	40	٠	1792	N	A57075	1
14	39	٠	325	2	F83503	eti
15	39	57.4	534	Н	A48529	$\vdash$
16	39		571	Ľ	DEECDL	D-lactate dehydrog
17	39	57.4	571	ุผ	E85850	hypothetical prot
18	. 39	٠	581	N,	G96811	unknown protein Tl
19	39	57.4	651	N	A26581	beta-glucuronidase
20	39		744	L	KIECG	GTP pyrophosphoki
21	39	٠	744	2	E85929	hypothetical prote
22	38	55.9	18	N	C81931	hypothetical prote
23	38	•	122	N	C53234	
24	38		236	N	T01662	-
25	38		407	N	T02258	ı
26	38		489	N	T36100	ATP
27	38	•	540	N	S21825	vicilin-like stora
28	38		573	N	A53234	-1s
20	٥		פח			

38 55.9 818 2 A48858 38 55.9 2422 2 T18201 38 55.9 2422 2 T18201 38 55.9 2422 2 T18201 38 55.9 2422 2 T18201 37 54.4 2 2 C83929 37 54.4 179 2 E83601 37 54.4 183 2 T51572 37 54.4 191 2 D96701 37 54.4 191 2 D96701 37 54.4 285 2 B83047 37 54.4 27 2 T39658 37 54.4 4 407 2 T39658 37 54.4 420 2 T39712 37 54.4 420 2 T39712 37 54.4 420 2 T39712 37 54.4 420 2 T39712 37 54.4 420 2 T39712 38 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.4 420 2 T39712 39 54.	45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30
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	473	427	426	426	420	407	339	285	191	183	179	64	511	5170	2422	818
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Na+/H+-exchanging fatty-acid synthas hypothetical prote beta-fructofurancs hypothetical prote proteinase PfpI PA hypothetical prote unknown protein, 9 hypothetical prote probable mitochond hypothetical prote probable oxidoredu probable oxidoredu hypothetical prote probable oxidoredu probable oxidoredu hypothetical prote probable oxidoredu probable oxidoredu hypothetical prote two-component sens	G83932	T42516	C85755	H64878	T39712	T39658	T06612	B83047	D96701	T51572	E83601	C83929	A37803	T15348	T18201	A48858
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## ALIGNMENTS

kininogen, HMW precursor (validated) - human
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen
N;Contains: bradykinin (kallidin 1); HMW kininogen I; HMW kininogen II; low molecular
C;Species: Homo sapiens (man)
C;Apecies: Homo sapiens exprision 28-May-1986 #text_change 08-Dec-2000
C;Apecies: 28-May-1986 #sequence_revision 28-May-1986 #text_change 08-Dec-2000
C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;
R;Ohkubo, II; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Blochemistry 23, 5691-5697, 1984
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide
A;Reference number: A90490; MUID:85122621

A; Molecule type: mRNA A; Residues: 1-389 <OHK>

A;Cross-references: GB:K02566; NID:g177889
R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs
A;Reference number: A92544; MUID:85234582
A;Accession: A25276 for human high molecular weight and

A; Molecule type: mRNA A; Residues: 1-592, 'I', 594-644 <TAK>

A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I. FEBS Lett. 321, 93-97, 1993 A;Title: Cloning, expression and characterization of human kininogen domain 3. A;Reference number: \$32422; MUID:93223854

A; Accession: S32422

A; Molecule type: mRNA A; Residues: 'ANSM', 253-377 < AUE>

A; Note: differences are due to known cloning artifacts R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl,

R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Bur. J. Blochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270
A;Accession: A91153

A; Molecule type: protein A; Residues: 379-644 <LOT>

A;Note: the bradykinin sequence preceding the light chain sequence was not determined R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. Eur. J. Blochem. 154, 471-478, 1986

A;Title: Completion of the primary structure of human high-molecular-mass kininogen. A;Reference number: A24871; MUID:86108361

A; Accession: A24871

A; Molecule type: protein A; Residues: 'Z', 20-380 <KEL1>

R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, A;Tille: Amino acid sequence of the light chain of human high molecular mass kini A;Reference number: A27899

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A;Residues: 1-19;189-192;310 31., A;Residues: 1-19;189-192;310 31., A;Residues: 1-19;189-192;310 31., A;Residues: 15:252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues of bradykinin A;Title: A61495; MUID:88211869
                                                                                                                                                                                                                                                             A; Molecule type: protein
A; Residues: 450-452,'X', 454,'X', 456 < LIT>
R; Straczek, J.; Maachi, F; le Nguyen, D.;
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V. FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C and kininogen by human cathepsin A;Reference number: S14303; MUID:91192133
A;Accession: S14447
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Accession: Output type: protein
A;Molecule type: protein
A;Residues: 1-19;189-192;310-314;381-389 <LEN1>
A;Residues: 1-19;189-192;310-314;381-389 <LEN1>
R;Kato, H.; Matsumura, Y.; Maeda, H.
R;Kato, H.; Matsumura, Y.; Maeda, H.
A; Title: Structural organization of the human kininogen gene and A; Reference number: A92545; MUID:85234583
                                                       A;Molecule type: protein
A;Residues: 431-434 <STR>
R;Rtstamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki,
J. Biol. Chem. 260, 8610-8617, 1985
                                                                                                                                                                           A; Reference number: S68059; A; Accession: S68059
                                                                                                                                                                                                                                                                                                                                                                                 R;Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms: separation A;Reference number: S55239; MUID:95251593
A;Accession: S55239
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 380-389 <KAT1>
A; Experimental source: urine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok, M.; Turk, Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors (CPIs) in A;Reference number: S02482; MUID:89076517
A;Accession: S02482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Sasaguri, M.; Ikeda, M.; Idelshi, M.; Arakawa, K. Biochem. Blophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin A;Reference number: A34030; MUID:88106632
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R:Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A;Title: Purification and identification of [hydroxyprolyl(3)]bradykinin
A;Reference number: A31905; MUID:89034061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 379-389, 'K',390-407, 'Q',409-644 <KEL2>
R;Mindroiu, T.; Carretero, O.A.; Proud, D.; Malz, D.; Scicli, Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A;Title: A new kinin molety in human plasma kininogens.
A;Reference number: A27699; MUID:88209021
                                                                                                                                                                                                                                        A; Title: Purification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 264-359,'N', 361-375 <LEN2>
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A; Accession: B61495
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A; Residues: 380-389 <SAS>
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                                                                                     Y.; Miyata,
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A. Hoss Teletences; Gubs: 12220; Owlm: 228900
A. Map position: 3q27-3q27
A. Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
C. Superfamily: kininogen; cystatin homology
C. Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-644/Product: HMW kininogen II #status experimental <MART2>
F;19-379,390-644/Product: HMW kininogen II #status experimental <HCH>
F;19-131/Domain: cystatin homology <CY1>
F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kalliddin II) #status experimental <HCH>
F;380-389/Product: bradykinin (kalliddin I) #status experimental <CH>
F;381-389/Product: bradykinin (kalliddin I) #status experimental <CH>
F;421-510/Region: glycine/histidine/lysine-rich 30-residue repeats
F;431-434/Product: low molecular weight growth promoting factor #status experimental
F;28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond
F;48/Binding site: carbohydrate (Asn) (covalent) #status absent
F;401,533,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;381-390-390/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;401,533,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;377/Binding site: carbohydrate (Ser) (covalent) #status experimental
F;377/Binding site: carbohydrate (Ser) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, February 1999 A; Reference number: Z21559 A; Accession: T34850 A; Statue:
C;Superfamily: 4-coumarate--CoA ligase; acetate--Co
C;Keywords: acid-thiol ligase
F;70-533/Domain: acetate--CoA ligase homology <ACL>
                                                                                                                                                                                                               A; Molecule type: DNA
A; Residues: 1-541 <OLI>
A; Cross-references: EMBL; AL035478; PIDN; CAB36604.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable acid--CoA ligase (EC 6.2.1.-) SC2G5.17 [similarity] -
C:Species: Streptomyces coelicolor
C:Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Title: Structural features of plasma kinins and kininogens. A;Reference number: A91455; MUID:90255622
A;Reference number: A91455; MUID:90255622
A;Contents: annotation; bradykinin
C;Comment: The HMW kininogen precursor and the LMW form are produced from the C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiat C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light characteristic Bradykinin, released from kininogen by kallikrein, is a potent vaso cyproline residue is present in the kininogen prior to the release of bradykin
                                                                                                                                                                                  A; Experimental source: strain A3(2)
                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: T34850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Pierce, J.V.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
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                                                                                                                    SCOEDB:SC2G5.17
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Pred. No.
                                                                                acetate--CoA
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,. 0.00058;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   J.; Barrell,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     #text_change 18-Aug-2000
                                                                                                                                                                                                                      GSPDB:GN00070;
                                                                                ligase homology
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Query Match
Best Local Similarity

64.7%; 66.7%;

Score Pred.

No .

DB 7.2;

2;

Length 541;

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C;Accession: S01433; SJULLER, Sinclair, R.B.; Bibb, M.J. R;Sinclair, R.B.; Bibb, M.J. 1988 Mol. Genet. 213, 269-277, 1988 Mol. Gen. Genet. 213, 269-277, 1988
                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:X12865; NID:g15458; PIDN:CAA31345.1; R;Hartley, N.M.; Murphy, G.O.; Bruton, C.J.; Chater, K.F. submitted to the EMBL Data Library, November 1993
A;Reference number: S38912
A;Accession: S38912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: phage phi-C31
C;Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 04-Mar-2000
C;Accession: S01433; S38912
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 31-Dec-2000
C;Accession: G83712
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A; Residues: 1-683 < HAR>
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A;Title: The repressor gene (c) of the Streptomyces
A;Reference number: S01433; MUID:89039715
A;Accession: S01433
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A83650; A; Accession: G83712
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
                                                                                                                                                                                                                                                                        A;Cross-references: EMBL:X76288; NID:g432610; PIDN:CAA53911.1; PID:g432611
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-683 <SIN>
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A; Residues: 1-174 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                hypothetical protein BH0503 [imported] - Bacillus halodurans (strain C-125)
                                                                                                                                                                                  Superfamily: phage phi-C31 repressor protein C; Superfamily: phage phi-C31 repressor protein C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Superfamily: Deinococcus radiodurans hypothetical
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474 DDDVERQGAH 483
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                                                                              Local Similarity hes 7; Conserv
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                                       DDDLEHQGGH 11
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58.3%;
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                                                                            Score 43; DB
Pred. No. 14;
1; Mismatches
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3.1;
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                                                                                                                     Length 683;
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A; Authors: Ferreira, V.C.A.; Fello, V.C.A.; Fello, V.C.A.; Reinger, J.E.; Kuramae, E.E.; La J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Marino, C.L.; Marques, M.V.; Martins chado, M.A.; Madeira, H.M.F.; Marino, C.F.M.; Miracca, E.C.; Miyaki, C. F.C.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, F.C.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de San, R.G.; Santelli, R.V.; Sawa Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa A; Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva, A; Authors: da Silva, A.C.R.; da Silva, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hemagglutinin-like secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Species: Xylella fastidiosa C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylella fastidiosa (strain C;Date: 18-Aug-2000 #secreted protein XF2196 [imported] - Xylel
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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717 A;Note: for a complete list of authors see reference number A59328 below A;Accession: E82589
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A; Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Experimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; Bl-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-3442 <SIM>
A;Cross-references: GB:AE004032; GB:AE003849; NID:g9107324; PIDN:AAF84995.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status:
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A; Reference number: A59328
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A;Cross-references: GB:AE003928; GB:AE003849; NID:g9105798; PIDN:AAF83699.1;
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C;Date: 18-Aug-2000 #sequence_revision
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Carrer
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C;Species: Candida maltosa
C;Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 03-Mar-2000
C;Accession: S08668; A56578; S65523
R;Schunck, W.H.; Gross, B.; Mueller, H.G.
                                                                                    A; Reference number: S08667
A; Accession: S08668
                                                                                                                                                                                                                                                                                                                                                                                    N; Alternate names: cytochrome P450-cm2 N; Contains: oxidoreductase (EC 1.-.-.)
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A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig J.D.; Jungueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laig Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D., F.G.; Nunes, L.R.; Oliveira, M.A.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasa A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silvai, Sundada, H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.; A;Reference number: A59328
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A;Residues: 1-3455 <SIN>
A;Residues: 1-3455 <SIN>
A;Cross-references: GB:AE004082; GB:AE003849; NID:g9108003; PIDN:AAF85560.1; GSPDB:GN001
A;Cross-references: GB:AE04082; GB:AE04082; GB:AE04082; NID:g9108003; PIDN:AAF85560.1; GSPDB:GN001
A;Cross-references: GB:AE04082; GB:AE04082; GB:AE04082; A;Cross-references: GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; GB:AE04082; G
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A;Note: for a complete list of authors see reference number A59328 below A;Accession: B82519
A;Accession: B82519
A;Status: preliminary
                                                                                                                                                                            submitted to the EMBL Data Library, February 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cytochrome P450 52A4 - yeast (Candida maltosa)
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        A; Residues:
                                                A; Molecule type: mRNA
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A; Contents: annotation
C; Genetics:
A; Gene: XF2196
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C;Species: Xylella fastidiosa
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1.2e+02;
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                                                                                                                            RESULT
S69790
fibronectin-binding protein II precursor -
C;Species: Streptococcus pyogenes
C;Date: 14-Feb-1997 #sequence_revision 13-M
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10

occus pyogenes
#sequence_revision 13-Mar-1997 #text_change 15-Oct-1999

Streptococcus pyogenes

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A;Gene: CYP52A4
C;Superfamily: Candida cytochrome P450 52A3; cytochrome P450 homology
C;Superfamily: Candida cytochrome P450 52A4; cytochrome P450 iron; metalloproto
F;2-538/Product: cytochrome P450 52A4 #status experimental <MAT>
F;331-507/Domain: cytochrome P450 homology <P45>
F;485/Binding site: heme iron (Cys) (axial ligand) #status predicted
                                                                                                                                                                                                                          A;Map position: 1
A;Introns: 56/3; 88/3; 203/1; 228/2; 383/1; 467/3
C;Superfamily: Caenorhabditis elegans hypothetical
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Arch. Biochem. Biophys. 328, 245-254, 1996
A;Title: Characterization of the n-alkane and fatty acid hydroxylating cytochrome
A;Reference number: S65522; MUID:96213873
A;Accession: S65523
A;Molecule type: protein
A;Residues: 2-15 <SCW>
                                                                                                                                                                                                                                                                                                            A; Gene: CESP: ZK1053.2
                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source:
                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-536 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            submitted to the EMBL Data Library, A; Reference number: Z20402 A; Accession: T27668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R; Kershaw,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein ZK1053.2 - Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Speckes: Caenorhabditis elegans C;Date: 15-Oct_1999 #sequence_revision 15-Oct-1999 #text_change 04-Mar-2000 C;Accession: T27668
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C; Genetics:
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A;Residues: 1-255,'D',257-538 <SC2>
A;Residues: 1-255,'D',257-538 <SC2>
A;Note: sequence inconsistent with nucleotide translation
A;Note: sequence extracted from NCBI backbone (NCBIN:64322, NCBIP:64324)
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A;Experimental source: strain EH15D
R;Schunck, W.H.; Vogel, F.; Gross, B.; Kargel, E.; Mauersberger, S.; Kopke, K.; Gengn Eur. J. Cell Biol. 55, 336-345, 1991
A;Title: Comparison of two cytochromes P-450 from Candida maltosa: primary structures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: A56578
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Best Local :
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511 LDDDVDHKPRHGGYV 525
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                                                  1 LDDDLEHQ----GGHV 12
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                                                                                                     Similarity
8; Conserv
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72.7%;
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ZK1053
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Pred. No.
                                                                                                                             Score 40.5;
Pred. No. 2
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R.Kreikemeyer, B.
submitted to the EMBL Data Library, December 1994
A;Reference number: $72666
A;Accession: $72666
В
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A; Residues: 1-1733 CCHE>
A; Cross-references: EMBL:M74165; NID:g212751; PID:g212752
A; Cross-references: EMBL:M74165; NID:g212751; PID:g212752
R; Weigt, C.; Gaertner, A.; Wegner, A.; Korte, H.; Meyer, H.E.
J. MOl. Biol. 227, 593-595, 1992
A; Title: Occurrence of an actin-inserting domain in tensin.
A; Reference number: S28973; MUID:93021103
A; Accession: S28973
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F:1-34/Domain: signal sequence *status predicted <SIG>F:35-1025/Product: fibronectin-binding protein II *status predicted F:848-868/Region: fibronectin binding F:869-907/Region: fibronectin binding F:908-946/Region: fibronectin binding F:908-946/Region: membrane anchor cleavage motif F:999-1016/Domain: transmembrane *status predicted <TMM>
                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 862-871,'X',873-875,'A',877-1212
C; Superfamily: SH2 homology
F;1461-1570/Domain: SH2 homology <SH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Chen, L.B. submitted to the EMBL Data Library, August 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Species: Gallus gallus (chicken)
C;Date: 17-Apr-1993 #sequence_revi
C;Accession: S27939; S28973
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A; Residues: 1-19,'T',21-145,'T',147-1025 <KRW>
A; Cross-references: EMBL:X83303; NID:g1070387;
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A;Cross-references: EMBL:X83303; NID:g1070387; PIDN:CAA58282.1; PID:g1552714
A;Experimental source: strain A75
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Mol. Microbiol. 17, 137-145, 1995
A;Title: Characterization of a novel fibronectin-binding surface protein in group A stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: S69790; S72666
R;Kreikemeyer, B.; Talay, S
Mol. Microbiol. 17, 137-145
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A; Accession: S27939
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                                                                                                              Query Match
Best Local
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Best Local
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568 LDDELPNQDGH 578
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                                         1 LDDDLEHQGGH 11
                                                                                        Similarity 7; Conser
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; S28973
                                                                                                                                                                                                     SH2 homology
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70.0%;
                                                                                                              58.8%;
                                                                                      Score 40; DB
Pred. No. 1.3e
2; Mismatches
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Pred. No. 72;
1; Mismatches
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1.3e+02;
-~ 2;
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C;Species: Gallus gallus (chicken)
C;Date: 11-Nov-1994 #sequence_revision 11-Nov-1994 #text_change 21-Jul-2000
C;Accession: A54970; S38330; S21544
R;Lo, S.H.; Ah, Q; Bao, S; Wong, W.K.; Liu, Y.; Janmey, P.A.; Hartwig, J.H.; Chen, J. Biol. Chem. 269, 22310-22319, 1994
A;Title: Molecular cloning of chick cardiac muscle tensin. Full-length cDNA sequence A;Reference number: A54970; MUID:94350987
A;Accession: A54970
hypothetical protein PA1130 [imported] - Pseudomonas aeruginosa (strain PAO1) C;Species: Pseudomonas aeruginosa (C;Species: Pseudomonas aeruginosa (C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000 C;Accession: F83503
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species: Gallus gallus (chicken)
C; Date: 05-Jan-1996 #sequence_revision
C; Accession: A57075
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A54970
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C;Superfamily: SH2 homology
F;1520-1629/Domain: SH2 homology <SH2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Chuang, J.Z.; Lin, D.C.; Lin, S.
J. Cell Biol. 128, 1095-1109, 1995
A;Title: Molecular cloning, expression, and A;Reference number: A57075; MUID:95204530
A;Accession: A57075
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C;Superfamily: SH2 homology
C;Keywords: cardiac muscle; heart
F;1472-1581/Domain: SH2 homology <SH2>
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R;van de Werken, R.; Gennari, M.; Tavella, S.;
Eur. J. Biochem. 217, 781-790, 1993
A;Title: Modulation of tensin and vimentin exprantation of tensin and vimentin exprantation of tensin and vimentin exprantation.
A;Reference number: S38330; MUID:94039118
A;Accession: S38330
                                                                                          F83503
                                                                                                                  RESULT
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A; Residues: 1-1792 <CHU>
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A; Residues: 1469-1744 <VAN>
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A; Residues: 1-1744 <LOA>
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A;Molecule type: mRNA
A;Residues: 1-534 <EMM>
A;Residues: 1-534 <EMM>
A;Residues: 1-534 <EMM>
A;Experimental source: var. Marfona, tuber
A;Experimental source: var. Marfona (NCBIP:136740)
A;Experimental source: var. Marfona (NCBIP:136740)
C;Superfamily: mitochondrial processing peptidase alpha chain
C;Keywords: hydrolase; metalloproteinase; mitochondrial matrix; mitochondrion; oxidative
F;1-32/Domain: transit peptide (mitochondrion) #status predicted <TNP>
F;33-534/Product: mitochondrial processing peptidase 55K protein #status experimental <A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mitochondrial processing peptidase (EC 3.4.24.64) 55K protein precursor - potato N;Alternate names: P-55; ubiquinol--cytochrome-c reductase (EC 1.10.2.2) core protein I c;Species: Solanum tuberosum (potato) C;Date: 28-Mar-1994 #sequence_revision 14-Jul-1994 #text_change 31-Dec-2000 C;Accession: A48529 R;Emmermann, M.; Braun, H.P.; Arretz, M.; Schmitz, U.K. J. Biol. Chem. 268, 18936-18942, 1993 A;Title: Characterization of the bifunctional cytochrome c reductase-processing peptidas A;Reference number: A48529; MUID:93366812 A;Accession: A48529; MUID:93366812
Search completed: July 6,
Job time: 644 sec
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A;Accession: F83503
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Nature 406, 959-964, 2000
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A; Residues: 1-325 <STO>
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RELA_ECOLI
GLB1_MAIZE
NAH1_PIG
SCRB_ZYMMO
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INVA_ZYMMO
Z138_HUMAN
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DISULFIDE BONDS.
Sueyoshi T., Miyata T., Kato H., Iwanaga S.;
"Disulfide bonds in bovine HMW kininogens.";

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Seikagaku

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JBBL; M11524; AAB5
JBBL; M11526; AV
JBBL; M11526; AV
JBBL; M11526; AV
JBBL; M11527; AV
JBBL; M11528; AV
JBBL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                 Alternative
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PTM: BRADYKININ IS RELEASED FROM KININOGEN BY
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION), INDIRECTLY VIA ENDOTHELIUM-DERLYDE RELAXING FACTOR ACTION); (5) LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING: TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN-AND PLASMININDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTOR AND ASSESSMENT OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY OF THE PROPERTY
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FUNCTION: (1) KININOGE
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S02482.
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B25276.
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KININOGEN HEAVY CHAIN
BRADYKININ.
                                                                                                                                                   Thiol protease inhibitor; Vasodilator; Inflammatory response; Signal;
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Best Local
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          SEQUENCE r.v...
STRAIN-C+-NORWICH;
STRAIN-B-89039715; PubMed=3185504;
Sinclair R.B., Bibb M.J.;
The repressor gene (c) of the Streptomyces temperate phage phi c31:
nucleotide sequence, analysis and functional cloning.";
C-1 Gen. Genet. 213:269-277(1988).
                                                                                 Lambda phage group.
NCBI_TaxID=10719;
[1]
[2]
SEQUENCE FROM N.A.
MEDLINE=94374705; PubMed=8088546;
MEDLINE=94374705; PubMed=8088546;
                                                                                                                                                      RPC_BPPHC
P08979;
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CARBOHYD
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DISULFID
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01-NOV-1988 (Rel.
01-NOV-1997 (Rel.
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nes 12; Conserv
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nilarity 100.0%;
Conservative 0
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593
71945
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Last annotation update
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                                                                                                     no RNA stage; Tailed phages; Siphoviridae;
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     Bruton C.J.,
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PFKAGAEPASSREVS (IN ISOFORM LAW).

MISSING (IN ISOFORM LAW).

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3132B4CBAF8FBB7E CRC64;
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
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                                                                                                                                                             PRT;
                                                                                                                                                                                                                                  Pred. No. 0.00032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACTIVITY).
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     Chater K.F.;
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Matches 7
  CHARACTERIZATION.

MEDLINE=96311366; PubMed=8713123;

Ximmer T., Ohkuma M., Ohta A., Takagi M., Schunck W.H.;

Zimmer T., Ohkuma M., Ohta A., Takagi M., Schunck W.H.;

"The CYP52 multigene family of Candida maltosa encodes

diverse n-alkane-inducible cytochromes P450.";

Biochem. Biophys. Res. Commun. 224:784-789(1996).

-I- FUNCTION: TOGETHER WITH AN NADPH CYTOCHROME P450 THE FUNCTION: TOGETHER WITH AN NADPH CYTOCHROME P450 THE CATALYZES THE TERMINAL HYDROXYLATION AS THE FIRST (
ASSIMILATION OF ALKANES AND FATTY ACIDS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P16141;
01-APR-1990
01-APR-1990
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15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 52A4 (EC 1.14.14.1) (CYPLITA4)
ALK3-A) (P450-CM2).
                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
MEDLINE-91229697; PubMed-2039569;
MEDLINE-91229697; PubMed-2039569;
Ohkuma M., Tanimoto T., Yano K., Takag
"CYP52 (cytochrome p450alk) multigene
molecular cloning and nucleotide seque
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Candida maltosa (Yeast).
Eukaryota; Fungi; Ascomycota;
Saccharomycetales; mitosporic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schunck W.-H., Kaergel E., Gross B., Wiedmann B., Mauersberger S., Koepke K., Kiessling U., Strauss M., Gaestel M., Mueller H.-G.; "Molecular cloning and characterization of the primary structure of the alkane hydroxylating cytochrome P-450 from the yeast Candida
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-89286595; PubMed-2735924;
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Gene 147:29-
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send an email to license@isb-sib.ch).
CATALYTIC POSITION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               147:29-40(1994).
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Similarity 70.0%;
7; Conservative
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; Candida.
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RESULT 4
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01-NOV-1995 (Rel. 32, C)
01-NOV-1997 (Rel. 35, La
01-NOV-1997 (Rel. 35, La
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Chuang J.Z., Lin D.C
                                                                                            Chen L.B.;
                                                                                                      MEDLINE=94350987; PubMed=8071358; Lo S.H., An Q., Bao S., Wong W.K.,
                                                                                                                                                                              Archosauria;
                                                                                                                                                                               Eukaryota; Metazoa;
Archosauria; Aves; l
                                                                                                                                                                                                    Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR002402; -. InterPro; IPR002974; -. Pfam; PF00067; p450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruce by non-profit institutions as long as its content
                    MEDLINE=95204530; PubMed=7896874;
                                SEQUENCE FROM N.A.
TISSUE=Heart;
                                                             "Molecular cloning of chick cardiac muscle sequence, expression, and characterization.
J. Biol. Chem. 269:22310-22319(1994).
                                                                                                                             TISSUE-Heart;
                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                          NCBI_TaxID=9031;
                                                                                                                                                                                                                TENSIN.
                                                                                                                                                                                                                                                                   TENS_CHICK
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SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
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8; Conserv
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  expression,
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                                                                                                       Janmey P.A.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
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SH2 DOMAIN.

SH2 DOMAIN.

MEDLINE=91220073; PubMed=1708917;

Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,

Davis S., Lu M.L., Lo S.H., Lin S., Butler J.A., Druker B.J.,

Roberts T.M., An Q., Chen L.B.;

"Presence of an SH2 domain in the actin-binding protein tensin.";

Science 252:712-715(1991)...

Science 252:712-715(1991)...

Science 252:712-715(1991)...

Science 252:712-715(1991)...

Science 352:712-715(1991)...

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EMBL; L06662; AAA73949.1; ALT_INIT.
EMBL; Z18529; CAA7915.1; ALT_INIT.
EMBL; M74165; AAA49087.1; --
EMBL; X66286; CAA46392.1; --
HSSP; P16277; 1BLJ.
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DOMAIN 6
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the European Bioinformatics Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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"Modulation of tensin and vimentin expression in chick embryo
developing cartilage and cultured differentiating chondrocytes.";
Eur. J. Biochem. 217:781-790(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Embryonic chondrocytes, and Embryonic heart; MEDLINE-94039118; PubMed-8223621; van de Werken R., Gennari M., Tavella S., Bet P., M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Chen L.B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 TENSIN DOMAIN. SIMILARITY: CONTAINS 1 SH2 DOMAIN.
   Similarity 7; Conserv
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128:1095-1109(1995).
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63.6%;
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C -> R (IN REF. 2).
M -> T (IN REF. 2).
Q -> PR (IN REF. 3).
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T -> A (IN REF. 2).
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Score 40; DB Pred. No. 62; 2; Mismatches
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                                                               Length 1744;
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RESULT 5
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                                                                                                                  RESULT 6
CBX4_HUMAN
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O55187;

O1-OCT-2000 (Rel. 4

O1-OCT-2000 (Rel. 4

O1-OCT-2000 (Rel. 4
CBX4_HUMAN
000257;
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Repressor.
DOMAIN
DOMAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Alkema M.J., Jacobs J., Voncken J.W., Jenkins N.A., Copeland N.G., Satijn D.P.E., Otte A.P., Berns A., van Lohnizen M.;
"MPC2, a new murine homolog of the Drosophila polycomb protein is a member of the mouse polycomb transcriptional repressor complex.";
J. Mol. Biol. 273:993-1003(1997).
J. MOL Biol. 273:993-1003(1997).
IN TATE OF GENES. MODIFIES CHROMATIN, RENDERING IT HERITABLY CHANGED IN ITS EXPRESSIBILITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:1195985; Cbx4.
InterPro; IPRO00953; -.
Pfam; PF00385; chromo; 1.
PRINTS; PR00504; CHROMODOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; U63387; AAB96874.1; -. HSSP; P23197; 1APO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. MEDLINE=98035734; PubMed=9367786;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chromatin regulator; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00598; CHROMO_1; 1. PROSITE; PS50013; CHROMO_2; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090
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                                                                                                                                                                                                                                  DLQYQGGH 177
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LDDELPNQDGH 577
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                                                                                                                                                                                                                                                                                                                                            6; Conserv
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551 AA;
(Rel. 40, Created)
(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                        STANDARD;
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40, Last sequence update)
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60581 |
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75.0%;
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4 (POLYCOMB 2 HOMOLOG) (PC2) (MPC2).
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Pred. No. 26;
2; Mismatches
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30CEB09A82C58400 CRC64;
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P06149;
01-JAN-1988
01-FEB-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Satijn D.P.E., Olson D.J., van der Vlag J., I
Masselink H., Gunster M.J., Sewalt R.G.A.B.,
"Interference with the expression of a novel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Fetal brain MEDLINE=97459707;
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Mammalia; I
                                                                                                                                                                                                                                                                                                                                         Chromatin
                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00385; chromo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-97342649;
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                                                                                                                                                                                                                                                                                                                                                         PROSITE;
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                                                                                                                                                                                                                                                                                                                                                                                                                      nterPro;
                                                                                                                                                                                                    Local
                                                                                                                                                       4 DLEHQGGH 11
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FUNCTION: INVOLVED IN MAINTAINING THE STATE OF GENES. MODIFIES CHROMATIN, REIN ITS EXPRESSIBILITY.
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transcriptional repressor.";
                                                                                                                          DLQYQGGH
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                                                                                                                                                                                    Similarity
6; Conser
                                                                                                                                                                                                                                                                                                                                                                                       PR00504; CHROMODOMAIN
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                                                                                                                                                                                                                                                                                                                                         regulator; Nuclear
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558 /
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(Rel.
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Chordata;
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                                              STANDARD;
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CHROMO_2; 1.
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06,
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DLOG 4 (POLYCOMB 2 HOMOLOG) (PC2) (HPC2).
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sequence update)
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POLY-ALA.
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Catarrhini; Hominidae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hamer K.M.,
                                                                                                                                                                                                                Length 558
                                                                                                                                                                                                                                                              CRC64;
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Dym O., Pratt E.A., Ho C., Eisenberg D.;
"The crystal structure of D-lactate dehydrogenase, a peripheral membrane respiratory enzyme.";
Proc. Natl. Acad. Sci. U.S.A. 97:9413-9418(2000).
-!- FUNCTION: FIRST COMPONENT OF THE MEMBRANE BOUND D-LACTATE OXIDAS WHICH IS BELIEVED TO PLAY AN IMPORTANT ROLE IN THE ENERGIZATION THE ACTIVE TRANSPORT OF A VARLETY OF SUGARS AND AMINO ACIDS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rule G.S., Pratt E.A., Chin C.C.Q., Wold "Overproduction and nucleotide sequence dehydrogenase of Escherichia coll."; J. Bacteriol. 161:1059-1068(1985).
Oxidoreductase; INIT_MET 0
                                                                                                                                                                                   EMBL; M10038; AAA23688.1;
EMBL; X01067; CAA25531.1;
EMBL; U00007; AAA60530.1;
                                                                                                                                                                                                                                                                    entities requires a license agreement (See or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Campbell H.D., Rogers B.L., "Nucleotide sequence of the of Escherichia coli.";
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                                       InterPro; IPR001575;
Pfam; PF01565; FAD_t
                                                                                 ECO2DBASE; H062.0; 6TH EcoGene; EG10231; dld.
                                                                                                                                                                                                                                                                                                              modified and this statement
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MEDLINE=97426617; PubMed=9278503;
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                   FAD; Membrane;
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VARIANTS MPS-VII CYS-382 AND VAL-619. MEDLINE-91090114; PubMed-1702266;
                                                  mucopolysaccharidosis
                                                                        MEDLINE=94154731;
Wu B.M., Sly W.S.;
                                                                                                                         Vervoort R., Lissens W., Liebaers I.;
"Molecular analysis of a patient with hydrops fetalis caused by beta-
glucuronidase deficiency, and evidence for additional pseudogenes.";
Hum. Mutat. 2:443-445(1993).
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Grubb J.H., Sly W.S., Tropak M., Guise K.S., Gravel R.A.;
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                                                          Nu B.M., Sly W.S.;
"Mutational studies in a patient with
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                                                                                                                                                                          MEDLINE=94154730; PubMed=8111412;
                                                                                                                                                                                                                                                                                                  Tanaka J., Gasa S., Sakurada K., Miyazaki T., Kasai M., Makita A.; "Characterization of the subunits and sugar moiety of human placen and leukemic beta-glucuronidase."; and leukemic beta-glucuronidase."; Biol. Chem. Hoppe-Seyler 373:57-62(1992).
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"Analysis of the 5' flanking region
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ONIDASE PRECURSOR (EC 3.2.1.31) (BETA-G1).
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PubMed=8111413;
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PROSITE; PS00608; GLYCOSYL_HYDROL_F2_2; 1.
Hydrolase; Glycosidase; Lysosome; Glycoprotein;
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                                                                                                                                                                                                                                                                                                                                                                                              InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mutational analysis of a patient with mucopolysaccharidosis type 
VII, and identification of pseudogenes.";
wm. J. Hum. Genet. 52:517-526(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SUBUNIT: HOMOTETRAMER.
SUBCELLULAR LOCATION: LYSOSOMAL.
PTM: GLYCOSYLATED WITH 3 TO 4 N-LINKED OLIGOSACCHARIDE CHAINS.
DISEASE: DEFECTS IN GUSB ARE THE CAUSE OF MUCOPOLYSACCHARIDOSIS
TYPE VII (MPS-VII) (ALSO KNOWN AS SLY SYNDROME).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE IN DEGRADATION OF DERMATAN AND KERATAN SULFATES.

CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = AN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CATALYTIC ACTIVITY: A BE ALCOHOL + D-GLUCURONATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                         A26581; A26581.
1BHG; 17-SEP-97.
                                                                                                                                                                                                                                                                                                                                                                                                              253220;
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                                                     651
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                                                                                                                                 611
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451
173
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420
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                                                   ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PubMed=7680524;
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651
451
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                                                   74715
57.4%;
60.0%;
                                                                                                                                                                                                                                                                                                                    Disease mutation;
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                                                                                                                                                                                                                                       N-LINKED
                                                                                                                                                                                /FTId=VAR_003196.
A -> V (IN MPS-VII).
                                                                                                                                                                                                          N-LINKED (GLCNAC. . R -> W (IN MPS-VII).
                                                                                                                                                                                                                                                                  N-LINKED
                                                                                                                                                                                                                                                                                            BETA-GLUCURONIDASE.
                                                                                                    /FTId=VAR_003199.
A -> V (IN MPS-VII).
                                                                                                                              /FTId=VAR_003198.
R -> W (IN MPS-VII).
                                                                                                                                                        /FTId=VAR_003197.
R -> 'C (IN MPS-VII).
                                                                                                                                                                                                                                                                             PROTON
                                                                                           /FTId=VAR_003200
                                                                 FTId=VAR_003201
                                                   6BA7A19935C9ABBD CRC64;
                                                                            -> C (IN MPS-VII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               в.м.,
            39;
                                                                                                                                                                                                                                                                              DONOR
                                                                                                                                                                                                                                    (GLCNAC . .
                                                                                                                                                                                                                                                              (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bachinsky D.R.,
                                                                                                                                                                                                                                                                                                                      3D-structure
                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                     (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Grubb J.H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a collaboration - MBL outstation
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RESULT 9
RELA_ECOLI

RELA_ECOLI P11585;

STANDARD;

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DTLEHEGGYL

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Best Local
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SEQUENCE
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InterPro; IPR002912; -.
Pfam; PF01842; ACT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34,
30-MAY-2000 (Rel. 39,
GTP PYROPHOSPHOKINASE
                                                                                                                                                                                                                                                                                                                                                                 PIR; A31996; KIECG.
                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; J04039; AAA03237.1; EMBL; U29580; AAA69294.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The nucleotide sequence Escherichia coli.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Metzger S., Dror I.B., A. Friesen J.D., Cashel M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; P
Escherichia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89008481; PubMed=2844820;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The complete genome sequence of Escherichia coli K-12.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (PPGPP SYNTHETASE
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BINCETION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5-'
FUNCTION: IN EUBACTERIA PPGPP (GUANOSINE 3'-DIPHOSPHATE 5-'
DIPHOSPHATE) IS A MEDIATOR OF THE STRINGENT RESPONSE THAT
COORDINATES A VARIETY OF CELLULAR ACTIVITIES IN RESPONSE TO
CHANGES IN NUTRITIONAL ABUNDANCE. THIS ENZYME CATALYSES THE
FORMATION OF PPPGPP WHICH IS THEN HYDROLYSED TO FORM PPGPP.
CATALYTIC ACTIVITY: ATP + GTP = AMP + GUANOSINE 3'-DIPHOSPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PATHWAY: FIRST STEP IN THE METABOLISM OF PPGPP. SIMILARITY: BELONGS TO THE RELA / SPOT FAMILY.
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                                             LDDDLEHQG
LDDELEHLG
                                                                                            Similarity 7; Conserv
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                                                                                                                                                                               307 307 83875 MW;
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                                                                                               Conservative
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77.8%;
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), Last annotation update)
BE (EC 2.7.6.5) (ATP:GTP 3'-PYROPHOSPHOTRANSFERASE)
((P)PPGPP SYNTHETASE)
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., Glaser G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gamma subdivision; Enterobacteriaceae;
                                                                                               ۳
                                                                                                                     Score 39; DB Pred. No. 36;
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                                                                                                                                                                                                                -> K (IN REF. 1).
FA269709F15E1F25 CRC64;
                                                                                               Mismatches
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                                                                                                                                       Length 744;
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NAH1_PIG P48762; 01-FEB-1996 01-FEB-1996

(Rel. 33, Created)
(Rel. 33, Last sequence

update)

STANDARD;

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RESULT 10
GLB1_MAIZE
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NAH1_PIG
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P15590;
01-APR-1990 (Rel. 14,
01-AUG-1990 (Rel. 15,
01-CCT-2000 (Rel. 40,
GLOBULIN-1 S ALLELE F
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SEQUENCE
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or send a
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Belanger F.C., Kriz A.L.;
"Molecular characterization of the major maize by the Glb1 gene.";
                                                                                                                                                                                                                                         MaizeDB; 30181;
                                                                                                                                                                                                                                                    EMBL; M24845; AAA33467.1;
HSSP; P50477; ICAW.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Biochem. Genet. 27:239-251(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; |
Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GLB1
                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                        Seed storage
                                                                                                                                                                                                                    Pfam; PF00546; Seedstore_7s;
                                                                                                                                                                                                                                                                                                            modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The European Bioinformatics Institutions as long
                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kriz A.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89374022; PubMed=2775172;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=4577;
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                                                                                                                                                                                               SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Characterization of embryo globulins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 87-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lant Physiol.
         11
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                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO THE 7S SEED STORAGE PROTEIN FAMILY.
                                                                 DDDLEHQGGH 11
                                            DDNHHHHGGH
                                                                                        Similarity 60. 6; Conservative
                                                                                                                                                                                                                                                                                        an email
                                                                                                                                                                                                                                                                                     requires a license agreement (San email to license@isb-sib.ch).
                                                                                                                                                                                                                               IPR001113;
                                                                                                                                                 349
573 AA;
                                                                                                                                                                                                      protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91:636-643(1989)
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15, Last sequence update)
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LE PRECURSOR (GLB1-S) (7S-
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573
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Poales; Poaceae;
                                                                                        Score 38; DB
Pred. No. 40;
1; Mismatches
                                                                                                                                                 N-LINKED (GLCNAC. . .) (P
525ED1D00A062976 CRC64;
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                                                                                              40;
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) (7S-LIKE).
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EMBL; S71135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Reilly R.F., Hildebrandt F., Biemesderfer D., Sardet C.,
Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi P.;
Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi P.;
Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi P.;
Pouyssegur J., Aronson P.S., Slayman C.W., Igarashi P.;

"CDNA cloning and immunolocalization of a Na(+)-H+ exchanger
LLC-PK1 renal epithelial cells.";
Am. J. Physiol. 261:F1088-F1094(1991).
-!- FUNCTION: INVOLVED IN PH REGULATION TO ELIMINATE ACIDS GE
BY ACTIVE METABOLISM OR TO COUNTER ADVERSE ENVIRONMENTAL
CONDITIONS. MAJOR PROTON EXTRUDING SYSTEM DRIVEN BY THE I
SEDDIUM ION CHEMICAL GRADIENT. PLAYS AN IMPORTANT ROLE IN
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Pfam; PF00999; Na_H_Exchanger;
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Mammalia; Eutheria;
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PTM: PHOSPHORYLATED (POSSIBLE).
SIMILARITY: BELONGS TO THE NA(+)/H(+) EXCHANGER FAMILY.
CAUTION: THE NUMBER, LOCALIZATION AND DENOMINATION OF HYD
DOMAINS IN THE NA(+)/H(+) EXCHANGERS VARY AMONG AUTHORS.
CAUTION: HYDROPHOBIC DOMAINS A, B AND L ARE NOT BELIEVED
TRANSMEMBRANAL, BUT ONLY MEMBRANE-ASSOCIATED.
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CYTOPLASMIC (POTENTIAL).
G (M5B) (POTENTTAT)
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C (M3) (POTENTIAL).
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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  CYTOPLASMIC
N-LINKED (G)
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EXTRACELLULAR (POTENTIAL)
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E (M5) (POTENTIAL)
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There are no restrictions
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DENOMINATION OF HYDROPHOBIC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-AUG-1991 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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ACT_SITE 43 43
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01-MAR-1992 (Rel. 21, Last annotation update)
SUCROSE-6-PHOSPHATE HYDROLASE (EC 3.2.1.26) (SUCRASE) (INVERTASE).
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EMBL; AE000228; AAC74383.1; --
EMBL; D90768; BAA14870.1; --
EMBL; M38433; AAA23429.1; --
                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sibor send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
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                                                                                                                                                                                                                                                                                                                                                                    bacterial genome.";
Nucleic Acids Res.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning an Escherichia coli gene similar to mammalian aldehyde dehy Gene 99:15-23(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 1-251 MEDLINE-91216440;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Horiuchi T., Ikemoto K., Inada T., Isono K., Isono S., Itoh T., Kanai K., Kasai H. Kashimoto K., Kim S., Kimura S., Kitagawa M., Kitakawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Mashimoto H., Nishio Y., Oshima T., Saito N., Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yanamoto Y., Yano M.; Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=97426617; PubMed=9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N. STRAIN=K12 / MG1
                                                                                                                                                EcoGene; EG11822; ordL.
                                                                                                                                                                                                                                                                                                                                                                                               Borodovsky M., Rudd K.E., Koonin E.V.; "Intrinsic and extrinsic approaches for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-K12
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174
                         5 LEHQGGHV 12
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SIMILARITY: SOME, TO NAD-BINDING SITES OF DEHYDROGENASES.
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LDHSGGHI 181
                                                    Similarity
5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            997 (Rel. 35, Last annotation update) OXIDOREDUCTASE ORDL (EC 1.-.-).
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                                                    Conservative
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PubMed=1840553;
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RESULT 14
BGLR_MOUSE
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                                                                                          the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entitles requires a license agreement (See lor send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gallagher P.M., D'Amore M.A., Lund S.D., Ganschow R.E.; "The complete nucleotide sequence of murine beta-glucur and its deduced polypeptide."; Genomics 2:215-219(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
MEDLINE=88085188; PubMed=2891607;
Gallagher P.M., DAmore M.A., Lund S
Gallagher F.M., Famore M.A., Ganschow
                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              murine beta-glucuronidase gene complex.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=YBR, AND C3H/HEJ; TISSUE=Sperm;
MEDLINE=89384641; PubMed=2779578;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "DNA determinants of structural and regulatory variation within
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biochemistry 27:7131-7140(1988).
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                                                                                                                                                                                                                                                  SUBCELLULAR LOCATION: LYSOSOMAL. SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
J02836;
M63836;
M28540;
                  J03047; AAA37696.1;
J02836; AAA98623.1;
M63836; AAA63309.1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. 9:4074-4078(1989).
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Sciurognathi; Muridae;
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Matches 5
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P06760;
P01-JAN-1988 (Rel. 06, Created)
O1-JAN-1988 (Rel. 06, Last sequence update)
O1-JUL-1998 (Rel. 36, Last annotation update)
T-JUL-1998 (Rel. 36, Last annotation update)
P06760;
P0707A-GLICURONIDASE PRECURSOR (EC 3.2.1.31).
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EMBL; M19279; AAA3769;
PIR; A28954; A28954
PIR; A29977; A29977.
HSSP; P08236; LBHG.
                                                                        Powell P.P., Kyle J.W., Miller R.D., "Rat liver beta-glucuronidase. cDNA expression of a chimeric protein in expression of a chimeric protein in Biochem. J. 250:547-555(1988).
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Hydrolase;
SIGNAL
CHAIN
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TISSUE-Preputial gland;

MEDLINE-8701633; PubMed-3463967;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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                                                                                                                                                                                                                                                             membranes.";
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                                                                                                                                                                 MEDLINE=88183378;
                                                                                                                                                                                                                                          Proc. Natl.
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                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                            'Nucleotide sequence of rat preputial and in vitro insertion of its encoded
                                                                                                                                                                                                                                                                                                                   Adesnik M., Andy R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MGD; MGI:95874; Gus-s
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FUNCTION: BETA-GLUCURONIDASE PLAYS AN IMPORTANT ROLE DEGRADATION OF DERMATAN AND KERATAN SULFATES.
CATALYTIC ACTIVITY: A BETA-D-GLUCURONOSIDE + H(2)O = ALCOHOL + D-GLUCURONATE.
'SUBUNIT: HOMOTETRAMER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                  Y., Rosenfeld M.G., Kreibich G., Gubler U., Sabatini D.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Glycosidase;
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AAA37697.1;
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SITE OF THIS CLEAVAGE HAS AS YET NOT BEEN DETERMINED.
SIMILARITY: BELONGS TO FAMILY 2 OF GLYCOSYL HYDROLASES.
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Q9SBF1
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Best Local Similarity
Watches 7; Conserve
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                                                                                                                            Query Match
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SEQUENCE
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Eukaryota; Viridiplantae; Embryoph;
Magnollophyta; Liliopsida; Poales;
Andropogoneae; Zea.
NCBI_TaxID=4578;
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01-MAY-2000 (TrembLrel.
01-OCT-2000 (TrembLrel.
GLOBULIN-1 (FRAGMENT).
                                                                                                                                                                                                                                       Pfam; PF00546; Seedstore_7s; 1.
PROSITE; PS00867; CPSASE_2; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                             evidence from the Globulin-1 genetics 0:0-0(1998). EMBL; AP064218; ARC31461.1; -HSSP; P50477; ICAU.
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. Hilton H., Gaut B.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilton H., Gaut B.S.;
"Speciation and domestication in maize evidence from the Globulin-1 gene.";
Genetics 0:0-0(1998).
GEMBL; AF064216; AAC31459.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      O81253;
01-NOV-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
01-OCT-2000 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00867; CPSASE_2; UNKNOWN_1.NON_TER 239 239
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Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001113; -
Pfam; PF00546; Seedstore_7s;
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                                                                                                                                                                                                                                                                                                                                                                                           Speciation and domestication in maize and its wild relatives: vidence from the Globulin-1 gene.";
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                                                                                                                                                                                                                                                                                                           nterPro; IPR000901; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nterPro; IPR000901;
26
                                                                                                          Local
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                                           N
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DDNLHHHGGH
                                      DDDLEHQGGH 11
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1; 31895; Zeam
                                                                                 7; Conserv
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                                                                                    Conservative
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                                                                                                                                                                                                                          239
                                                                                                                                                                                                 AA;
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35
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                                                                                                        66.2%;
70.0%;
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08, Last sequence update)
15, Last annotation update)
                                                                                                                                                                                                 MW;
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Last sequence update)
Last annotation update)
                                                                                 Score 45; DB 1
Pred. No. 4.5;
1; Mismatches
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Pred. No.
                                                                                                                                                                                              147C4F61F65307FA CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tracheophyta; Spermatophyta;
ceae; PACC clade; Panicoideae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and
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                                                                                                                          Length 239;
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RESULT
Q9KFH6
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Q9Z5A6
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Best Local
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STRAIN-C-125 / JCM 9153;
Takami H., Nakasone K., Takaki Y.;
Submitted (MAR-2000) to the EMBL/Ger
EMBL; APO01508; BAB04222.1; -.
InterPro; IPR000182; -.
InterPro; IPR000182; -.
Pfam; PF00583; Acetyltransf; 1.
SEQUENCE 174 AA; 19690 MW; 11D88
                                                                                                                                                                                                                                                                                                         Q9KFH6;
01-OCT-2000 (TrEMBLrel. 1
01-OCT-2000 (TrEMBLrel. 1
01-MAR-2001 (TrEMBLrel. 1
BH0503 PROTEIN.
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SEQUENCE
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Bentley S.D.,
Submitted (FEB
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0925A6;
01-MAY-1999 (TrEMBLrel. 10,
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
                                                                                                                                                                                                                       Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                         Bacillus halodurans.
                                                                                                                                                                                                                                                                                                  вн0503.
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Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a detailed genetic and "A set of ordered cosmids" and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set of ordered cosmics and a set o
                                                                                                                                                                                                     NCBI_TaxID=86665;
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EMBL; AL035478: CAB36604.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Streptomyces coelicolor.
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InterPro; IPR000873; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=1902;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 LDDDLEHQGGHV 12
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8; Conserv
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                                                                                                                                                          FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (FEB-1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    541 AA;
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66.7%;
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16,
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e EMBL/GenBank/DDBJ databa
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Last annotation update)
                                                                                    EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                          Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL/GenBank/DDBJ
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Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CEB7374431F28CE5 CRC64;
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databases.
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Q9VXP2;
Q9VXP2;
01-MAY-2000 (TrEMBLrel. 13, C
01-MAY-2000 (TrEMBLrel. 13, L
01-MAR-2001 (TrEMBLrel. 16, L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9T215
Q9T215;
Q9T215;
01-MAY-2000
01-MAY-2000
                                                                    Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith M.C.M., Burns N., Wilson R.N., Gregory M.A.;
"The complete genome sequence of the Streptomyces temperate phage C31:
evolutionary relationships to other viruses.";
Nucleic Acids Res. 27:2145-2155(1999).
EMBL; AJ006589; CAA07123.1;
EMBL; AJ006589; CAA07123.1;
SEQUENCE 683 AA; 73980 MW; EC114A061EECA4BD CRC64;
     SEQUENCE FROM N.A.
                                                                                                                                                                        RHP OR CG8497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=NORWICH STOCK;

MEDLINE=99162580; PubMed=10051617;

Hendrix R.W., Smith M.C.M., Burns N., Ford M.E., Hatfull G.F.;

"All the world's a phage.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Viruses;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriophage phi-C31.
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MEDLINE=99238410; PubMed=10219087;
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Pred. No. 7.1;
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                                                                                                Brachycera; Muscomorpha;
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RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brothier P.,

RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

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RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gelbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,

RA Harris N.L., Kalush F., Karpen G.H., Ke Z., Kulp D., Lai Z.,

RA Lisko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Mshrefi A.,

RA Rainert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Syler E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Yelds S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Yelds S.R., Wers E. W., Rubin G.M., Venter J.C.,

RA Yelds S., Zhong W., Shong W., Zhou S., Zhao Q., Zheng L.,

RA Shong S.O., Sarafashi A., Norley K., Zhou S., Zhu X., Smith H.O.,

RA Shong S.O., Sarafashi A., Shong W
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RHP OR CG8497.

Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Bukaryota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Prerygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Prerygota; Neoptera; Drosophilia.
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                                                                                                                                                                                                                                                                                        01-MAR-2001 (TrEMBLrel. RHOPHILIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR001478; - Pfam; PF00595; PDZ; 1.
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RESULT
Q9PEY9
       Qy
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Best Local Similarity
7; Conserv
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                                                                                                                                                                              RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furlan L.R.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA HO P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manck C.F.M., Miracca E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T., O., Netto L.E.S.,
RA Moon D.H., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Souza M.E., Jr., de Sa R.G., Santelli R. V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.,
RA da Silva A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Marghe S. S. Santelli R. V., Sawasaki M.H.,
RA Marghe S. Sa R.G., Santelli R. V., Sawasaki M.B.,
RA Marghe S. Silva M.A., Verjovski-Almeida S., Vettore A.L.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe M. S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe S. Sa R.G., Setubal J.C.,
RA Marghe 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIINE-20365717; PubMed-10910347;
Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
Alvarenga R., Alves L.M.C., Araya J.E., Bala G.S., Baptista C.S.,
Barros M.H., Bonaccorsi E.D., Bordin S., Bove J.M., Briones M.R.S.,
Bueno M.R.P., Camargo A.A., Camargo L.E.A., Carraro D.M., Carrer H.
Colauto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.
Coutinho L.L., Cristofani M., Dias-Neto E., Docena C., El-Dorry H.,
Faccincani A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
                            PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2001
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01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9PEY9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00595; PDZ; 1.
Pfam; PF02185; HR1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FlyBase; FBgn0026374; Rhp. InterPro; IPR000861; -. InterPro; IPR001478; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases EMBL; AF132025; AAD31273.1; -
                                                                                                                   EMBL; AE003928; AAF83699.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Xylella fastidiosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HEMAGGLUTININ-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Edwards K.A.,
                                                                                              InterPro; IPR000267; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=2371;
                                                                         InterPro; IPR001424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2 DDDLEHQGGH 11
                                                                                                                                           genome sequence of the plant pathogen re 406:151-159(2000).
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CE 718 AA; 8
PS00144; ASN_GLN_ASE_1; UNKNOWN_1.
PS00087; SOD_CU_ZN_1; UNKNOWN_1.
3282 AA; 343744 MW; F0796430BC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Proteobacteria; gamma subdivision; Xanthomonas group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 15, (TrEMBLrel. 15, (TrEMBLrel. 16,
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the Drosophila Rhophilin g
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Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
    F0796430BC9A2194 CRC64;
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46;
                                                                                                                                                                Xylella fastidiosa.",
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     D.M., Carrer H.,
Costa-Neto C.M.,
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RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Garnier M., Goldman G.H., Goldman M.H.S., Gomes S.L., Kitajima J.P.,
RA HO.P.L., Hoheisel J.D., Junqueira M.L., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.E., Lalgret F., Lambais M.R., Leite L.C.C.,
Lemos E.G.M., Lemos M.V. F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Lemos E.G.M., Lemos M.V. F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira A.M.B.N., Madeira H.M.F., Matsukuma A.Y.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Manchado M.A., Nascimento A.L.T., Nonteiro-Vitorello C.B.,
RA Moon D.H., Nagai M.A., Nascimento A.L.T., Netto L.E.S.,
Nhani A. Jr., Nobrega F.G., Nunes L.R., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Pasquero J.B.,
RA Quaggio R.B., Roberto P.G., Rodrigues V., de Rosa A.J.M.,
A de Rosa V.E. Jr., de Sa R.G., Santelli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A. Jr.,
RA da Silva A.C.R., da Silva A.M., da Silva F.R., Silva W.A.,
RA de Souza A.P., Terenzi M.F., Truffi D., Tsai S.M., Tsuhako M.H.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
The Groome Seguence of the plant pathogen XVIella fastidiosa ""
The Groome Seguence of the plant pathogen XVIella fastidiosa ""
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-MAR-2001 (TrEMBLrel. 16,
HEMAGGLUTININ-LIKE SECRETED
XF2196.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The genome sequence of the plant pathogen Xylella fastidiosa."; Nature 406:151-159(2000).
EMBL; AE004032; AAF84995.1; -.
                                                                                                                                                                                                                                                                                                           PROSITE; PS00144; ASN_GLN_ASE_1; UNKNOWN_1.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
SEQUENCE 3442 AA; 360148 MW; AAE30CDE92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xylella fastidiosa
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                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001424;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000267;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20365717; PubMed=10910347;
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472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    472 LENDIDNRGGHI 483
                                                                                                                                                                  Local Similarity
                                                         1 LDDDLEHQGGHV 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10
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5; Conserv
                                                                                                                                     Conservative
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                                                                                                                                                                  61.8%;
41.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                  Score 42; DB 2;
Pred. No. 2.4e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 42; DB
Pred. No. 2.2e
                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                  AAE30CDE923E3C6E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3442 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
                                                                                                                                                                                                  Length 3442;
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PRELIMINARY;

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01-OCT-2000 01-MAR-2001

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045994;
01-JUN-1998 (Tremblrel. C
01-JUN-1998 (Tremblrel. C
01-JAN-1999 (Tremblrel. C
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InterPro; IPRO00267; ..
InterPro; IPRO01424; ..
InterPro; IPRO01424; -.
IPROSITE; PS00144; ASN_GLN_ASE_1; UNKNOWN_1.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
PROSITE; PS00087; SOD_CU_ZN_1; UNKNOWN_1.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
                                  Caenorhabditis elegans
                                                                        ZK1053.2 PROTEIN.
ZK1053.2.
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EMBL; AE004082; AAF85560.1; -.
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Best Local
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Nature 368:32-38(1994).
NATURE 368:32-38(1994).
EMBL; Z82084; CAB04976.1;
EMDL; Z82084; CAB04976.1;
Q54507 PRELIMINARY; PRT;
Q54507;
01-NOV-1996 (TrEMBLrel. 01, Created)
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O9LWC2;
01-OCT 2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
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                                                                                                                                                                                                                                      clone:P0483F08.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AP002094; BAA96222.1; -.
                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Magnoliophyta; Liliopsida;
                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                            Sasaki T., Matsumoto T., Yamamoto K.;
                                                                                                                                                                                                                                                                                                        STRAIN=CV.
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Pred. No. 61;
4; Mismatches
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Pred. No.
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Best Local S
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Matches 7; Conservative
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P72532;
01-FEB-1997 (TrEMBLrel. 0)
01-FEB-1997 (TrEMBLrel. 0)
01-OCT-2000 (TrEMBLrel. 1)
FIBRONECTIN-BINDING PROTE
                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CLINICAL ISOLATE A75;
MEDLINE-96020668; PubMed-7476200;
Kreikemeyer B., Talay S.R., Chhatwal G.S.;
"Characterization of a novel fibronectin-binding surface protein in group A streptococci.";
MOI. Microbiol. 17:137-145(1995).
EMBL; X83303; CAA58282.1; -.
HSSP; P02188; IHRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PFO
SEQUENCE
                                                                                                               InterPro; IPR001899; -.
InterPro; IPR002035; -.
Pfam; PF00746; Gram_pos_anchor; 1.
SEQUENCE 1025 AA; 112680 MW; CE6E52FE45CFF5D5 CRC64;
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                                                                                                                                                                                                                                                                                                                                        Streptococcus pyogenes
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Rakonjac J.V., Robbins J.C., Fischetti V.A.;
Rakonjac J.V., Robbins J.C., Fischetti V.A.;
Planta sequence of the serum opacity factor of group A streptococci:
identification of a fibronectin-binding repeat domain.";
Infect. Immun. 63:622-631(1995).
EMBL; U02290; AAA85219.1; -.
EMBL; P02188; 1HRM.
                                                                                                                                                                                                                                                                                                                Streptococcus
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Bactlaria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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InterPro; IPR002035; -.
InterPro; IPR002035; -.
Pfam; PF00746; Gram_pos_anchor; 1.
SEQUENCE 1025 AA; 112770 MW; 327C9C1DFFBD0394 CRC64;
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                                                Score 40; DB 2; Le
Pred. No. 1.5e+02;
l; Mismatches 2;
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Search completed: July 6,

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Result
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4.260 Million cell updates/sec
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US-09-177-858-2
US-09-107-858-2
US-09-303-318A-8
US-08-93-318A-8
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US-08-172-331B-2
US-08-172-331B-2
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US-08-072-064-4
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AT.TCMWEMTS	US-09-115-032-1	US-08-255-457-1	US-08-651-818A-23	US-08-651-818A-19	US-08-780-496-8	US-08-584-031-8	US-08-405-496A-24	US-08-480-604A-24	US-08-651-818A-21	US-08-293-284A-53	US-08-346-849-53	US-09-434-065-2	US-09-252-571-2	US-08-677-862-2	US-09-107-858-4	US-08-758-621-4	US-08-007-107-4	US-09-456-287-2	
	Sequence 1, Appli	Sequence 1, Appli	Sequence 23, Appl	Sequence 19, Appl	Sequence 8, Appli	Sequence 8, Appli	Sequence 24, Appl	Sequence 24, Appl	Sequence 21, Appl	Sequence 53, Appl	Sequence 53, Appl	Sequence 2, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli	Sequence 2, Appli	

ALIGNMENTS

## ; MOLECULE TYPE: US-08-188-582-20 RESULT 1 US-08-188-582-20 TELEPHONE: (415) 781-1989 TELERAX: (415) 398-3249 TELEX: 910 277299 INFORMATION FOR SEQ ID NO: 20: SEQUENCE CHARACTERISTICS: LENGTH: 1213 amino acids Patent No. Sequence GENERAL INFORMATION: COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA: ATTORNEY/AGENT INFORMATION: NAME: OSMAN, Richard A REGISTRATION NUMBER: 36,627 REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989 APPLICANT: Wang, Edith APPLICANT: Weinzierl, Robert O.J. TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS NUMBER OF SEQUENCES: 36 CORRESPONDENCE ADDRESS: APPLICANT: APPLICANT: APPLICANT: Dynlact, Brian D. APPLICANT: Hoey, Timothy APPLICATION NUMBER: US/0 FILING DATE: 28-JAN-1994 CLASSIFICATION: 435 CITY: San Francisco STATE: California TOPOLOGY: ZIP: 94111-4187 COUNTRY: STREET: ADDRESSEE: 20, Er 5534410 amino acid Application US/08188582 4 Embarcadero Center, Tjian, Robert Comai, Lucio USA Ruppert, Siegfried Tanese, Naoko FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT US/08/188,582 20: Suite 3400 Version #1.25 ę

64.6%;

Score 51;

DB 1;

Length 1213;

72.78;

Pred. No. 6.7;

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Sequence 7, Application US/08918727 Patent No. 5849528
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Best Local (
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Patent No.
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Matches 8; Conservative
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TELEX: 910 277299
INFORMATION FOR SEQ ID NO:
                                                                                                    1160 HKHKHKHRHSK 1170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
US/08/646,715
FILING DATE: 09-MAY-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/188,582
FILING DATE: 28-JAN-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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APPLICANT: Weinzierl, Robert O.J.
TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS,
TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE
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nes 8; Conserva
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REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
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RESULT 4
US-09-205-680A-7
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                                                                                                                                                                                     Sequence 7, Application US/09205680A Patent No. 6103497
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Best Local
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                                                                                                                       APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,727
FILING DATE: Herewith
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
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NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                             CORRESPONDENCE ADDRESS
                                                             APPLICANT: Lal, Preeti
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN S100 PROTEINS
NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            IMMEDIATE SOURCE:
LIBRARY: GenBa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                102 GHDHRHGKGCGK 113
 ADDRESSEE: Incyrcan Drive
STREET: 3174 POI
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                       Local Similarity 66.7 nes 8; Conservative
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3174 Porter Drive
                                                                                                                         Bandman, Olga
Corley, Neil C.
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Corley, Neil C.
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                               Incyte Pharmaceuticals, Inc
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N: HUMAN S100 PROTEINS
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Pred. No. 0.91
1; Mismatches
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0.91;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
             FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION UNMBER: 60/018
APPLICATION:
FILING DATE: 29-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: $11ver! Jean M.
REGISTRATION NUMBER: 39,03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                        SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Guerino TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Colette C. Muenzen
REGISTRATION NUMBER: 39,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530 PRIOR APPLICATION DATA:
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LIBRARY: GenBai
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REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                         Guerinot, Mary Lou, and Eide, David J.
VENTION: Metal-Regulated Transporters and Uses Therefor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                39,030
DCI-099CP
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Pred. No. 0.
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                                                                                                                                                      Version #1.25
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0.91;
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US-09-107-858-14
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                                                                                                                                                                                                                                                                                                           Sequence 2, Application US/08758621
Patent No. 5846821
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Best Local Similarity
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TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/107,858
                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 08/758,621 EARLIER FILING DATE: 1996-11-27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT FILING DATE: 1998-06-30
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TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 34
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Ver. 2.0
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                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE &
                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                           APPLICANT: Guerinot, Mary Lou, and Eide, David J.
TITLE OF INVENTION: Metal-Regulated Transporters and Uses Therefor NUMBER OF SEQUENCES: 21
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APPLICATION NUMBER:
                                                                                                                       ZIP: 02109-1875
                                                                                                                                      COUNTRY:
                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                       STREET:
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77.8%;
US/08/758,621
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Pred. No.
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                                 Version #1.25
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2.7;
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FILING DATE: PRIOR APPLICATION DATA:

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US-09-032-315-8
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Best Local Similarity
7; Conserv
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; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-107-858-2
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Best Local Similarity
7; Conserve
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US-09-107-858-2
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FILING DATE: 29-MAY-LYCATION:

ATTORNEY/AGENT INFORMATION:

NAME: $11ver1, Jean M.

REGISTRATION NUMBER: 39,030

REFERENCE/DOCKET NUMBER: DCI-(
TELECOMMUNICATION: 10FORMATION:

TELEPHONE: (617)227-7400

TELEFAX: (617)227-5941

TELEFAX: (617)227-5941
                                                                                  Sequence 8, Application US/09032315
Patent No. 5985818
GENERAL INFORMATION:
APPLICANT: Svendsen, Allan
APPLICANT: Xu, Feng
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: Guerinot, Mary Lou et al.
APPLICANT: Guerinot, Mary Lou et al.
TITLE OF INVENTION: METAL-REGULATED TRANSPORTERS AND USES THEREFOR
FILE REFERENCE: DCI-099CPDV
CURRENT APPLICATION NUMBER: US/09/107,858
CURRENT FILING DATE: 1998-06-30
CURRENT FILING DATE: 1998-06-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2, Application US/09107858 Patent No. 6162900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: 08/758,621
EARLIER FILING DATE: 1996-11-27
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 339 amino acids
                                            CORRESPONDENCE ADDRESS:
                                                         NUMBER OF SEQUENCES:
                                                                           TITLE OF INVENTION:
                                                                                                                                                                                                                                    154 HGHGHGHG 161
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 CITY:
                STREET:
                             ADDRESSEE:
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                                                                                                                                                                                                                                                                  4 HKHGHGHG 11
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OGY: linear
New York
             E: No. 59858180 No. 5985818disk of No. 5985818th America, Inc. 405 Lexington Avenue
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                                                                          LACCASE MUTANTS
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Pred. No. 5;
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Pred. No. 5;
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Best Local
                                                                             APPLICATION NUMBER: US/08/9
FILING DATE: December 18, 1
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION UMBER: 33,728
REFERENCE/DOCKET NUMBER: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 59983530 No. 5998353disk of No.
                                               TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
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NAME: ROZEK, Carol
REGISTRATION NUMBER: 36,993
                                                                                                                                                                                                SOFTWARE: Patentin Rel
                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cherry, Joel TITLE OF INVENTION: LAC
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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LENGTH: 575 amino acids
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MEDIUM TYPE: Diskett
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Rasmussen, Grethe
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SEQUENCE CHARACTERISTICS:

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                                                     Query Match
Best Local Similarity
Matches 9; Conserv
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Patent No. 6140092
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                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/93
APPLICATION NUMBER: 18,
FILING DATE: December 18,
ATTORNEY/AGENT INFORMATION:
NAME: Gregg, Valeta A.
REGISTRATION NUMBER: 33,72
REGISTRATION NUMBER: 33,72
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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APPLICANT:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
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331 HKHKHGRGLLSGHG 344
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CITY: New York
                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC
OPERATING SYSTEM:
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE:
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                         2 HKHKHGH----GHG 11
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Schneider, Palle
Rasmussen, Grethe
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                   linear
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                                                                  Score 48;
Pred. No.
                                                                                                                                                                                                                                                                                             5032.200-US
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                                                                                DB 4;
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RESULT 13
US-08-172-331B-2
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                                                                                                                                                                                    GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
                                                                                                                                    APPLICANT: Wahleithner,
APPLICANT: Christensen,
APPLICANT: Schneider, Pa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: 52
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 61840150 No. 6184015disk of No. 6184015th America,
                                                                                                         TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Rozek, Carol
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                                                                           CORRESPONDENCE ADDRESS:
                                                                                           NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                              331 HKHKHGRGLLSGHG 344
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SOFTWARE: FastSEQ for Windows Version
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/396,260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CENGTH:
                                                                                                                                                                                                                                                                                                                           2 HKHKHGH----GHG 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10174
                              New York
                                                                                                                                                                                                                   Application US/08172331B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              amino acid
New York
                                               405
                                                                                                                                       Schneider, Palle
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                                                                                                                                                                 Wahleithner, Jill A.
                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                            No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          212-867-0123
                                            Lexington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            amino acids
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                                                         54808010 No. 5480801disk of No.
                                                                                                                                                                                                                                                                                                                                                                       60.8%;
                                                                                                       PURIFIED PH NEUTRAL ACIDS ENCODING SAME
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                                                                                                                                                                                                                                                                                                                                                                                      DB 4;
                                                                                                                       LACCASES
                                                                                                                                                                                                                                                                                                                                                                                      Length 575;
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                                                            5480801th America,
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COMPUTER READABLE FORM: MEDIUM TYPE: Floppy

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

Floppy disk

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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 26, Application US/08137614A Patent No. 5487976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                            STREET: CLL...
CITY: Rochester
CTATE: New York
                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit
ATTORNEY/AGENT INFORMATION:
                                                                       CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 08/162,827 FILING DATE: 03-DEC-1993 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 00 FILING DATE: 17-SEP-1993 PRIOR APPLICATION DATA:
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APPLICATION NUMBER: US 08/122,230
FILING DATE: 17-SEP-1993
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             332 HKHKHGRGLLSGHG 345
                                                                                        COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                  APPLICATION NUMBER: US/08/137,614A
FILING DATE: 15-OCT-1993
                     CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: 212-878-9655
                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity les 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Lowney Dr., Karen A REGISTRATION NUMBER: 31,2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                   ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 22-DEC-1993
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                                                                                                                                                                                           14603
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 576 amino acids amino acid
                                                                                                                                                                                                                                                          Clinton Square, p.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                               Nixon, Hargrave, Devans & Doyle
                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein
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US-08-072-064-1
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Best Local Similarity
7; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-137-614A-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (716)263-160
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                          TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
                                                  POSITION IN GENOME:
                                                                                    ORIGINAL SOURCE:
                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                         REFERENCE/DOCKET NUMBER: OP TELECOMMUNICATION INFORMATION:
                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: FFRENCH-CONSTANT, RICHARD H. APPLICANT: JACKSON, MEYER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 617 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION: TELEPHONE: (716)263-1636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               434 GPEHGHGHGH 443
                                  CHROMOSOME/SEGMENT:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 19930
                MAP POSITION:
                                                                    ORGANISM:
                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32,837
                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: San Francisco
STATE: California
                                                                                                                      FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: PETER G. CARROLL STREET: 220 Montgomery Street,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,103 REFERENCE/DOCKET NUMBER: 19
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GY: linear
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                                                                                                                      unknown
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                                                                Drosophila melanogaster
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                                                                                                  peptide
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            MENT: III; polytene subregion approximately map unit 26
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59.5%;
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Pred. No.
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. 12;
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OY 1 GHENHEHH 10
Db 455 GPENGHEHH 464
Search completed; July 6, 2001, 09:10:21
Job time: 187 sec
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Scoring table:
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   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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  PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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  US-09-437-912-3
79
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Copyright (c) 1993 - 2000 Comp
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  2038
5038
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1334
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                 A25486
T34937
S75947
T49164
C27115
A27115
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T48099
T34168
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S54302
                                                                                             C25486
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hypothetical prote hypothetical prote zinc transporter-1 hypothetical prote probable transcrip
                                                                                                                                                                  kininogen, HMW pre
kininogen, HMW II
kininogen, HMW II
kininogen, HMW I p
peptidyl-prolyl ci
hypothetical prote
probable zinc tran
hypothetical prote
zinc transporter z
zinc transport pro
                                         zinc transporter-l
K-kininogen, LMW p
major acute phase
                                                                 hypothetical prote
                                                                                                                    gene pipsqueak pro
gene pipsqueak pro
                                                                                                                                                                                                                                                       Description
                                                                                  K-kininogen, HMW
kininogen, HMW I
                                                                                                                                           histidine-rich pro
hypothetical prote
                                                                                                   hypothetical prote related to spliceo
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51	51	51	51	51	52	52	52	53	53	53	53	53	53.5	54	54
64.6	64.6	64.6	64.6	64.6	65.8	65.8	65.8	67.1	67.1	67.1	67.1	67.1	67.7	68.4	68.4
1213	1213	1028	457	203	436	314	110	529	196	196	177	160	173	1920	1891
Ν	Ν	Ν	N	N	N	Ν	Ν	2	N	N	Ν	2	N	N	ν
A54063	S16356	A56038	S39079	T36240	149714	T35241	T07618	T08684	A49987	D85999	S65780	T07180	T51469	T13893	T13594
TATA-binding prote	ovo protein - frui	DNA-binding protei	puff C-8 protein -	hypothetical prote	MHC H-2K/t-w5-link	hypothetical prote	cold stress protei	hypothetical prote	probable fkbP-type	hypothetical prote	glycine/proline-ri	hypothetical prote	glycine/proline-ri	gene hindsight pro	hypothetical prote

## ALIGNMENTS

A;Title: Completion of the primary structure of human high-molecular-mass kininogen. A;Reference number: A24871; MUID:86108361 A;Accession: A24871 A;Molecule type: protein A;Residues: 'Z',20-380 <kell> R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins TV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New A;Title: Amino acid sequence of the light chain of human high molecular mass kininoge A;Reference number: A27899 A;Accession: A27899</kell>	A;Molecule type: mRNA A;Molecule type: mRNA A;Residues: 'ANSM', 253-377 <aue> A;Residues: 'ANSM', 253-377 <aue> A;Residues: 'ANSM', 253-377 <aue> A;Residues: 'ANSM', 253-377 <aue> A;Residues: 'ANSM', 253-377 <aue> Cut. J. Biochem. 152, 307-314, 1985 A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270 A;Accession: A91153 A;Accession: A91153 A;Molecule type: protein A;Residues: 379-644 <lot> A;Note: the bradykinin sequence preceding the light chain sequence was not determined R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. Eur. J. Biochem. 154, 471-478, 1986 A:Title: Completion of the primary structure of human high-molecular-mass kiningen</lot></aue></aue></aue></aue></aue>	A;Residues: 1-389 < OHK> A;Cross-references: GB:K02566; NID:g177889 A;Cross-references: GB:K02566; NID:g177889 R;Takagaki, Y; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A;Reference number: A92544; MUID:85234582 A;Accession: A25276 A;Molecule type: mRNA A;Residues: 1-592, 'I', 594-644 < TAK> A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I. FEBS Lett. 321, 93-97, 1993 A;Title: Cloning, expression and characterization of human kininogen domain 3. A;Reference number: S32422; MUID:93223854 A;Accession: S32422	RESULT 1 KGHUH1 Kininogen, HMW precursor [validated] - human kininogen, daludated] - human N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen N;Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular C;Species: Homo sapiens (man) C;Date: 28-May-1966 #sequence_revision 28-May-1986 #text_change 08-Dec-2000 C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030; C;Okcusion: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030; C;Okcubo, I; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M. Biochemistry 23, 5691-5697, 1984 A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide A;Reference number: A90490; MUID:85122621 A;Accession: A01279 A;Molecule type: mRNA

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A; Molecule type: protein
A; Residues: 264-359, 'N', 361-375 <LEN2>
A; Residues: 254-359, 'N', 361-375 <LEN2>
A; Rittle, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A; Title: Human mast cell tryptase isoforms: separation and examination of substrate-spec A; Reference number: S55239; MUID:95251593
A; Accession: S55239
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A; Molecule type: protein
A; Residues: 380-389 <MIN>
A; Residues: 380-389 <MIN>
R; Maeda, H.; Matsumura, Y.; Kato, H.
R; Maeda, H.; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A; Title: Purification and identification of [hydroxyprolyl(3)]bradykinin
A; Title: Purification and identification of [hydroxyprolyl(3)]bradykinin
                                                                A;Molecule type: protein
A;Residues: 431-434 <STR>
A;Residues: 431-434 <STR>
R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, Y.; Miyata,
J. Biol. Chem. 260, 8610-8617, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lenarcic, B.; Krasovec, M.; Ritonja, A.;
FBBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C
A;Reference number: S14303; MUID:91192133
A;Accession: S14447
                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 450-452, 'X', 454, 'X', 456 <LIT>
R; Straczek, J: Maachi, F: le Nguyen, D.;
FEBS Lett. 373, 207-211, 1995
A; Reference
A; Contents:
                    A; Title: Structural organization of the human A; Reference number: A92545; MUID:85234583
                                                                                                                                                                                            A; Accession: S68059
                                                                                                                                                                                                                      A; Title: Purification from human plasma of A; Reference number: S68059; MUID: 96033974
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A;Residues: 380-389 <KAT3>
R;Lenarcic, B.; Krasovec, N
FEBS Lett. 280, 211-215, 19
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FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues
A;Reference number: A61495; MUID:88211869
A;Accession: A61495
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A; Molecule type: protein
A; Residues: 1-19;189-192;310-314;381-389 < LEN1>
A; Residues: Matsumura, Y.; Maeda, H.
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A;Residues: 379-389, K', 390-407, 'Q', 409-644 <KEL2>
A;Residues: 379-389, K', 390-407, 'Q', 409-644 <KEL2>
R;Mindrolu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scicli, Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A;Title: A new kinin molety in human plasma kininogens.
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A;Note: this peptide had Pro-383 modified to
A;Accession: B61495
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A;Residues: 380 389 <SAS>
R;Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok,
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors
A;Reference number: 802482; MUID:89076517
A;Accession: 802482
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Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from
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A;Residues: 381-389 <KAT2>
A;Experimental source: urine
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A; Residues: 380-389 < KAT1>
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A;Accession: A34030
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h, Accession: C61495
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A; Accession: A91923
A; Molecule type: protein
A; Residues: 376-391 <KAT>
                                                                  R;Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine kininogen:
A;Reference number: A91923; MUID:70180420
                                                                                                                                                                                                                                                                                                                                                       C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01282; A91923; A91941; A91938; B29559
                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-619 < KIT>
                                                                                                                                                                                                                                                                                     R;Kitamura, N.; Takagaki,
Nature 305, 545-549, 1983
A;Title: A single gene for
                                                                                                                                                                                                                                                                                                                                                                                                                          kininogen, HMW II precursor – bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokinin
                                                                                                                                                                A;Cross-references: GB:V01492; GB:K01758; NID:g493; PIDN:CAA24736.1;
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F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>
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C;Superfamily: kiningen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
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                                                                                                                                                                                                                                           A; Accession: A01282
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ininogen; cystatin homology
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Pred. No.
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Kato, H.;

Iwanaga,

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Suzuki,

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C;Superfamily: kininogen; Cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-619/Product: HMW kininogen II #status predicted <MAT>
F;19-376/Product: HMW kininogen II #status predicted <MAT>
F;19-130/Domain: cystatin homology <CY1>
F;141-352/Domain: cystatin homology <CY2>
F;141-352/Domain: cystatin homology <CY3>
F;261-372/Domain: cystatin homology <CY3>
F;261-372/Domain: cystatin homology <CY3>
F;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;377-38-386/Product: bradykinin (kallidin I) #status experimental <CH>
F;377-38-386/Product: bradykinin (kallidin I) #status experimental <CH>
F;387-619/Product: hmw kininogen II light chain #status experimental <CCH>
F;418-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment
F;27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
F;47-168 fig 304-306/dialetic (Asn) (covalent) #status absent
                                                                                                                                                                                                                                                             F;47/Binding site: carbohydrate (Asn) (covalent) #status absent #s87,168,169,204,280/Binding site: carbohydrate (Asn) (covalent) (covalent) #status experimental F;136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental F;197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F;376-377/Cleavage site: Met-Lys (kallikrein) #status experimental F;380/Modified site: 4-hydroxyproline (Pro) #status predicted F;380-387/Cleavage site: Arg-Ser (kallikrein) #status experimental F;396-387/Cleavage site: Arg-Ser (kallikrein) #status experimental F;396,400,404,510/Binding site: carbohydrate (Ser) (covalent) #status experimental F;397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) #status F;496-497/Cleavage site: Arg-Thr (kallikrein) #status experimental
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xyproline residue is present in the kininogen prior 
C;Superfamily: kininogen; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: The amino acid sequence of the light chain of A;Reference number: A91153; MUID:86030270
A;Contents: annotation; bovine cleavage sites; bovine c R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S. Seikagaku 56, 808, 1984
A;Title: Disulfide bonds in bovine HMW kininogens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: A91941; A; Accession: A91941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 J. Biochem. 79, 1201-1222, A; Title: Primary structure
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Contents: annotation; disulfide bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A94300
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                                                                                                                                                       Query Match
Best Local
                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biochem.
470
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                                                             СНКНКНСНСНСК 12
GHGHKHGHGHGK
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                                                                                                                                                Similarity
                                                                                                                      Conservative
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152, 307–314, 1985
481
                                                                                                                                                   91.1%;
91.7%;
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                                                                                                                      0;
                                                                                                                                                Score 72; D
Pred. No. 0.
                                                                                                                      Mismatches
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Suzuki, T.
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                                                                                                                                                       DB 1;
0.0029;
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                                                                                                                                                                             Length 619;
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RESULT

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A; Molecule type: protein
A; Molecule type: protein
A; Residues: 458-498 < HANN
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.
R; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.
A; Title: Bovine high molecular weight kininogen. Th
A; Title: Bovine high molecular weight kininogen. Th
A; Reference number: A92627; MUID:87137530
A; Recession: A29559
A; Molecule type: protein
A; Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 < SUE
R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: article in Japanese C; Comment: The HMW kininogen precursor is produced from the same gene as the LMW form C; Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of C; Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is in C; Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator xyproline residue is present in the kininogen prior to the release of bradykinin. C; Superfamily: kininogen; cystatin homology C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bur. J. Blochem. 152, 307-314, 1983
A;Title: The amino acid sequence of the light chain of A;Reference number: A91153; MUID:86030270
A;Contents: annotation; bovine cleavage sites; bovine c R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
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N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininc
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-
C;Accession: A01181; A91923; A91938; A29559
C;Accession: A01181; A91923; A91938; A29559
R;Kitamura, N; Takagaki, Y; Furuto, S; Tanaka, T; Nawa, H; Nakanis
                                                                                                                                                                                                                                                                                                                                                     F;141-252/Domain: cystatin homológy <CY2>
F;263-974/Domain: cystatin homológy <CY3>
F;263-974/Domain: cystatin homológy <CY3>
F;379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
F;380-388/Product: bradykinin (kallidin I) #status experimental <BDY>
F;389-621/Product: HMW kininogen I light chain #status experimental <LCH>
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A;Accession: A91938
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A; Residues: 1-621 <KIT;
A; Cross-references: GB: V01491; GB: K01757;
R; Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
                                                                                               F:417-488/Region: glycine/histidine/lysine-rich
F:19/Modified site: pyrrolidone carbonic acid (Gln) (in mature form) #status ex
F:27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-359/Disulfide
F:87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:136/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F:197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F:197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
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                           F;382/Modified site: 4-hydroxyproline (Pro) #status predicted F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experime
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F;19-621/Product: HMW prokininogen I *status predicted <MAT>F;19-379/Product: HMW kininogen I heavy chain *status experiF;19-130/Domain: cystatin homology <CY1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      c;neyworus: arcernative spricing; blood coagulation; cysteine
F;1-18/Domain: signal sequence #status predicted <SIG>
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Seikagaku 56, 808, 1984
A;Title: Disulfide bonds in bovine HMW kininogens
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A;Contents: annotation; disulfide bonds
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J. Biochem. 77, 55-68, 1975
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J. Biochem. 152, 307-314, 1985
site: carbohydrate (Ser)
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(COValent) #status
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                                       experimenta.
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experimental
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R.Theologis, A.; ECALL, CONN, L.; CURTE, Chin, C.W.; Chung, M.K.; Conn, L.; CURTE, Chin, C.W.; Chung, M.K.; Conn, L.; CURTE, C.M.; Chin, C.; Khan, S.; Khaykin, E.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A.Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; C.A.; Li, J.H.; Li, Y.; Liu, Y.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; J. Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vener, J.C.; Davis, R.W.

ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Vener, J.C.; Davis, R.W.
                                                                                                     A; Map position: 1
C; Superfamily: Ar
                                                                                                                                                                                           A;Cross-references: GB:AE005173; NID:g6751686; PIDN:AAF27669.1; GSPDB:GN00141
                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-389 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Hulzar, L.
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A:Accession: C81428
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Campylobacter jejuni
C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 31-Mar-2000
C;Accession: C81428
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: GB:AL139074; GB:AL111168; NID:g6967505; PIDN:CAB72599.1; PID:g69676(
A;Experimental source: serotype O2, strain NCTC 11168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-189 < PAR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Parkhill, J.; Wren, B.W.; Mungall, K.; Ketley, J.M.; Churcher, C.; Basham, D. C.W.; Quail, M.; Rajandream, M.A.; Rutherford, K.M.; VanVliet, A.; Whitehead, Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   hypothetical protein T7P1.10 [imported] - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Status: preliminary
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                                                                                                  ;Superfamily: Arabidopsis thaliana zinc transporter
                                                                                                                                                                          Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 23-Mar-200;
;Accession: B96635
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;Species: Arabidopsis thaliana (mouse-ear cress
Query Match
Best Local Similarity
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                                                                                                                                                      Gene:
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Best Local
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                                                                                                                                                      T7P1.10
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81.8%;
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81.8%;
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    Score
Pred.
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Pred. No. 0.026;
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Pred. No. 0.0029;
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  No.
    DB 2;
0.052;
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                        Length 389
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A; Experimental source: strain A3(2) C; Genetics:
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                                                                                                                                                                                                                                                                                                                                            C;Accession: T36920
R;Seeger, K.; Harris
                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein SCI7.24c - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Ve Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: D84907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:AC005310; NID:g3510247; PID:g3510254
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fuji
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; T
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  R;Rounsley, S.D.; Lin, X.; Kaul, S.; Shea, T.P.; Fujii, C.Y.; Mason, T.M.; Shen, submitted to the EMBL Data Library, September 1998
A;Description: Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence. A;Reference number: 214698
A;Accession: T02681
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                                                                                                                   A;Gene:
                                                                                                                                                                                   A;Cross-references: EMBL:AL096743; PIDN:CAB46407.1; GSPDB:GN00070;
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                                                                                                                                                                                                                               A; Molecule type: DNA
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A; Residues: 1-398 <STO>
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A; Residues: 1-398 < ROU>
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                       Query Match
Best Local
  Matches
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Similarity 9; Conserv
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9; Conser
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  Conservative
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Data Library, July
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                     78.5%;
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81.8%;
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Score 62; DB 2;
Pred. No. 0.064;
0; Mismatches
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Pred. No.
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1999
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                                          Length 490;
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E.; Umayam, L.; Tallon,
                                                                                                                                                                                                                                                                                                                                         B.G.; Rajandream,
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0;
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1 GHKHKHGHGHG

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zinc transport protein ZnT-1 - rat
N;Alternate names: zinc transporter ZnT-1
C;Species: Rattus norvegicus (Norway rat)
C;Date: 15-Uul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
C;Accession: S54303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBO J. 14, 639-649, 1995
A;Title: Cloning and functional characterization
A;Title: S54302; MUID:95188868
                                                                                                                                             chorion protein s36 - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 01-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 21-Jul-2000
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S07193
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EMBO J. 14, 639-649, 1995
A;Title: Cloning and functional characterization
A;Reference number: S54302; MUID:95188868
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
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 A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1-286 <SPR>
                                                  A; Reference number: A; Accession: S07193
                                                                 A; Title: Amplification of the X-linked Drosophila A; Reference number: S07193; MUID:87246506
                                                                                                R; Spradling,
EMBO J. 6, 1
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A; Residues: 1-507 < PAL>
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A;Molecule type: DNA
A;Residues: 1-503 <PAL>
A;Cross-references: EMBI
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A; Accession: S54302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Accession:
                                                                                                                                 C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:U17133; NID:g577842; PIDN:AAAA79234.1; PID:g577843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary
                                                A; Accession:
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
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Best Local
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                                                                                                                                                                                                                                                                     145
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                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                g, A.C.; de Cicco, D.V.; Wakimoto,
1045-1053, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            203/1
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9; Conserv
                                                                                                                                   S07193
                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL:U17132; NID:g577840; PIDN:AAA79233.1; PID:g577841
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                59
                                                                                                                                                                                                                                                                                                                                                    78.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          78.5%;
81.8%;
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                                                                                                                                                                                                                                                                                                                                                    Score 62; DB 2;
Pred. No. 0.066;
                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                  в.т.;
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                                                                                 chorion
                                                                                                                Levine, J.F.; Kalfayan, L.J.;
                                                                                                                                                                                                                                                                                                                                     2;
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                                                                                                                                                                                                                                                                                                                                                                  Length 507
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                 gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       zinc transporter that
                                                                                                                                                                                                                                                                                                                                     0;
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                                                                                 requires a
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                                                                                                                Cooley
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B32473
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Query Match
Best Local S
Matches 9
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C; Genetics:
A; Gene: 50
C; Superfamily: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Note: 18-Gly and 18-His were also C; Superfamily: period clock protein; C; Keywords: egg yolk F; 1, 5/Modified ~ 1.
                                                                                                                                                                                                                                                                   A; Note: host
C; Date: 17-Au
C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Gene: FlyBase:Cp36
A;Cross-references:
A;Introns: 16/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R; Waite, J.H.: Rice-Ficht, A.C. Biochemistry 28, 6104-6110, 1989 A; Title: A histidine-rich protein from the A; Reference number: A32473; MUID:89375343 A; Accession: B32473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X05245; NID:g7725; C;Genetics:
                                                                 A; Reference number: A39447; A; Contents: annotation
                                                                                                                                                                                        A; Description: Channel cat
A; Reference number: A36804
A; Accession: F36791
                                                                                                                                                                                                                       submitted to GenBank, January 1 A; Description: Channel catfish
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: protein A; Residues: 1-18 <WAI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     histidine-rich protein C, peptide P-5 - liver fluke (fragment) C;Species: Fasciola hepatica (liver fluke) C;Date: 25-Sep-1989 #sequence_revision 03-May-1994 #text_chang C;Accession: B32473
                                                    A; Note:
                                                                                               Virology 186, 9-14, 1992
A; Title: Channel catfish virus:
                                                                                                                            R; Davison, A.J
                                                                                                                                             A;Cross-references: GB:M75136; NID:g331209; PIDN:AAAB8153.1;
                                                                                                                                                            A; Molecule type: DNA
A; Residues: 1-670 < DAV>
                                                                                                                                                                                                                                                        R; Davison, A.J.
                                                                                                                                                                                                                                                                                                                                 hypothetical protein ORF50 - ictalurid herpesvirus 1
                                                                                                                                                                                                                                                                                                                  Species: ictalurid herpesvirus
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              sywords: egg yolk
5/Modified site: 3',4'-dihydroxyphenylalanine (Tyr) #status
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                                                                                                                                                                                                                                                                     17-Aug-1992
sion: F36791
                                                                                                                                                                                                                                                                                  host Ictalurus punctatus (channel catfish) 17-Aug-1992 #sequence_revision 17-Aug-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 СНКНКНСНСНСК 12
                                                      neither
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9; Conser
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9; Conser
                                                                                                                  9-14, 1992
       period
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       clock protein;
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                                                                                  rus: a new type
MUID:92087490
                                                    nucleic acid sequence
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Pred. No. 0.
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         EGF
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                                                                                                                                                                                                                        new
       homology
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                                                                                                 of herpesvirus
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                                                                                                                                                                                                                        type
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0.0054;
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                                                                                                                                               PID:g331260
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hep

Similarity 9; Conserv

75.9%; nilarity 81.8%; Conservative

0;

Score 60; DB 2; Pred. No. 0.17; 0; Mismatches

2;

Indels

0;

Gaps

0;

Length 670;

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A;Gene: fsh
A;Gene: fsh
A;Cross-references: FlyBase:FBgn0004656
A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status predicted
F;1-205/Product: female sterile homeotic protein, 110K #status predicted
F;59-116/Domain: bromodomain homology <BRO1>
F;59-116/Domain: bromodomain homology <BRO1>
                                                                                                                   A;Gene: pipsqueak
C;Superfamily: PO;
F;21-123/Domain: N
                                                                                                                                                                                                                                                                        C;Accession: S66148
R;Weber, U.; Siegel, V.; Mlodzik, M.
EMBO J. 14, 6247-6257, 1995
A;Title: pipsqueak encodes a novel nuclear protein required downstream of seven-up for A;Reference number: S66148; MUID:96134923
A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                 gene pipsqueak protein A short form - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Sep-1999
C;Accession: A43742; B43742
R;Haynes, S.R.; Mcozer, B.A.; Bhatia-Dey, N.; Dawid, I.B.
Dev. Biol. 134, 246-257, 1989
A;Title: The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent mem A;Reference number: A43742; MUID:89276730
A;Accession: A43742
                                                                                                                                                                                           A;Molecule type: DNA
A;Residues: 1-535 <WBB>
A;Cross-references: EMBL:X90986; NID:g1149498; PIDN:CAA62473.1; PID:g1149499
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A; Residues: 1-1106 <HA2>
A; Cross-references: EMBL:M23222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-2038 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              female sterile homeotic protein, 205K - fruit fly N;Alternate names: membrane protein fsh, 205K N;Contains: female sterile homeotic protein, 110K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Accession: B43742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:M23221; NID:g157452; PIDN:AAA28540.1; PID:g157453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary
                        Query Match
Best Local Similarity
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Best Local (
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  8;
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9; Conservative
                                                                                                              POZ domain homology
n: POZ domain homology
  Conservative
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81.8%;
                     74.7%;
80.0%;
  1;
                        Score 59; DB 2
Pred. No. 0.19;
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Pred. No. 0.49
0; Mismatches
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  Mismatches
                                                                                                                   <P02>
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Gaps
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6,

2001, 09:17:59

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A; Molecule type: DNA
A; Residues: 'MQ', 428-1085 <WE2>
A; Cross-references: EMBL: X90986; NID:g1149498; PIDN:CAA62475.1; PID:g1149501
R; Horowitz, H; Berg, C.A.
Development 122, 1859-1871, 1996
A; Title: The Drosophila pipsqueak gene encodes a nuclear BTB-domain-containing protei
A; Accession: T45461
밁
                                                                                                                                                                                                              A;Description: required for establishing polarity of the developing egg chamber C;Superfamily: POZ domain homology F;21-123/Domain: POZ domain homology <POZ>
                                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-355,'E',357-1005,'H',1007-1020,'Q',1021-1061,'ERS' <HOR>
A;Cross-references: EMBL:U48358; NID:g1203906; PIDN:AAC47153.1; PID:g1203907
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A; Introns: 427/3
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A;Map position: II
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A; Residues: 1-1085 <WEB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 01-Dec-2000 C;Accession: S66149; S66150; T45461 C;Accession: U; Siegel, V; Mlodzik, M. EMBO J. 14, 6247-6257, 1995
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"Disulfide bonds in bovine HMW kininogens.";

Seikagaku

56:808-808(1984)

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ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN H
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
FIN: BRADYKININ IS RELEASED FROM KININOGEN BY
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
PERMEDABILITY, (4E2) STIMULATION OF NCCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM DERIVED RELAXING FACTOR ACTION); (5)
LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
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                                       Kitamura N., Takagaki Y., Furuto S., Tanaka T., Nawa H., "A single gene for bovine high molecular weight and low meight kininogens.";
                                                              SEQUENCE FROM N.A. MEDLINE=84014106; PubMed=6571699;
                                                                                             Eukaryota; Metazoa;
Mammalia; Eutheria;
Bovidae; Bovinae; Bo
 Sueyoshi T., Miyata T., Hashimoto N., Kato H.,
        SEQUENCE OF 19-376
MEDLINE=87137530; I
                                Nature 305:545-549(1983).
                                                                                     NCBI_TaxID=9913;
                                                                                                                      Bos taurus (Bovine).
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EMBL; V01492; CAA24736.1;
EMBL; V01492; CAA24737.1; /
PIR; A01282; KGBOH2.
PIR; B29559; B29559.
HSSP; P04129; 1AFI.
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HAW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMM-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGRECATION OF THROMBOLYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIORESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLICOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4EI) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDIS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal; Inflammatory response.
                                                            InterPro; IPR000010; -.
InterPro; IPR002395; -.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
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J. Biochem. 77:55-68(1975).
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MEDLINE=75170265; Po
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Han Y.N., Kato H., Twanaga S., Suzuki T.;
Primary structure of bovine plasma high-molecular-weight kininogen.
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus of the bradykinin moiety.";
J. Blochem. 79:1201-1222(1976).
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"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
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"Bovine high molecular weight kininogen. The amino acid sequence,
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                                                                                                                                                                                                                                                                                                                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ALTERNATIVE PRODUCTS: HMW II AND LMW II KININOGEN PRECURSORS PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LINE=75170265; PubMed=1169237;
Y.N., Komiya M., Iwanaga S., Suzuki T.;
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SEQUENCE OF 378-393.
MEDLINE-70180420; PubMed-4986212;
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Miyata T., Iwanaga S.;
                                                                                                                                                                                                               SEQUENCE OF 19-378.
MEDLINE=87137530; F
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
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                                                                     J. Biol.
                                                                                              chain
                                                                                                                     positions of carbohydrate
                                                                                                                                           Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The amino acid sequence,
                                                                                                                                                                                                                                                                                       Nature 305:545-549(1983).
                                                                                                                                                                                                                                                                                                                weight kininogens."
                                                                                                                                                                                                                                                                                                                                                           Kitamura N., Takagaki Y.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bovidae;
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PRECURSOR (THIOL PROTEINASE INHIBITOR) [CONTAINS:
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CYSTATIN-LIKE 3.
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ılar weight
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                                                                                                                                                                                                                                                                                                         Pfam; PF00031; cystatin; 3.
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PIR; A29559; A29559.
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                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kininogen. Amino acid sequence of a fragme peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
-!- FUNCTION: (1) KININOGENS ARE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bonds
                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        between
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kininogen. Amino acid sequence of a fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 458-498
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        European Bioinformatics Institute.
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ALTERNATIVE PRODUCTS: HAW I AND LAW I KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JE SPECIFICITY: PLASMA.

BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
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N-LINKED (GLCNAC. . .).
INTERCHAIN.
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CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
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LIGHT CHAIN.
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            EMBL; D84435; BAA EMBL; D84415; BAA MGD; MGI:1097705;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (APR-1996) to the EMBL/GenBank/DDBJ-!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF
                                                                                        entities
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=C57BL/6 x CBA; TISSUE=Liver;
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Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mus musculus (Mouse)
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"Molecular cloning of cDNAs for mouse low-
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SUBGELLULAR LOCATION: SECRETED.
SUBGELLULAR LOCATION: SCRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HAW (SHOWN HERE) AND LAW; ARE PRODUCED BY ALTERNATUS ESPLICING.
                                                                                                                                 ween the Swiss Institute of Bioinf
European Bioinformatics Institute.
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                                                                                     and this statement is not removed. requires a license agreement (See
                                                                       equires a license agreement (See email to license@isb-sib.ch).
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247
266
339
369
                                                                                                                    institutions as long as its content
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91.7%;
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CHAIN
SEQUENCE OF 45-82 FROM STRAIN-NEW ZEALAND WHIT MEDLINE-94198229; PubMe
                                                                       Underwood J.R., Robinson H.C.;
"Rabbit polymorphonuclear neutrophils form
calgranulin C when incubated with inorganic
J. Biol. Chem. 271:19802-19809(1996).
                                                                                                                        STRAIN-NEW ZEALAND WHITE; TISSUE-Neutrophils; MEDLINE-96355278; PubMed-8702688; Yang Z., de Veer M.J., Gardiner E.E., Devenis Underwood J.R., Robinson H.C.;
                                                                                                                                                                                                                                                       Oryctolagus cuniculus (Rabbit).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolao
                                                                                                                                                                                                                                                                                                                   S100A9 OR MRP-14.
                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
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Pfam; PF00031;
                                                                                                                                                                                                   SEQUENCE FROM N.A.
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661 AA;
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 PubMed=8148323;
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73102
                   WHITE;
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BY SIMILARITY.
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                                                                                        inorganic [35S]sulfate.";
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                                                                                                                                              Devenish R.J., Handley C.
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Q60738;
30-MAY-2000
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REPEAT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CA_BIND
                                                                                                  Palmiter R.D., Findley S.U.; "Cloning and functional characterization of a mammalian zinc "Cloning and functional characterization of a mammalian zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Dynamic changes in mRNA expression of neutrophils during to facute inflammation in rabbits.";
Int. Immunol. 6:149-156(1994).
-i- SIMILARITY: BELONGS TO THE S-100 FAMILY.
-i- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS
                        transporter that confers resistance to zinc.";
EMBO J. 14:639-649(1995).

-i- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF
LETHALITY OF KNOCKOUT EARLY IN GESTATION SUGGESTS
PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.

-i- SUBGULTI MULTIMER (PROBABLE).

-i- SUBGULTULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
                                                                                                                                                                                                                    Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS00018; EF_HAND; 1.
PROSITE; PS00303; S100_CABP;
Calcium-binding; Repeat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                  TISSUE=Brain;
MEDLINE=95188868;
                                                                                                                                                                                                                                                            SLC30A1 OR ZNT1
                                                                                                                                                                                                                                                                          ZINC TRANSPORTER 1 (ZNT-1).
                                                                                                                                                                                                                                                                                       30-MAY-2000 (Rel. 01-OCT-2000 (Rel.
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                                                                                                                                                                             SEQUENCE FROM N.A.
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LOCALIZED ON THE PLASMA MEMBRANE TISSUE SPECIFICITY: WIDELY EXPRES
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118
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. 39, Last sequence. 40, Last annotations.
                                                                                                                                                    PubMed=7882967;
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81.8%;
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SITE II (HIGH AFFINITY) (POTENTIAL).
2 X 8 AA TANDEM REPEATS OF G-H-G-H-G-H-S-H.
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Pred. No. 0.0057;
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                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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of neutrophils during the course
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Best Local
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SEQUENCE
         McMahon R.J., Cousins R.J.;

"Regulation of the zinc transporter ZnT-1 by dietary zinc.";

Proc. Natl. Acad. Sci. U.S.A. 95:4841-4846(1998).

-!- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE C

-!- SUBUNIT: MULTIMER (PROBABLE).
                                                           TISSUE=Intestine;
MEDLINE=98226729; PubMed=9560190;
                                                                                                         EMBO
                                                                                                                "Cloning and functional characterization of a mammalian zinc transporter that confers resistance to zinc.";
                                                                                                                                                   TISSUE=Kidney;
MEDLINE=95188868;
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                         SLC30A1 OR ZNT1.
                                                                                                                                                                                                                                                  30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence up
01-CCT-2000 (Rel. 40, Last annotation
ZINC TRANSPORTER 1 (ZNT-1).
                                                                                                                                                                                                                                                                                               Q62720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                        Palmiter R.D.,
                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                             NCBI_TaxID=10116;
                                                                                                                                                                                                                              Rattus norvegicus (Rat).
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                                                                                    NDUCTION BY ZINC.
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 SUBCELLULAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Transport;
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                                                                                                        14:639-649(1995).
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9; Conserv
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32
36
57
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                                                                                                                                                                                                                                                                                                         STANDARD;
LOCATION:
                                                                                                                                                                                                                                                                                                                                                             155
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                                                                                                                                                   PubMed=7882967;
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35
56
78
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113
113
124
303
303
1563
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                                                                                                                                                                                                                                                                                                                                                                                                                78.5%;
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INTEGRAL MEMBRANE PROTEIN
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6 X 2 AA APPROXIMATE REPEATS OF H-G.
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7C4FF93FC13CDA22 CRC64;
                                                                                                                                                                                                                                                                        update)
                                                                                                                                                                                                                                                                                                         507
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0.024;
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TRANSCRIPTION INITIATION
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CAUP_DROME
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Best Local S
Matches 9
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01-OCT-1996 (Rel. :
01-OCT-1996 (Rel. :
01-OCT-2000 (Rel. :
                                                                                                                                                                                                                     Drosophila |
Eukaryota;
                                                        encode homeoproteins that control Cell 85:95-110(1996).
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DOMAIN
                                                                                                   Gomez-Skarmeta J.-L., del Cor
Ferres-Marco D., Modolell J.;
                                                                                                                                                                                                                                                   CAUP.
                                                                                                                                                                                                                                                                                                                                         CAUP_DROME
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                                                                                                                                MEDLINE=96180722;
                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                          Ephydroidea;
                                                                                                                                                                                                       Pterygota; Neoptera;
                                                                                                                                                                                                                                                                  HOMEOBOX PROTEIN CAUPOLICAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                      "Araucan and caupolican, two members
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE BASOLATERAL SURFACE OF THE ENTEROCYTES.
TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN IS DETECTED DUODENUM AND JEJUNUM BUT NOT IN ILEUM AND COLON.
INDUCTION: SLIGHTLY BY ZINC IN THE INTESTINE, BUT NOT THE LIVE SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.
FUNCTION: CONTROLS PRONEURAL AND VEIN FORMING GENES. POST:
TRANSCRIPTIONAL CONTROLER OF AC-SC (ACHAETE-SCUTE). MAX AX
ACTIVATOR THAT INTERACTS WITH THE TRANSCRIPTIONAL COMPLEX
ASSEMBLED ON THE AC AND SC PROMOTERS AND PARTICIPATES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IPR002524;
                                                                                                                                                                                                                     melanogaster (Fruit fly).
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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                                                                                                                                                                                          Drosophilidae;
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34, Last sequence update)
40, Last annotation update)
                                                                                                                                PubMed=8620542;
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Pred. No. 0.02
0; Mismatches
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                                                                                                                 de la Calle-Mustienes E.,
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0.024;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 507;
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                                                                                                                                                                                                       Muscomorpha;
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Best Local
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DNA_BIND 226 28
DOMAIN 300 303
DOMAIN 405 418
DOMAIN 501 516
DOMAIN 517 528
DOMAIN 565 572
DOMAIN 613 624
                                                                                                                                                                                                                                                                                  CH36_DROME
P07182;
01-APR-1988
01-APR-1988
01-NOV-1990
                                                                                                                                                                                                                                                                       01-APR-1988 (Rel. 07,
01-APR-1988 (Rel. 07,
01-NOV-1990 (Rel. 16,
CHORION PROTEIN S36.
                                                                                                                                                                                                                                                                                                                                       DROME
          PIR;
                                                                                                                                          Spradling A.C., de Cicco D.V., Wakimoto B.T., Levine J.F., Kalfayan L.J., Cooley L.;
"Amplification of the X-linked Drosophila chorion gene cluster
                                                                                                                                                               MEDITINE=87246506; PubMed=3036489; Spradling A.C., de Cicco D.V., Wakimoto B.T.,
                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                               CP36 OR S36.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the
                   EMBL; X05245; CAA28870.1;
                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                  the
                                                                                            between
                                                                                                       This
                                                                                                                                                                                                                     Pterygota; Neoptera; Endopterygota; Diptera; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Transcription regulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00046; homeobox; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase; FBgn0015919;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                                                                                                                                                                                        SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                649
                                                s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way lifted and this statement is not removed. Usage by and for commercial ities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                   1 GHKHKHGHGHG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
SIMILARITY: BELONGS TO THE TALE/IRO FAMILY OF HOMEOBOX PROTEINS.
          S07193;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                GHGHSHGHGHG
                                                                                                                          s a region upstream from the s38 chorion gene."; 6:1045-1053(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
9; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  requires allocatement is not removed. Usage by and for com requires a license are accompanies.
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81.8%;
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Pred. No. 0.032;
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Q00130;
01-DEC-1992
01-DEC-1992
01-OCT-1996
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                                                                                                                                                                                                                                                                                                   Hypothetical
REPEAT
                                                                                                                                                                                                                                                                                                                           EMBL; M75136; AAA88153.1; -. PIR; F36791; F36791.
                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute. Thuse by non-profit institutions as long
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL GENE
  SEQUENCE
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         А.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            catfish virus: a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Rel.
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34, Last annotation updat
50 PROTEIN.
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75.0%;
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  MW.
           Score 61; DB 1;
Pred. No. 0.019;
                                                                                                                                                                                                               987654321
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2B64A781C519E8B4 CRC64;
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EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; --
EMBL; M15763; AAA70423.1; --
EMBL; M15764; AAA70422.1; --
EMBL; M15764; AAA7042.1; --
EMBL; M15764; AAA704; --
EMBL; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FSH_DROME STANDARD; PRT; 2038 AA.
P13709; P13709; P13700;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
O1-OCT-1996 (Rel. 34, Last annotation update)
FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE PROTEIN).
FS(1)H OR FSH.
                                                                                                                                                        TRANSMEM
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                                                                                                                                                                                                                                                                                                                PROSITE;
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                                                                                                                                                                                                                                                                                                                                                              PRINTS; PR00503;
                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00439; bromodomain; 2.
                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P04002; 1WFA.
FlyBase; FBgn0004656; fs(1)h.
InterPro; IPR001487; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -i- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF OTHER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS UBX.
-i- SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN.
-i- SIMILARITY: CONTAINS 2 BROMODOWAINS.
-i- SIMILARITY: CONTAINS 1 ET DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         apparent membrane proteins.";
Dev. Biol. 134:246-257(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.; "The Drosophila fsh locus, a maternal effect homeotic gene, encodes apparent membrane proteins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89276730; PubMed=2567251;
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BROMODOMAIN_2;
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81.8%;
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POTENTIAL.
G -> A.
H -> RKPYY
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RKPYY
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RESULT 13
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KE4L_CAEEL
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
HYPOTHETICAL KE4-LIKE PROTEIN H13N06.5 IN CHROMOSOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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247
297
386
429
463
92
                                                                                                                                                                                                              Conservative
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27 47
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Pred.
                                                                                                                                                                                                                                          Score 58; DB 1;
Pred. No. 0.093;
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KE4_HUMAN ID KE4_H AC Q9250

KE4_HUMAN Q92504; Q9UIQ0;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tubby B.;
Submitted
                                                                                                                                                                                                                                                                                                                       EMBL; D82060; BAA11528.1; -. EMBL; AF117221; AAD12305.1; -. EMBL; AL031228; CAA20238.1; -. MIM; 601416; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=97001166; PubMed=8812499;
Ando A., Kikuti Y.Y., Shigenari A., Kawata H., Okamoto Chen L., Ikemura T., Abe K., Kimura M., Inoko H.;
"CDNA cloning of the human homologues of the mouse Ke4 at the centromeric end of the human MHC region.";
                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        flanking region.";
Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Vergara A., Lana I., Corella A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Kidney;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HISTIDINE-RICH MEMBRANE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
01-OCT-2000 (Rel. 40,
                                                                                                                                                                                                     CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Molecular cloning and characterization of the human KE4 gene
 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the centromeric end of nomics 35:600-602(1996).
                      ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          nitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE) TISSUE SPECIFICITY: MAJOR EXPRESSION IN PLACENTA, LUNG, KI AND PANCREAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
           GHKHKHGHGH 10
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80.0%;
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Last sequence update)
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A -> G (IN REF. 1 AND 2).
E -> G (IN REF. 1 AND 2).
S -> T (IN REF. 1 AND 2).
CALLTEGGAVGSEIAGGAGPGWVLPFTAGGFIYVATVSVLPELLREASPLQSLLEVLGLLGGVIMMVLIAHLE -> VPFSL
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POTENTIAL.
                                                        Score 57; DB 1 Pred. No. 0.12;
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6504A1EF5AA6A5B9 CRC64;
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                                             Mismatches
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                                                                   Length 469;
                                             Indels
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RESULT 15
KE4_BRARE
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AC C9PUB8
DT 01-OCT
DT 01-OCT
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GN HKE4.
OS Brachy
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Q29175; Q9XT01;
01-OCT-2000 (Rel. 4
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                                                                 KE4_BRARE
Q9PUB8;
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                                           01-0CT-2000 (Rel. 40, Created)
01-0CT-2000 (Rel. 40, Last sequence update)
01-0CT-2000 (Rel. 40, Last amoutation update)
HISTIDINE-RICH MEMBRANE PROTEIN KE4 HOMOLOG (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
-!- SIMILARITY: BELONGS TO THE KE4/CATSUP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Physical organization of the swine major histocompatibility complex class II region.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Evaluation and characterization of a porcine small intestine library: analysis of 839 clones.";
Mamm. Genome 7:509-517(1996).
Brachydanio rerio (2ebrafish) (2ebra danio)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; F14787; CAA23256.1; -. EMBL; AF146397; AAD44801.1; -.
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Chardon P., Rogel-Gaillard C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 125-155 FROM N.A.
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NCBI_TaxID=9823;
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NCBI_TaxID=7955;
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OM protein - protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Maximum Match 100%
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Sp_archea:*

sp_bacteria:

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sp_fungi:*

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## ALIGNMENTS

ID 027920 ID 027920 ID 027920 PRELIMINARY; PRT; 450 AA. AC 027920; DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 08, Last annotation update) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) DT 01-NOV-1996 (TrEMBLrel. 05, Created) DT 01-NOV-1996 (TrEMBLrel. 05, Created)																•							
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TISSUE-ROOT NOBULES;
Dobritsa S.V., Mullin B.C.;
"In vitro expression of actinorhizal nodulin AgNOD-GHRP demonstration of its toxicity of Escherichia coli.";
(In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);
the Biology of Plant-Microbe Interactions:
Proceedings of the 8th International Symposium on Molecinic Advances of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the State of the S
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SEQUENCE
TISSUB-ROOT NODULES;
Pawlowski K., Twigg P.G., Dobritsa S.V., Guan C., Mullin B.C
"A nodule-specific gene family from Alnus glutinosa encodes
and histidine-rich proteins expressed in the early stages of
actinorhizal nodule development.";
Submitted (EEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U69156; AAD00171.1; -.
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Thesis (1993), The
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                                                                                                                                                                                                                                                                     "Isolation of a nodule-specific cDNA encoding a protein from Alnus glutinosa."; Thesis (1993), The University of Tennessee, Knox
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gene family from Alnus glutinosa encodes glycine-
proteins expressed in the early stages of
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SEQUENCE
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PUTATIVE ZINC TRANSPORTE
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                                                                                                  Brassicales; Brassicaceae; NCBI_TaxID=3702;
                                                                                                                                          Eukaryota; Viridiplantae; Embr
Magnoliophyta; eudicotyledons;
                                                                                                                                                                                     Arabidopsis thaliana
                                                                                                                                                                                                            F19D11.8
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"The genome sequence of the food-borne reveals hypervariable sequences.";
Nature 403:665-668(2000)
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PRINTS; PRO0334; KININOGEN.
99 AA; 10567 MW;
                     Rounsley
                                                             SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PS50059; FKBP_PPIASE_3; 2.
189 AA; 20132 MW; 47B5F5D047549D7F CRC64;
                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                             TRANSPORTER.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   78.5%;
81.8%;
                                                                                                                                          (Mouse-ear cress).
ntae; Embryophyta; Tracheophyta; S
otyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
  Kaul S., Shea
Fraser C.M., S
                                                                                                                                                                                                                                             08,
13,
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16,
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Last
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Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 62;
Pred. No.
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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annotation updat
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No.
  a T.P., Fujii C.Y., Mason T.M.
Somerville C.R., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                  398
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e: eurosids II;
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RESULT
Q9GRW9
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REMBL, ALD96743; CAB46407.1; -.

W Hypothetical protein.

SEQUENCE 490 AA; 52666 MT.
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Q9X9W6
ID Q
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Best Local S
Matches 9
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Best Local S
Matches 9
         ZINC/IRON
                          01-MAR-2001
01-MAR-2001
                                                                       Q9GRW9;
01-MAR-2001
                                                                                                                     Q9GRW9
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Bacteria; Firmicutes; Actinobacteria;
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01-NOV-1999 (TrEMBLrel. 12, La
01-NOV-1999 (TrEMBLrel. 12, La
NYPOTHETICAL 52.7 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9X9W6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Arabidopsis thaliana chromosome II BAC F19D11 genomic sequence."; Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AC005310; AAC33498.1; -. InterPro; IPR002524; -. Pfam; PF01545; Cation_efflux; 1. SEQUENCE 398 AA; 43827 MW; 7E20E0B29237BB23 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=A3(2);
Bentley S.D., Parkhill J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "A set of ordered cosmids and a detailed genetic and physical map the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=A3(2);
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                                                                                                                                                                                                                                   GHDHHHGHGHG
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9; Conserv
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01 (TREMBLrel. 16, Created)
01 (TREMBLrel. 16, Last sequence update)
01 (TREMBLREl. 16, Last annotation update)
REGULATED TRANSPORTER-RELATED PROTEIN 3, DZIP3 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (JUL-1999)
                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                     PRELIMINARY;
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81.8%;
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86
87
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                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                          Score 62; DB
Pred. No. 0.05
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Created)
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Pred. No.
                                                                                                                     PRT;
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                                                                                                                     494
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0.044;
                                                                                                                                                                                                                                                                                                                                                  DB 2;
0.054;
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                                                                                                                                                                                                                                                                                                                                                                     Length 490;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 398,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         physical map for
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RESULT
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Ffannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bernana B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Chandra I.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C. Davasport L.B., Davies P.,
RA Cherry J.M., Cawley S., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
Dodson K., Doup L.E., Downes M., Dugan Rocha S., Dunkov B.C., Dunn P.,
RA Borlos G. Schart W. Glassor K.
           RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,

AG Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

AG Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

AG Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

AG Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

AG Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.

AG Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

AG Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

AG Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

AG Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

AG Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Liang Y., Lin X.,

AG Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

AG Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

AG Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

AG Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

AG Mount S.M., Nolson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

AG Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

AG Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

AG Reinert K., Remington K., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Remington K., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler F., Shen H.,

AG Nolon R., Sannders R.D.C., Scheeler R.D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ
EMBL; AJ401615; CAC14874.1; -
SEQUENCE 494 AA; 54201 MW; 2FB595C6E3BE88E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-BERKELEY,
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01-MAY-2000
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NCBI_TaxID=7227;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=20196006;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Identification of three zinc-iron regulated transporter-like
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81.8%;
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Pred. No. 0.05
0; Mismatches
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a; Brachycera; Musc
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                                               Reese M.G.,
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                                                                                                  D.L.,
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RESULT
Q9W4C1
   RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adamstides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Baster E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Beesson K.Y., Bernan B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Hoyland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit Z.S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravit Z.S., Kulp D., Lai X.,
RA Melkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Nelson K.A., Nuxon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Remington K., Samonders R.D.C., Scheeler F., Shen H.,
RA Syler E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Weinstock G.M., Weinstock G.M., Weissenbach J.,
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Williams
Ye J., Ye
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Gibbs
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Svirskas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ephydroidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pier E., Spradling A.C., Stapleton M., Strong R., Sun E., virskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., lang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., villams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Lee J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., 3ibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

Science 287:2185-2195(2000).

EMBL, AE003712; AAF5295.1; -.

FlyBase; FBgn0038412; CG6898.

SEQUENCE 495 AA; 54292 MW; A41DBEE85446FFCB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006;
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Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Drosophilidae; Drosophila.
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81.8%;
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Last sequence update)
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Weinstock
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P.,
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RA Ballew R.M., Basu A., Baxendale J., Bayraktarglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Berson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davepport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davepport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davepport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davepport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Daveport R., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dodson K.J., Bvangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.Y., Mobarry C., Morris J., Moshrefi A.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Wand Z.-Y., Wassarman D. A., Weinstrock G. M., Weissenbach J.
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Best Local :
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Q9VU00;
01-MAY-2000
01-MAY-2000
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Ye J., Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Zheng X.H., Zhong F.N., Zhong W., Zhu X., Zhu S., Zhu Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

EMBL; AE003434; AAF46035.1; -. ElyBase; FBgn0029766; CG15784.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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PRINTS; PRO0334; KININOGEN.
PS54 AA; 62329 MW;
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               Z.-Y., Wassarman D.A.,
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9; Conser
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Woodage
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75.0%;
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                   Weinstock G.M., Weissenbach
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Last annotation updat
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 ₩u D.,
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G., Zhao (
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X., Smith
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OggTNO
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Ol-Mar-2001 (TremBLrel. 16, Created)
Ol-Mar-2001 (TremBLrel. 16, Last sequence update)
Ol-Mar-2001 (TremBLrel. 16, Last annotation update)
Ol-Mar-2001 (TremBLrel. 16, Last annotation update)
D1-Mar-2001 (TremBLrel. 16, Last annotation update)
D2-201-201 (TremBLrel. 16, Last annotation update)
D3-201-201 (TremBLrel. 16, Last annotation update)
D3-201-201 (TremBLrel. 16, Last sequence update)
D3-201-201 (TremBLrel. 16, Last sequence update)
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Q9M435;
Q1-QCT-2000
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Quercus robur (English oak).

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Identification of a phase-change related mRNA in oak shoot cultures derived from basal sprouts and crown branches.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gil B.,
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01-OCT-2000 (TYEMBLEE). 15, Last sequence update)
01-OCT-2000 (TYEMBLEE). 15, Last annotation update)
PHASE-CHANGE RELATED PROTEIN PRECURSOR.
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pfam; PF00046; homeobox; 1.
pROSITE; PF00027; HOMEOBOX_1;
pROSITE; PS50071; HOMEOBOX_2;
SMART; SM00389; HOX; 1.
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-:- SIMILARITY: TO OTHER HOMEOBOX DOMAINS.
EMBL; AE003540; AAF49895.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GHKHKHGHGHG 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GHGHSHGHGHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yeh R.-F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pastoriza E.M.,
                                                                                                                       Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ÃĄ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8414 MW;
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81.8%;
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballester
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Pred. No. 0.013;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8E45CABF40F00B6F CRC64;
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FBEB1616493F7EC9 CRC64;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E. Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Calle R.F., Yandell M.D., Zhang Q., Chen L.X.,
RA Burtton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Baril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayaktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadleu E., Center A., Chandra I.,
RA Ghory J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Gerry J.M., Cawley S., Dahlke C., Dew I., Dietz S.M.,
RA Gerry J.M., Cawley S., Dahlke C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Morherson D.L.,
RA Merkulov G., Milshina N.V., Wobarry C., Morris J., Mosheri A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Shue B.C., Kohlen T., Worley R., Sun B.,
RA Willians S.M., Wodaer C., 
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Best Local
      Wang Z.-Y
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "The evolutionary analysis of 'orphans' from the Drosophila genome identifies incorrectly annotated and rapidly evolving genes."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF264920; AAG10259.1; -. NON_TER 213 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-BERKELEY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ephydroidea; Drosophilidae; Drosophila
NCBI_TaxID-7245;
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9; Conserv
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13,
16,
Weinstock G.M., Wei
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
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Pred. No.
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RESULT 15
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ID Q9GTN1
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AC Q9GTN1
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Q1-MAR-2001 (TrEMBLrel. 16, Created)
Q1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
Q1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
DS06238.4-LIKE PROTEIN (FRAGMENT).
Drosophila simulans (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda.
Pterygota; Neoptera; Endopterygota; Diptera; Brachy.
Ephydroidaa; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001 (Trembirel. 16, Last annotation update)
E0:84H4.4 PROTEIN.
E0:84H4.4 PROTEIN.
EG.884H4.4 OR CG3081.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Everyota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
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EMBL, AE003431; AAR45965.1: -
FlyBase; FBG10025613; EG:84H4.4.
SEQUENCE 457 AA; 48919 MW; 70B4B7ADDD0ZE0AD CRC64;
STRAIN-NORTH CAROLINA 17;
Schmid K.J., Aquadro C.F.;
                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.

Ferraz C., Vidal S., Brun C., Bucheton A., Demaille J.G.;

Feguencing the distal X chromosome of Drosophila melanogaster.";

"Seguencing the distal X chromosome of Drosophila melanogaster.";
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## ALIGNMENTS

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A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                      WPI; 2000-376483/32.
                                                                                                                                                                                                                                                         Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
anglogenesis inhibition; tumour; cancer; ocular disorder;
                                                                                     (UTEM ) UNIV TEMPLE. (MCCR/) MCCRAE R K.
                                                                                                                         10-NOV-1998;
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                                                                                                                                                                                                                       Homo sapiens.
                                                                                                                                                                                                                                               rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                         Human high molecular weight kininogen domain 5 fragment #4
                                                                                                                                                                                                                                                                                                                                16-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                         AAY81995;
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Best Local Similarity
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The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 kD
                                                                    Claim 15; Page 29; 52pp; English.
                                                                                                                       endothelial cell proliferation, and
                                                                                                                                      A pharmaceutical composition used to inhibit angiogenesis, inhibit
                                                                                                                                                                            WPI; 2000-376483/32
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                                                                                                                                                                                                                                                                                                     98US-0107833
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 74; L
Pred. No. 1.
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                                                                                                                     induce endothelial cell apoptosis
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                                                 The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting anglogenesis. Anglogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain occular disorders. It can also occur in a chamber of disease trates occurs in a number of disease states.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting anglogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit anglogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell proliferation or by inducing endothelial cell proliferation or by inducing endothelial cell proliferation may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis methods.
rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelia
                                                                                                                                                                                                                                Claim 13; Page 29; 52pp; English.
                                                                                                                                                                                                                                                                                        A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376483/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          angiogenesis inhibition; tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; high molecular weight kininogen; HK; two-chain high molecular weight kininogen; HKa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human high molecular weight kininogen domain 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY81997 standard; peptide; 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200027866-A1
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(MCCR/) MCCRAE R K.
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Pred. No. 1.7
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RESULT
AAY93351
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Best Local S
Matches 12
                                                                                       high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim
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Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain
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Pred. No. 3.1e-05;
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Query Match

100.0%;

Score

74; DВ 21;

Length

94;

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45

1 GKKNGKHNGWKT

12 56

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RESULT
AAY93353
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                   Query Match
Best Local
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    Matches
                                                                                                   high molecular weight Kiningen. High molecular weight kiningen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kiningen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kiningen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                           Sequence
                                                                                                                                                                                                                                                                                             Claim 11; Page 40-41; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                  Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                            (COLM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    04-SEP-2000
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                                                                                                                                                                                                                                                                  The present sequence represents an analogue of the light chain of human
                                                                                                                                                                                                                                                                                                                          Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-376306/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Light chain of human high molecular weight kininogen analogue
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||||||||||
| 73 gkkngkhngwkt 84
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cn 100.0%;
l Similarity 100.0%;
l2; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          standard; peptide;
                                                                            179
                                                                                                                                                                                                                                                                                                                                                                                                  Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                            AA;
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      0;
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    Score 74; DB 21;
Pred. No. 0.00021;
; Mismatches 0;
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                               Length 179;
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AAY9334
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AC AA
AC AA
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AC AA
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Best Local
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                                                                                                                                                                                                                                                                                                                   endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also k used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                  high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI;
              Light chain of human high molecular weight kininogen
                                         04-SEP-2000
                                                                     AAY93342;
                                                                                             AAY93342 standard; protein;
                                                                                                                 342
                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents an analogue of the light chain of human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Page 38; 41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Colman WR, Mousa AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
endothelial cell proliferation; endothelial cell migration; vitronec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Light chain of human high molecular weight kininogen analogue
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                                                                                                                                                                                            GKKNGKHNGWKT 12
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                                                                                                                                                                                                                      l Similarity
12; Conser
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                                                                                                                                                                                                                                                                                          186
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                                        (first entry)
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                                                                                                                                                                    63
                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell migration
                                                                                                255
                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                     Score 74; DB 21;
Pred. No. 0.00022;
); Mismatches 0;
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                                                                                                                                                                                                                                                Length 186;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vitronectin
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Best Local S
Matches 12
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                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                            Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (UTEM )
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121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COLM/)
                1 GKKNGKHNGWKT 12
gkkngkhngwkt 132
                                                            ch 100.0%;
l Similarity 100.0%;
12; Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DUPONT PHARM CO COLMAN W R.
                                                                                                                                                     255 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mousa AS
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                                                                                                                                                                                                                                                                                                                                                                                                            English.
                                                                   0;
                                                                 Score 74; DB 21;
Pred. No. 0.00031;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cell migration; vitronectin
                                                                                                 Length 255;
                                                                                                                                                                                                                                                                                                                                                                            high molecular
                                                                   0;
                                                                 Gaps
                                                                 0;
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RESULT
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Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                        Light chain of human high, molecular weight kininogen fragment.
                                                                                                                           04-SEP-2000
                                                                                                                                                                                                                        AAY93345 standard; peptide;
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                                                                                                                           (first entry)
                                                                                                                                                                                                                          47
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PD OS S XXX

WO200027415-A2

Synthetic endothelial

proliferation;

endothelial

cell migration;

vitronectin-

Homo sapiens.

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В
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(UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
                                                                               09-NOV-1999;
                                                                                                         18-MAY-2000
                                                                                                                                 WO200027415-A2
                                                                                                                                                                       Synthetic
                                                                                                                                                                                              Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                                                                                                                                                                                                                    Light chain of
                                                                                                                                                                                                                                                                              04-SEP-2000
                                                                                                                                                                                                                                                                                                       AAY93348;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Method for inhibiting endothelial cell proliferation, using compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-376306/32.
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                                                      10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               inhibit migration of endothelial cells to vitronectin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (/SDOM)
                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                          1 GKKNGKHNGWK 11
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                                                                                                                                                                                                                                                                                                                                                                                                gkkngkhngwk 47
                                                                                                                                                           sapiens.
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) DUPONT PHARM CO.
') COLMAN W R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Page 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       47 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                   human high molecular weight kininogen
                                                      98US-0107844
                                                                               99WO-US26377.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                93.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 69; DB 21; 
; Pred. No. 0.00032;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                           A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                  Claim
                                                                                                                                                                                                                                                                                                                                                                  high molecular weight; kininogen; fragment; 1.2; 1; 2; partial;
                                                                                                                                                                                                                                                                                                                                                                                              Partial peptide of human HMW kininogen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                           05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR75186 standard; peptide; 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Page 37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration \cdot
                                         fragment
                                                     AAR75186
                                                                                                                                                                               (FARH ) HOECHST JAPAN
                                                                                                                                                                                                           17-SEP-1993;
                                                                                                                                                                                                                                         17-SEP-1993;
                                                                                                                                                                                                                                                                   28-MAR-1995
                                                                                                                                                                                                                                                                                               JP07082172-A.
                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   wound treating agent; bovine; growth promotion; fibroblast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman WR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (MOUS/) MOUSA A S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    present sequence represents an analogue of the light chain of human
                                                                                                                                                      1995-158909/21.
                                                                                  8
                                                                                 Page

    amino acids

                                                     is a partial
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                  8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ΑA;
          ino acids 458-520. Partial peptides of bovine and in fragments 1.2, 1 and 2, are used in wound treating and act as the active component. The fragments are
                                                                                                                                                                                                           93JP-0230616
                                                                                                                                                                                                                                         93JP-0230616
                                                                              8pp;
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                                                                                                                                                                                  XX
                                                                                  Japanese.
                                                     peptide corresponding
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Pred. No. 0.00043;
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                                                     ç
                                                     human kininogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 62;
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0;

human kininogen : agent compsns. au useful in wound :

treating

because

component. The fragments are have growth promotion activity

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AAY93347
Query Match
Best Local Similarity
"-+ hes 11; Conserve
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                           The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                       Sequence
                                                                                                                                                                                                                                                                    Claim 5; Page 37;
                                                                                                                                                                                                                                                                                           Method for inhibiting endothelial cell proliferation, using compound that inhibit endothelial cell migration {\ \ }
                                                                                                                                                                                                                                                                                                                                   WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                                                                            Colman WR,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; high molecular weight kininogen; glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93347;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-NOV-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         plasma kallikrein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     18-MAY-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              fibroblasts.
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                                                                                                                                                                                                                                                                                                                                                                                      MOUSA A S.
                                                                       83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      63 AA;
       93.2%; Score 69; ilarity 100.0%; Pred. No. Conservative 0; Mismatc
                                                                                                                                                                                                                                                                                                                                                           Mousa AS;
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                                                                       ΑĄ;
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                                                                                                                                                                                                                                                                  41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy
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100.0%; Pred. No. 0.0
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chain;
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          Mismatches
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                      DB 21; I
0.00058;
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0.00044;
hes 0;
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                                 Length 83;
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          Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    endothelial cell;
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RESULT 1
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                                                                                                                                                                                                                                                                     Query Match
Best Local S
Matches 11
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         JP07082172-A
                                 Bos taurus
                                                                                                                05-DEC-1995
                                                                                                                                                            AAR75180 standard; peptide; 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        05-DEC-1995
                                                                   high molecular
                                                                                        Partial peptide of HMW kininogen fragment
                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                       on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-SEP-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; human; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR75181;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (FARH ) HOECHST JAPAN KK
                                                                                                                                                                                                                                                                     y Match 93.2%;
Local Similarity 100.0%;
hes 11; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
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                                                                                                                                                                                                                                              1 GKKNGKHNGWK 11
                                                                                                                                                                                                                       GKKNGKHNGWK 11
                                                     treating
                                                                                                                                                                                                                                                                                                                                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                131 AA;
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                     7; 8pp;
                                                     agent;
                                                                  weight;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     peptide; 131 AA
                                                     ;; kininogen; fragment; 1.2; 1; 2; partial;
bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Japanese.
                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                     Score 69; DB 16;
Pred. No. 0.00093;
0; Mismatches 0;
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ARR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compens. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
  Claim 4; Page 6;
                     A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                      17-SEP-1993;
                                                                                                                                                                 JP07082172-A
                                                                                                                                                                                                 Misc-difference
                                                                                                                                                                                                                      Misc-difference
                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                           Bos taurus
                                                                                                                                                                                                                                                                                                          high molecular weight; kininogen; fragment; 1.2; 1; 2; partial;
                                                                                                                                                                                                                                                                                                                               Partial peptide of HMW kininogen fragment 1
                                                                                                                                                                                                                                                                                                                                                      05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                          AAR75178;
                                                                                                                                                                                                                                                                                                                                                                                               AAR75178 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
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                                                                           (FARH ) HOECHST JAPAN
                                                                                                 17-SEP-1993;
                                                                                                                                                                                                                                                                                                wound treating agent; bovine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    31 gknngkhydwr 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity les 7; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1995-158909/21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 AA;
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                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                 69
8pp; Japanese
                                                                                                                                                                                    /label= Lys or Arg
                                                                                                                                                                                                          'label= Val or Leu
                                                                                                                                                                                                                               'label= Pro,
                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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                                                                                                                                                                                                                                                                                               growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 41;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                    29-APR-1999;
06-MAY-1999;
01-OCT-1999;
01-OCT-1999;
                                    The patent discloses a method for preventing or treating a disorder resulting from the release of bradykinin in a mammal which produces a heparin-binding protein (HBP) that binds to a HBP antagonist. This method involves administration of a mammalian HBP antagonist (especially aprotinin) and/or monoclonal antibodies that bind to prekallikrein-kininogen complexes in the HBP, to decrease the release of bradykinin in the mammal. The antagonists of HBP (e.g. aprotinin) decrease the permeability of the endothelial cells and are used to prevent or treat disorders resulting from the release of bradykinin such as systemic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR75178 is a partial peptide corresponding to bovine kininogen fragment 1.2, amino acids 387-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent componens. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunosuppressive; vasotropic; prevention; treatment; bradykinin;
aprotinin; H-kininogen; HK; systemic inflammatory response syndrome;
pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
                                                                                                                                                                                                                                           Treating systemic inflammatory response syndrome, ischaemia reperfusion, anaphylaxis and allograft rejection by modulating release of bradykinin
                                                                                                                                                                                                                                                                                                                         Flodgaard HJ,
            inflammatory response syndrome, ischaemia and/or allograft rejection. They are also
                                                                                                                                                                                                Example 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200066151-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; heparin binding protein; HBP; antiinflammatory;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human HKH20 peptide derived from domain 5 of H-Kininogen (479-498 aa).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-MAR-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      adult respiratory
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                                                                                                                                                                                                Page 39; 75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                        NORDISK AS
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                                                                                                                                                                                                                                                                                                                                                                                    99DK-0000613.
99DK-0001402.
99US-0157384.
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                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0132748
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    patent No. 5851760
    GENERAL INFORMATION:
    APPLICANT: Evans,
    APPLICANT: Smith, 1
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Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL: 1
ANTI-SENSE: NO
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LENGTH: 376 amino acid
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APPLICATION NUMBER: 60/006,838
FILING DATE: 16-NOV-1995
ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: THOMPSON, Timothy C:
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                     FRAGMENT TYPE
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SOFTWARE: FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 52.7%;
Best Local Similarity 53.3%;
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 619-546-9392 INFORMATION FOR SEQ ID NO:
                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                             NERAL INFORMATION.

APPLICANT: Evans, Glen A.

APPLICANT: Smith, Michael W.

APPLICANT: Smith, METHOD FOR GENERATION OF SEQUENCE

AMORED MAPS OF COMPLEX GENOMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US 08/078,471
FILING DATE: 15-JUN-1993
ATTORNEY/AGENT INFORMATION:
NAME: Relter, Stephen E.
REGISTRATION NUMBER: 31,192
REFERENCE/DOCKET NUMBER: P41 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/117,95
FILING DATE: 07-SEP-1993
                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
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                                                                                                                                                                                      STREET: 444 South CITY: Los Angeles STATE: CA
                                                                                                                                                COUNTRY: UZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 GKKNSPHEGKRIWWK 24
FILING DATE:
                  APPLICATION NUMBER:
                                                                                                                                                                                                                                             ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: UZIP: 90071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 444 South
CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GKKNGKHNG----WK 11
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                                                                                                                                                                                                                                                                                                                                                                                                       788, Application US/08117952
5. 5851760
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                                                                                                                                                                                                                        E: Pretty, Schroeder, Bru
444 South Flower Street,
                                                                                                                                                                      USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein
internal
07-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METHOD FOR GENERATION OF SEQUENCE SAMPLED MAPS OF COMPLEX GENOMES
                                                                                                                                                                                                                          Schroeder, Brueggemann & Clark
Flower Street, Suite 2000
                  US/08/117,952
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 39;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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CLASSIFICATION:

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; TOPOLOGY: unb;
; MOLECULE TYPE:
; FRAGMENT TYPE:
US-08-117-952-788
                                                                  TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-477-451-4
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-UN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MCCLUNG, BATBATA G.
REFERENCE/DOCKET NUMBER: 33,113
REFERENCE/DOCKET NUMBER: 0335.002
Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 4, Application US/08477451 Patent No. 5928865
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-546-4737
TELEFAX: 619-546-9392
TRIEFFAX: 619-546-9392
INFORMATION FOR SEQ ID NO: 788:
                                                                                                                                                                                                      NFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
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                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 3177 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Covacci, Antonello TITLE OF INVENTION: Helicobact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity hes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 4560 Hort CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid
TOPOLOGY: unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10 GKKNSPHEGKLIWWK 24
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REFERENCE/DOCKET NUMBER: P41 9423
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 GKKNGKHNG----WK 11
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52.7%;
60.0%;
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53.3%;
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Score 39; DB 2;
Pred. No. 4.3e+02;
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Pred. No.
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RESULT 7
5514582-43
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Best Local Similarity
6; Conserve
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; TYPE: PRT
; ORGANISM: Gallus sp.
US-09-203-716-2
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US-09-203-716-2
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                                                                                                                                                                                                                                                                                                                                                                       ;Patent No. 5514582
; APPLICANT: CAPON, DANIEL J.;LASKY, LAURENCE A.; TITLE OF INVENTION: RECOMBINANT DNA ENCODING HYBRID; IMMUNOGLOBULINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWALE,
SEQ ID NO 2
                                                                                                                                                               SEQ ID NO:43:
                                                          Matches
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                                                                        Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/067,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Crooke, Stanley T.
APPLICANT: Lima, Walter F.
APPLICANT: Lima, Wolfter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 21-JAN-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                           APPLICATION NUMBER: 986,931
FILING DATE: 08-DEC-1992
APPLICATION NUMBER: 808,122
FILING.DATE: 16-DEC-1991
APPLICATION NUMBER: 440,625
FILING DATE: 22-NOV-1989
APPLICATION NUMBER: 315,015
FILING DATE: 23-FEB-1989
                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 43
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75 NGRHNGYE 82
                                                        Local Similarity
les 5; Conserv
                                                                                                                                                 LENGTH: 126
                          4 NGKHNGWK 11
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                                                        Conservative
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                                                                     50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              51.4%;
60.0%;
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                                                                      Score 37;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 38; DB 3; Pred. No. 53;
                                                       core 37; DB red. No. 32; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                   Length 126;
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RESULT

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-203-716-1
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                                                                                                                                                                                                                                                                                                                                                                 US-09-203-716-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; MOLECULE TYPE: protein US-07-906-983-2
                                                                       SOFTWARE: PatentIn Ver. 2.0 SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                           Sequence 1, Application US/09203716 Patent No. 6001653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 62.9
Matches 5; Conservative
                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: Crooke, Stanley T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent No.
                                                                                                         APPLICANT: Lima, Walter F.
APPLICANT: Wu, Hongjiang
TITLE OF INVENTION: Human RNase H Compositions and Uses Thereof
FILE REFERENCE: ISPH-0333
CURRENT APPLICATION NUMBER: US/09/203,716
CURRENT FILING DATE: 1998-12-02
EARLIER APPLICATION NUMBER: 60/67,458
EARLIER FILING DATE: 1997-12-04
NUMBER OF SEQ ID NOS: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Kotwal, Giris.
APPLICANT: Moss, Bernard
TITLE OF INVENTION: Synthetic, Anti-Complement Protein and
TITLE OF INVENTION: the Gene Encoding Same
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Steuart Tower, Suite 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NFORMATION FOR SEQ ID NO: 2:
                                                     LENGTH: 286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                           156 NGRHNGYE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US
FILING DATE: 19920701
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1: 263 amino acids
AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Application US/07906983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     415-543-5043
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
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                                                         US-07-783-706-2
                                                                         RESULT
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US-08-183-214-12
              Sequence 2, Application US/07783706 Patent No. 5714376 GENERAL INFORMATION:
                                                                                                                                                                                  Best Local Similarity
Matches 6; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 12, Appr
Sequence 12, Appr
No. 571687
                                                                                                                                                                                                                 Query Match
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                    TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 415-543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
PAPPLICATION DATA:
PAPPLICATION NUMBER: US 07/888,231
FILING DATE: 22-MAY-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/183,214
FILING DATE: 14-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: APPLICANT:
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 APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        226 KKNGWKT 232
                                                                                                                         99 KPGKPNGWR 107
                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 31,677
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY; UZIP: 94105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STREET: One Market I
                                                                                                                                           3 KNGKHNGWK 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6 KHNGWKT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                            Weber, Kenneth A
                                                                                                                                                                                                                                                                                                          : 345 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application US/08183214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          E: Townsend and Townsend
One Market Plaza, Steuart Street Tower
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
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Sasisekharan, Ramnath
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Monaco, Lucia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Stanley, Sally J.
Nightingale, Maria S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADP-RIBOSYLARGININE HYDROLASES
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85.7%;
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                                                                                                                                                                                                 Score 37;
Pred. No.
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                                                                                                                                                                                    Pred. No. 90;
; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                  DB 1;
90;
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Query Match
Best Local Similarity
6; Conserve
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US-08-445-342A-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/783,706
FILING DATE: 19911023
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT5546
TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                         Sequence 2, Application US/08445342A Patent No. 5830726
                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acid
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AN AMINO ACID

STRANDEDNESS: Sin

TOPOLOGY: 1:

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ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                 APPLICANT:
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                                                                                                         CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                           PPLICANT: Langer, Robert, S.
TITLE OF INVENTION: The Heparinase gene from Flavobacterium
TITLE OF INVENTION: Heparinum
                                                                                                                                                                                                                 PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                    220 GKPNGWK 226
                                   CITY: Atlanta
STATE: GA
                COUNTRY:
                                                                     STREET:
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                                                                                      ADDRESSEE:
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30309-3450
                                 GA
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7: US
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100 Peachtree Street, Suite 3100
                                                                   2800 One Atlantic Center, 1201 West Peachtree Street
                  USA
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                                                                                                                                                                                                             Moreman, Kelley
Cooney, Charles, I.
                                                                                                                                                                                                Zimmerman, Joseph, J.
                                                                                                                                                                                                                                                       Sasisekharan, Ramnath
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                          Patrea L. Pabst
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-terminal
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Pred. No. 1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 384;
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; SOFTWARE: FastSEQ for Windows Version 3.0; SEQ ID NO 2; LENGTH: 384; TYPE: PRT; ORGANISM: Flavobacterium Heparinum US-09-066-481-2
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US-09-066-481-2
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                                                                      Matches
                                                                                         Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL
                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/066,481B
CURRENT FILING DATE: 1999-01-19
EARLIER APPLICATION NUMBER: US 60/008,069
EARLIER FILING DATE: 1995-10-30
NUMBER OF SEQ ID NOS: 38
                                                                                                                                                                                                                                                                                                                                                            SENERAL INFORMATION:

APPLICANT: GODAVARTI, RANGANATHAN
APPLICANT: SASISEKHARAN, RAMNATH
APPLICANT: GANESH, YENKATARAMAN
APPLICANT: GANESH, YENKATARAMAN
APPLICANT: COONEY, CHARLES L
APPLICANT: LANGER, ROBERT
TITLE OF INVENTION: LYASES DERIVED FROM HEPARINASE I
FILE REFERENCE: M0656/7038/HCL
EILE REFERENCE: M0656/7038/HCL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (404) 873-87 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 384 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: PADST, PATTEA L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: MIT 5546 div
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/783,706
FILING DATE: 23-OCT-1991
CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
220 GKPNGWK 226
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STRANDEDNESS: sir
                                                                                     Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                5 GKHNGWK 11
                                                                    Similarity
6; Conser
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                                                                      Conservative
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) 873-8795
NO: 2:
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85.7%;
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    Mismatches

                                                                                 Score 37; DB 4;
Pred. No. 1e+02;
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Pred. No. 1e+02;
                                                                      Mismatches
                                                                                                      Length 384;
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                                                                      Indels
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RESULT 14 PCT-US92-09124-2

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RESULT 15
US-08-221-817-14
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Best Local Similarity
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                                                                                                                                                                                 Patent No. 5532151
GENERAL INFORMATION:
                                                                                                                                                                                                  Sequence 14, Application US/08221817 Patent No. 5532151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: 404-815-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                     APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              FRAGMENT TYPE:
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYPOTHETICAL: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: MI
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-815-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Massachusetts Institute, of Technology TITLE OF INVENTION: The Heparinase Gene from Flavobacterium TITLE OF INVENTION: Heparinum
                                                                          CORRESPONDENCE ADDRESS:
                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
STREET: but.
STREET: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                           220 GKPNGWK 226
                                           ADDRESSEE:
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STATE: Georgia
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TOPOLOGY: lin
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Y: US
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                           6300 Sears Tower, 233 South Wacker Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      384 amino acids
                                                                                                                    Chantry, David
Gray, Patrick W.
Hoekstra, Merle F.
VENTION: A.No. 5532151el G Protein-Coupled Receptor
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                                                       Marshall, O'Toole, Gerstein, Murray &
                                            Borun
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1e+02;
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Search completed: July Job time: 188 sec
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                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 590 amino acids
TYPE: amino acid
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/123,932
FILING DATE: 17 SEP 1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                               Local Similarity hes 6; Conserv
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TELEFAX: (312) 474-0448
TELEX: 25-3856
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                                                                                          21 GKRKGKSKKWK 31
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REGISTRATION NUMBER: 35,302
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Pred. No. 1.6e+02;
1; Mismatches 4
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Perfect score:
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length: 2000000000
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Match Length
     July 6, 2001, 09:17:59; Search time 73.59 Seconds (without alignments)
12.421 Million cell updates/sec
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Copyright (c) 1993 - 2000
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## ALIGNMENTS

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A; Molecule type: protein A; Molecule type: protein A; Residues: '2',20-380 <kell> R; Residues: '2',20-380 <kell> R; Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. In Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp.85-89, Plenum Press, New A; Title: Amino acid sequence of the light chain of human high molecular mass kininoge A; Reference number: A27899 A; Accession: A27899</kell></kell>	A; Molecule Lype: protein A; Residues: 379-64 <lotp. 154,="" 1986="" 379-644="" 471-478,="" <lotp.="" a.;="" a24871;="" a24871<="" a;="" biochem.="" bradykinin="" chain="" completion="" determined="" eur.="" f.;="" henschen,="" high-molecular-mass="" human="" j.="" j.;="" kellermann,="" kininogen.="" light="" lottspeich,="" mueller-esterl,="" muid:86108361="" not="" note:="" number:="" of="" preceding="" primary="" r;="" recession:="" reference="" residues:="" sequence="" structure="" td="" the="" title:="" w.="" was=""><td>A;References 'ASSM', 253-377 <aue> A;Residues: 'ASSM', 253-377 <aue> A;Note: differences are due to known cloning artifacts R;Lottspetch, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985 A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270 A;Accession: A91153</aue></aue></td><td>A; MOLECULE LyPE: INKNA A; Residues: I -389 COHK&gt; A; Cross-references: GB:KO2566; NID:g177889 A;Cross-references: GB:KO2566; NID:g177889 R;TakagakI, Y:; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 J. Biol. Chem. 260, 8601-8609, 1985 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A; Reference number: A92544; MUID:85234582 A;Accession: A5276 A;Accession: A5276 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Reference number: S32422; MUID:g3223854 A;Reference number: S32422; MUID:g3223854 A;Accession: S32422; MUID:g3223854 A;Accession: RNAA</td><td>RESULT 1  KGHUHI  kininogen, HMW precursor [validated] - human  kininogen, HMW precursor [validated] - human  N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen  N;Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular  C;Species: Homo sapiens (man)  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.  Biochemistry 23, 5691-5697, 1984  A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide  A;Accession: A01279  A;Accession: A01279</td></lotp.>	A;References 'ASSM', 253-377 <aue> A;Residues: 'ASSM', 253-377 <aue> A;Note: differences are due to known cloning artifacts R;Lottspetch, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985 A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini A;Reference number: A91153; MUID:86030270 A;Accession: A91153</aue></aue>	A; MOLECULE LyPE: INKNA A; Residues: I -389 COHK> A; Cross-references: GB:KO2566; NID:g177889 A;Cross-references: GB:KO2566; NID:g177889 R;TakagakI, Y:; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 J. Biol. Chem. 260, 8601-8609, 1985 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A; Reference number: A92544; MUID:85234582 A;Accession: A5276 A;Accession: A5276 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852 A;Reference number: S32422; MUID:g3223854 A;Reference number: S32422; MUID:g3223854 A;Accession: S32422; MUID:g3223854 A;Accession: RNAA	RESULT 1  KGHUHI  kininogen, HMW precursor [validated] - human  kininogen, HMW precursor [validated] - human  N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen  N;Contains: bradykinin (kallidin I); HMW kininogen I; HMW kininogen II; low molecular  C;Species: Homo sapiens (man)  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.  Biochemistry 23, 5691-5697, 1984  A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide  A;Accession: A01279  A;Accession: A01279

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A;Molecule type: protein
A;Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
R;Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; S
Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A;Title: A new kinin moiety in human plasma kininogens.
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A; Residues: 380-389 < SAS>
R; Lenarcic, B.; Gabrijelcic, D.; Rozman, B.; Drobnic-Kosorok,
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A; Title: Human cathepsin B and cysteine proteinase inhibitors
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A;Reference number: A27699;
A;Accession: A27699
A;Molecule type: protein
A;Residues: 380-389 <MIN>
                     R;Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki, 1
J. Biol. Chem. 260, 86.10-8617, 1985
A;Title: Structural organization of the human kininogen
A;Reference number: A92545; MUID:85234583
                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: protein
A; Residues: 264-359, 'N', 361-375 <LEN2>
R; Little, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A; Title: Human mast cell tryptase isoforms: separation
A; Reference number: S55239; MUID:95251593
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lenarcic, B.; Krasovec, M.; Ritonja, A.; Olafsson, I.; Turk, V. FEBS Lett. 280, 211-215, 1991 A;Title: Inactivation of human cystatin C and kininogen by human cathepsin A;Reference number: S14303; MUID:91192133 A;Accession: S14447
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A;Accession: A61495
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A; Residues: 1-19;189-192;310-314;381-389 < LEN1>
R; Kato, H; Matsumura, Y; Maeda, H.
FEBS Lett. 232, 252-254, 1988
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Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A;Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from A;Reference number: A34030; MUID:88106632
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A; Reference number: A31905;
A; Accession: A31905
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A;Contents: annotation; gene organization
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H; Matsumura, Y; Kato, H.
Chem. 263, 16051-16054, 1988
Purification and identification of number: A31905; MUID:89034061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           $02482; MUID:89076517
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                                                                                             Takagaki, Y.; Miyata, T.; Nakanishi,
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C;Superfamily: kiningen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-644/Product: HMW kiningen I (prokiningen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kiningen II #status experimental <HAT1>
F;19-379/Domain: HMW kiningen heavy chain #status experimental <HCH>
F;19-379/Domain: cystatin homology <CY1>
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F;142-253/Domain: cystatin homology <CY2>
F;264-375/Domain: cystatin homology <CY2>
F;381-389/Product: lysyl-bradykinin (kallidin II) #status experimental <HCH>
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F;381-389/Product: bradykinin (kallidin I) #status experimental <CH>
F;431-434/Product: low molecular weight growth promoting factor #status experimental F;39-614,83-94,107-126,142-145,206-218,299-248,264-367,338-340,351-370/Disulfide bond F;48/Binding site: carbohydrate (Asn) (covalent) #status experimental F;39-380/Cleavage site: Aty-Ser (kallikrein) #status experimental F;39-390/Cleavage site: Aty-Ser (kallikrein) #status experimental F;301-310,531,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-310,531,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-310,531,542,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-310,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-320,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-320,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status experimental F;301-320,546,557,571,593,628/Binding site: carbohydrate (Asn) (covalent) #status
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A;Map position: 3q27-3q27
A;Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                     F;577/Binding site: carbohydrate (Ser) (covalent) #status experimental
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Matches
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GKKNGKHNGWKT 521
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A; Title: Studies on the structure of bovine A; Reference number: A91923; MUID:70180420 A; Accession: A91923 C;Species: Bos primigenius taurus (cattle) (c;Date: 14-Nov-1983 #text_change 22-Jun-1999 C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999 C;Accession: A01282; A91923; A91941; A91938; B29559 R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, Nature 305, 545-549, 1983 A;Title: A single gene for bovine high molecular weight and low molecular weight kini A;Reference number: A93317; MUID:84014106
A;Accession: A01282 A; Molecule type: protein A; Residues: 376-391 <KAT> R;Kato, H.; J. Biochem. A; Cross-references: GB: V01492; GB: K01758; A; Molecule type: mRNA A; Residues: 1-619 < KIT> N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokinin kininogen, H.; Nagasawa, S.; Suzuki, hem. 67, 313-323, 1970 HMW II precursor bovine NID: 9493; PIDN: CAA24736.1; kininogen: cleavages prokininogen of disulfide bonds PID:9494

Kato, H.; Iwanaga,

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Suzuki,

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C;Superfamily; kininogen; cystatin homology
C;Reywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl
F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-619/Product: HMW kininogen II #status predicted <MAT>
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F;241-252/Domain: cystatin homology <CY2>
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F;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;387-619/Product: bradykinin (kallidin I) #status experimental <KBDY>
F;387-619/Product: bradykinin (kallidin I) #status experimental <CH>
F;387-619/Product: bradykinin (kallidin I) #status experimental <F;389, as 93, 106-125, 141-144, 205-217, 228-247, 261-264, 325-337, 348-367/Disulfide bonds:
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F;386/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
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F;386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;386-387/Cleavage site: Arg-Ser (kallikrein) #status experimental
F;387-388, 525, 534, 546, 551, 568/Binding site: carbohydrate (Fhr) (covalent) #status experimental
F;387-388, 525, 534, 546, 551, 568/Binding site: carbohydrate (Fhr) (covalent) #status experimental
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A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984
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A;Title: Bovine high molecular weight kininogen. A;Reference number: A92627; MUID:87137530
A;Accession: B29559
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A; Residues: 387-455 < HAN>
A; Residues: 387-455 < HAN>
A; Note: 398-Pro, 401-Val, and 455-Lys
R; Han, Y.N.; Komiya, M.; Iwanaga, S.;
J. Biochem. 77, 55-68, 1975
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Disulfide bonds in bovine HMW kininogens
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A;ACCESSION.
A:Molecule type: protein
A;Residues: 'Z',20-104,'E',106-256,'XX',257-376
A;Residues: 'Z',20-104,'E',106-256,'XX',257-376
A;Residues: 'Z',20-104,'E',106-256,'XX',257-376
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486
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GKNNGKHYDWRT 497
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8; Conser
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                                                                                                                                                                             . 78;
                                                                                                                                      Score 51; DB : Pred. No. 2; 1; Mismatches
                                                                                                                                                                                                                                                                                                                               (kallikrein) #status
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hayashida, H.; Miyata,
                                                                                                                                                                                                                                                                                                                           experimental
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RESULT

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F;141-252/Domain: cystatin homology <CY2>
F;263-374/Domain: cystatin homology <CY3>
F;263-374/Domain: cystatin homology <CY3>
F;379-388/Product: lysyl-bradykinin (kallidin II) #status experimental <RBDY>
F;380-388/Product: bradykinin (kallidin I) #status experimental <BDY>
F;380-388/Product: HMW kininogen I light chain #status experimental <LCH>
F;417-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experi
F;27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond
F;87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;197/Binding site: carbohydrate (Thr) (covalent) (partial) #status experimental
F;197/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental
F;378-379/Cleavage site: Met-Lys (kallikrein) #status experimental
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A, Title: The amino acid sequence of the light chain of human high-molecular-mass kini A, Reference number: A, 1153, MUID: 86030270
A; Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R; Sueyoshi, T; Miyata, T.; Kato, H.; Iwanaga, S. Seikagaku 55, 808, 1984
Seikagaku 55, 808, 1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in init C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent v xyproline residue is present in the kininogen prior to the release of brady C;Superfamily: kininogen; cystatin homology
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N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos prinigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01281; A91923; A91938; A29559
C;Accession: A01281; A91923; A91938; A29559
R;Kitamura, N; Takagaki, Y; Furuto, S; Tanaka, T; Nawa, H; Nakanishi,
Nature 305, 545-549, 1983
                             F;382/Modified site: 4-hydroxyproline (Pro) #status predicted F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;19-130/Domain: cystatin homology <CY1>F;141-252/Domain: cystatin homology <CY2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             F; 19-621/Product:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F;1-18/Domain: signal sequence #status predicted <SIG>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; \mbox{Note:} \mbox{ article in Japanese } \mbox{$C$; Comment: The } \mbox{HMW} \mbox{ kininogen precursor is produced from the same} \mbox{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Disulfide bonds in bovine HMW kininogens A;Reference number: A94300 A;Contents: annotation; disulfide bonds
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A; Residues: 'z', 20-123,'I', 125-127,'I', 129-378 <SUE>
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J. Biochem. 77, 55-68, 1
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A;Reference number: A91923;
A;Accession:.A91923
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A; Residues: 1-621 <KIT>
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A;Reference number: A93317;
A;Accession: A01281
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Biochem. 67, 313-323, 1970
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19–621/Product: HMW prokininogen I #status predicted <MAT>
19–379/Product: HMW kininogen I heavy chain #status experimental
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experimental
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B.; Holland, R.;

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A;Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete A;Reference number: A71250; MUID:9832770
A;Accession: G71333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable ribonuclease H (rnhA) - syphilis spirochete
C;Species: Treponema pallidum subsp. pallidum (syphilis spirochete)
C;Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 22-Jun-1999
C;Accession: G71333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, July 1999
A;Reference number: Z21567
A;Accession: T35064
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-275 <SEE>
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R;Seeger, K.J.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell
                                                                                                                                                                                                                                                                                               A; Cross references:
                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-169 <COL>
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                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; nucleic acid sequence not shown; translation not shown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 8
                                                                                                    Query Match
Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                             Superfamily:
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Best Local
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                           103 KHNGWKT 109
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                                                                                                                                                                                                                                     TP0353
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                                                                KHNGWKT 12
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8; Conserv
                                                                                                                                                                                                                ribonuclease H
                                                                                                                                                                                                                                                                       nces: GB:AE001215; GB:AE000520; NID:g3322631; source: strain Nichols
                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                             sequence of Treponema pallidum, the syphilis spirochete.
50; MUID:98332770
                                                                                                                          62.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         68.9%;
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Pred.
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Pred. No.
                                                                                                                            Score 46;
Pred. No.
                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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No.
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4.1;
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3.8;
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                                                                                                                                                                                                                                                                                           PIDN: AAC65340.1; PID: g33226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         05-Nov-1999
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                                    R:Hayashi, Y.; Ichinose, M.; Yuasa, H.; Tatematsu, FEBS Lett. 405, 147-150, 1997 A;Title: Cca3, the mRNA level of which transiently A;Reference number: 220971; MUID:97263491 A;Accession: T31081
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-516 <SCH>
A:Cross-references: EMBL:AL355926; GSPDB:GN00116; NCSP:B17C10.30
A:Experimental source: BAC clone B17C10; strain OR74A
C:Genetics:
                   A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                             C; Accession: T31081
                                                                                                                                                                C;Species: Rattus norvegicus (Norway rat)
C;Date: 22-Oct-1999 #sequence_revision 22
                                                                                                                                                                                                         cca3 protein
                                                                                                                                                                                                                                                                                                                В
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A; Note: SPAC6F12.11c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Barrell, B.G.; Rajandream, submitted to the EMBL Data L: A;Reference number: Z17305 A;Accession: T11662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Species: Schizosaccharomyces pombe
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: T11662
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Gene: NCSP:B17C10.30
A; Map position: 6
A; Introns: 31/3
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A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Cross-references: EMBL: Z98533;
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A; Accession: T49422
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable transcription factor 44K chain - fission yeast (Schizosaccharomyces pombe)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT
                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genetics:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                            56.8%;
72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        M.A.; Wood, V
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NID:e1071719; PID:e334060
                                                                                                                                                                                                                                                                                                                                                                                                            Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                August 1997
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32;
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30;
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                                                                                                                            Ishibashi,
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before initiation

of DNA

0

Gaps

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ribonuclease HI NMB1618 [imported] - Neisseria meningitidis (strain MC58 serogroup C;Species: Neisseria meningitidis C;Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Superfamily: ribonu
C;Keywords: hydrolase
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A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Cross-references: GB:AL162757;
A;Cross-references: GB:AL162757;
A;Cross-references: GB:AL162757;
                                                                                                                                           A; Molecule type: DNA
A; Residues: I-145 <TET>
A; Cross references: GB: AE002512;
A; Experimental source: serogroup
                                                                                                                                                                                                                                  A;Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; A;Title: Complete genome sequence of Neisseria meningitidis serogroup B A;Reference number: A81000; MUID:20175755
A;Accession: H81061
                                                                                                                                                                                                                                                                                                       R; Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; ri, H.; Oin, H.; Vamathevan, J.; Gill, J.; Scarlato, V.; Masignani, V.; Science 287, 1809-1815, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QУ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Complete DNA sequence of a serogroup A strain of Neisseria menigitidis Z2491. A;Reference number: A81775; MUID:20222556
A;Accession: F81807
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Parkhill, J.; Achtman, M.; James, K.D.; Bentley, ; Holroyd, S.; Jagels, K.; Leather, S.; Moule, S.; Nature 404, 502-506, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ribonuclease H (EC 3.1.26.4) I NMA1817 [imported] - Neisseria meningitidis (strain C;Species: Neisseria meningitidis C;Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001 C;Accession: F81807
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 Query Match
Best Local S
Matches 9
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Matches
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Best Local
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 Similarity
9; Conserv
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9; Conser
                                                                                                                                                                                                                                                                                                                                                                                 H81061
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                                                                                           ribonuclease
   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       70
                    55.4%;
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Score 41; DB Pred. No. 20; 0; Mismatches
                                                                                                                                             GB:AE002098; NID:g7226866; PIDN:AAF41970.1; PID:g722686
B, strain MC58
 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 41; DB Pred. No. 20; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0
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Pred. No.
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                DВ
20;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          <u>ن</u>
                                   Length 145;
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 Indels
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 Gaps
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                                                                                                                                                                                                                                                                      Rappuoli, R.; strain MC58.
                                                                                                                                                                                                                                                                                                                          Dougherty,
Pizza, M.
                                                                                                                                                                                                                                                                                                                                                             K.E.;
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                                                                                                                                                                                                                                                                                                                                          ю, J.
В.А.
                                                                                                                                                                                                                                                                                                                                                                                                                                  8)
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                δÃ
                                                                                                                                                                                                 C; Function
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                                                       Matches
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A;Cross-references: EMBL:X95535; NID:g1524034; PIDN:CAA64780.1; PID:g1524035 R;Flashner, Y.; Shlomai, J.; Shafferman, A. Mol. Microbiol. 19, 985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-996, 1985-9
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C;Species: Drosophila hydei
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995
                                                                                                                                                                                                                                                         A;Description: catalyzes a sequence-specific cleaving-joining C;Superfamily: Escherichia coli plasmid R6K nickase taxC C;Keywords: DNA binding; plasmid DNA replication
                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 20.3
A; Genome: plasmid R6K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Gene: taxC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: DNA
A; Residues: 1-227, 'A', 229-255, 'K', 257-385 <FLA>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-385 <AVI>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Plasmid R6K contains two functional oriTs which can assemble simultaneously A; Reference number: S72275; MUID:96346167
A; Accession: S72275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R:Avila, P.; Nunez, B.; de la Cruz, F.
J. Mol. Biol. 261, 135-143, 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 21-Jul-2000
C;Accession: S72275; S70937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N;Alternate names: DNA distortion C;Species: Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nickase taxC -
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A;Cross-references: FlyBase:FBgn0011816
C;Superfamily: neurofilament triplet H
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: X73480; NID: g313199; PID: g313200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-344 < NEE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Reference number: S34153
A; Accession: S34153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C; Accession: S34153 R; Neesen, J.; Heinl
                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       304 GKKNGKKNDMK 314
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
mes 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      75 KNGMENWIHGWKRNGWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              w
KNGKHNGWKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KNG-----KHNGWKT
                                                                   7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Heinlein, U.A.O.; Buenemann, H.
the EMBL Data Library, June 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli plasmid R6K
nes: DNA distortion protein 2
                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                           55.4%;
70.0%;
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72.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12
                                                                       0
                                                                   Score 41; DB Pred. No. 47; O; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in concert to distort DNA within the
                                                                                                                                              2;
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                                                                                                                                              Length 385;
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312 KNGIQQGWKT 321

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hypothetical protein Y54B2A.9 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #teaccession: T27150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein F8B4.120 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999 C; Accession: T05352 R; Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, R.; De Clerck, R.; ewes, H.W.; Mayer, K.F.X.; Schueller, C.
                                                                                                                                                                                           Д
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                                                                                                                                                                                                                                                                                                                                                               C;Superfamily: cyclophilin homology F;6-162/Domain: cyclophilin homology <CYP>
                                                                                                                                                                                                                                                                                                                                                                                                       A; Map position: 4
A; Introns: 26/3; 45/1; 74/3; 83/1; 122/2; 165/1; 270/2; 307/1; 731/2; 754/2
A; Note: F8B4.120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary.
A;Molecule type: DNA
A;Residues: 1-552 <PAR>
A;Cross references: GB:AL139078;
A;Experimental source: serotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R; Lloyd,
                                                                                                                 RESULT 15
T27150
   submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-857 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z15409
A; Accession: T05352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     submitted to the Protein Sequence Database, February 1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Title: The genome sequence of the food-borne pathogen Campylobacter jejuni reveals hypela;Reference number: A81250; MUID:20150912
A;Accession: D81290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone F8B4
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T05352
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Nature 403, 665-668, 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                           171 GKKNGKH 177
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nes 7; Conserv
                                                                                                                                                                                                               1 GKKNGKH 7
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to the EMBL
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ilarity 100.0%;
Conservative
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                                                     #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
Data Library, October 1998
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77.8%;
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                                                                                                                                                                                                                                                                                   Score 41;
; Pred. No.
                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 41;
Pred. No.
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                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                   DB
. 97;
                                                                                                                                                                                                                                                                                                         2;
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                                                                                                                                                                                                                                                                                                     Length 857;
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                                                                                                                                                                                                                                                                   Indels
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A;Introns: 145/1
C;Superfamily: Caenorhabditis elegans hypothetical protein Y38H6C.19
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A:Molecule type: DNA
A:Molecule type: DNA
A:Residus: 1-198 <WIL>
A:Cross-references: EMBL:AL032646; PIDN:CAA21683.1; GSPDB:GN00019; CESP:Y54E2A.9
A:Experimental source: clone Y54E2A
C:Genetics:
C:Genetics:
C:Genetics:
C:Genetics:
Search completed: July Job time: 646 sec
                                                                                      B
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A; Accession: T27150
                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                        Matches
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| 131 GQPNGKRNSW 140
                                                                                                                      1 GKKNGKHNGW 10
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                 2001, 09:18:00
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Result
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Perfect score:
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Listing first 45 summaries
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10.936 Million cell updates/sec
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   Вd
 PDI_ASPNG
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GC4BP_RAT
GRK5_BOVIN
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NMT_CRYNE
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RNH_STRCO
GRK4_HUMAN
TOPL_BUCAII
MTDM_ARATH
YB33_SCHPO
RK32_ODOSI
RR52_ODOSI
RR52_ODOSI
RR52_OCHPO
VCCP_VCCCS
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VCP_VCCS
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TPR_PORGI
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P37371
P34881
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3 saccharomyc
6 homo sapien
9 cryptococcu
4 escherichia
6 streptomyce
8 homo sapien
1 buchnera ap
1 arabidopsis
8 schizosacch
9 odontella s
9 porphyra pu
3 lycopersico
8 vaccinia vi
8 schizosacch
8 schizosacch
                                                            6 porphyromon
0 aspergillus
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4 rattus norv
9 bos taurus
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bos taurus
bos taurus
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pedobacter
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R R

Sueyoshi T., Miyata T., Kato H., Iwanaga S.; "Disulfide bonds in bovine HMW kininogens.";

RY SEQUENCE OF 379-644.  RX MEDLINE-86030270; PubMed=4054110;  RA Lottspeich F., Kellermann J., Henschen A., Foertsch B.,  RA Mueller Esterl W.;  RT "The amino acid sequence of the light chain of human high-molecular-  RT mass kininogen.";  RL Eur. J. Biochem. 152:307-314(1985).
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PROSITE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; 7
Bradykinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
     PEPTIDE
                                                                                                                                                                                                                                                         Pfam; PF00031; cystatin;
                                                                                                                                                                                                                                                                                                                                                                          SWISS-2DPAGE; P01043; HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Seikagaku 56:
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ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN E PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
FTM: BRADYKININ IS RELEASED FROM KININOGEN BY SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRUTESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN PASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HE A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA BRADYKININ ACTION); (5) LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMEOCYTES; (6) LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
                                                                                                                                                                                                                                                                                                                                                                                                    K02566
M11438
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLOTTING.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SWISS-PROT entry is copyright. It is produced through sen the Swiss Institute of Bioinformatics and the EN
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AN IMPORTANT ROLE IN BLOOD COAGULATION I
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Best Local
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Eukaryota; Metazoa; C
Mammalia; Eutheria; C
Bovidae; Bovinae; Bos
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P01045;
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               SEQUENCE OF 19-376
MEDLINE=87137530; 1
                                                                  Kitamura N., Takagaki Y.,
"A single gene for bovine
weight kininogens.";
Nature 305:545-549(1983).
                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=84014106; PubMed=6571699;
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PRECURSOR (THIOL PROTEINASE
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 Hashimoto N.,
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CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
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CYSTATIN-LIKE 3.
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HWA-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HEMP-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMM-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOYTES; (4) THE ACTIVE
PEPTIDE BRADYKININ THAT IS RELEASED FROM HMM-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Han Y.N., Kato H., Iwanaga S., Suzuki T.;
"Primary structure of bovine plasma high-molecular-weight kininogen.
The amino acid sequence of a glycopeptide portion (fragment 1)
following the C-terminus ot the bradykinin moiety.";
Biochem. 79:1201-1222(1976).
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"Bovine high molecular weight kininogen. The amino acid sequence,
positions of carbohydrate chains and disulfide bridges in the hea
                                                 InterPro; IPR000010; -.
InterPro; IPR002395; -.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine high-molecular-we kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J. Biochem. 67:313-323(1970).
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MEDLINE=70180420; Pu
            Glycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
                                                                                                                                                                                                        EMBL; V01492; CAA24736.1; -.
EMBL; V01492; CAA24737.1; ALT_SEQ.
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                                                                                                                                                                                                                                                                                                                                           s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the Exercise Bioinformatics Institute. There are no resti
                                                                                                                                                                                                                                                                                                                                                                                                                      TO RESIDUE 398.
TISSUE SPECIFICITY: PLASMA.
PIM: BRADYKININ IS RELEASED FROM KININOGEN BY
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HAW II AND LAW II KININOGEN PRECURSORS
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                   A01282; КGBOH2.
B29559; B29559.
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MEDLINE=70180420; PubMed=4986212;
                                                                                                           Sueyoshi T., Miyata
Miyata T., Iwanaga S
                                                                                                                                                                         weight kininogens.";
Nature 305:545-549(1983).
[2]
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MEDLINE-84014106; PubMed-6571699;
Kitamura N., Takagaki Y., Furuto
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MEDLINE=87137530; F
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Eukaryota; Metazoa;
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"A single gene for bovine high molecular weight
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J. Biochem. 77:55-68(1975).
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PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS ARE
PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA
SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
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NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAMSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTACLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: (1) KININGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HAW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKERIN AND FACTOR XI NEXT TO FACTOR XII; (3) HAW-KININGEN INHIBITS THE THROMBIN- AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HAW-KININGEN SHOWS A VARRETY OF PHYSIOLOGICAL EFFECTS; (4A) INFLUENCE IN SMOOTH
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tructure of bovine kininogen: cleavages of disulfide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Treponema pallidum.
Bacteria; Spirochaetales;
CBI_TaxID=160;
                                                                                                                                                                                                                                 entities requires a license agreement (Son send an email to license@isb-sib.ch).
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                                                                                                                                                                    TIGR; TP0353;
                                                                                                                                                                                        EMBL; AE001215;
                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 281:375-388(1998).
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Bowman C., Cotton M.D., Fujii C., Garland S
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Q08695;
"The Drosophila hydei gene Dhmst101(1) repetitive, axoneme-associated protein Y chromosomal deletion mutant flies.":
                                                                                            Eukaryota; Metazoa; Arthropoda; Trac
Pterygota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosophi
NCBI_TaxID=7224;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Badcock K., Churcher C.M., Barrell B.G., Rajandream M.A., Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).

Eukaryota; Fungi; Ascomycota; Schizosaccharomycete
Schizosaccharomycetales; Schizosaccharomycetaceae;
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                                    Neesen J., Buenemann H.,
                                              MEDLINE=94200512; PubMed=8150205;
                                                                                                                                             Drosophila hydei (Fruit
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                                    Heinlein U.A.;
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                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                            Deckert G., Warren P.V., Gaasterland T., Young W.G., Ler Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M. Feldman R.A., Short J.M., Olson G.J., Swanson R.V.; "The complete genome of the hyperthermophilic bacterium
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-i- FUNCTION: POSSIBLE STRUCTURAL ROLE IN THE
-i- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMI
-i- TISSUE SPECIFICITY: TESTIS. LOCATED IN SPE
                                                 EMBL; AE000669; AAC06392.1;
                                                                                                                                                                                                                                                                                                            Nature 392:353-358(1998).

1 - FUNCTION: THIS PROTEIN IS A PRIMARY 23S RRNA-BINDING PROTEIN-HAS PEPTIDYLTRANSFERASE ACTIVITY (BY SIMILARITY).

-!- SIMILARITY: BELONGS TO THE L2P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                         aeolicus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-VF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Aquificales; NCBI_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=98196666; PubMed=9537320;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Aquifex aeolicus.
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DOMAIN: THE PREDOMINANT STRUCTURE IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN: THE PREDOMINANT STRUCTURE IS ALPHA-HELICAL. POLYMORPHISM: THE NUMBER OF REPEATS VARIES BETWEEN STRAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     $34153; $34153.
; P01032; 1C5A.
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19 x 16 AA APPROXIMATE TANDEM REPEATER STANDEM 
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. 37, Last sequ
. 39, Last anno
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Aujay M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X77688; CAA54757.1;
EMBL; Z49475; CAA89495.1;
PIR; S46631; S46631
HSSP; P16276; 6ACN.
SGD; S0003736; YJL200C.
                                                                                                                                                                METAL
SEQUENCE
                                                                                                                                                                                                                                                                                                                                PRINTS; F
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CDC6, CRY2, the gene for S24, a homologue to the aconitase general two homologues to chromosome III genes."; reast 10:1235-1249(1994).

YEAST 10:1235-1249(1994).

YEAST 10:1235-1249(1994).

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                                                                                                                                                                                                                                                               Hypothetical protein; Lyase; 4Fe-4S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Purnelle B., Coster F., Goffeau A.;
"The sequence of a 36 kb segment on the left arm of yeast chromosome x identifies 24 open reading frames including NUC1, PRP21 (SPP91), CDC6, CRY2, the gene for $24, a homologue to the aconitase gene ACO1
                                                                                                                                                                                                                                                                                                             PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000573; -.
InterPro; IPR001030; -.
Pfam; PF00694; Aconitase_C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Fungi; Ascomycota; Saccharon Saccharomycetales; Saccharomycetaceae;
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                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00330; aconitase;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Saccharomyces cerevisiae (Baker's yeast).
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                                           7; Conserv
                                                                                                                                                                                                                                                                                                                              PRO0415; ACONITASE.; PS00450; ACONITASE_1; 1.
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8; Conser
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                                              Conservative
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CAA89495.1;
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IRON-SULFUR (4FE-4S)
IRON-SULFUR (4FE-4S)
; FABA4FE482D3F993 CR
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                                                                                                                                                             (BY CRC64;
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                                              Indels
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Best Local S
Matches 8
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Pfam; PF02022; Integrase_Zn; 1
Pfam; PF00552; integrase; 1.
Pfam; PF00075; rnaseH; 1.
Pfam; PF00076; rve; 1.
Pfam; PF00078; rvt; 1.
Pfam; PF00078; rvt; 1.
                                                                                                                                                                                                                                                                                                                    01-FEB-1994
01-FEB-1994
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
RETROVIRUS-RELATED POL POLYPROTEIN [CONTAINS:
(EC 2.7.7.49); ENDONUCLEASE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POL1_HUMAN
P10266;
01-MAR-1989
                                                                                                                                                                                                                                                                                                                                                                                     NMT_CRYNE P34809;
MEDLINE=94132075; PubMed=8300631;
Lodge J.K., Johnson R.L., Weinberg R.A., "Comparison of myristoyl-CoA:protein N-my three pathogenic fungi: Cryptococcus neof
                                                                                                                                                                                   Eukaryota; Fungi; Basidiomycota; Tremellaceae; Filobasidiella.
                                                                                                                                                                                                                                                                           N-MYRISTOYLTRANSFERASE)
                                                                                                                                                                                                                                                                                                    GLYCYLPEPTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87036922; PubMed=3021993; Ono M., Yasunaga T., Miyata T., Ushikubo "Nucleotide sequence of human endogenous the mouse mammary tumor virus genome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HUMAN
                                                                                            SEQUENCE FROM N.A. STRAIN=L210425;
                                                                                                                                          NCBI_TaxID=5207;
[1]
                                                                                                                                                                                                                               Cryptococcus neoformans (Filobasidiella neoformans)
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InterPro; IPR001037; -.
InterPro; IPR001584; -.
InterPro; IPR002156; -.
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PIR; D24483; GNHUER.
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Eukaryota; Me
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874 AA;
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                                                                                                                                                                                                                                                               (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 40, Last annotation update)
DE N-TETRADECANOYLTRANSFERASE (EC 2.3.1.97) (PEPTIDE
TRANSFERASE) (MYRISTOYL-COA:PROTEIN N-MYRISTOYLTRANSF
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98936 MW;
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Primates;
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Pred.
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      neoformans,
                       N-myristoyltransferases
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                                                Gordon J.I.;
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P56614;
15-DEC-1998
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               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                   Unpublished observations (AUG-1998).
-!- SIMILARITY: BELONGS TO THE CON-10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                      Science
                                                                                                                                                                                                                                                                                                                                                                                                                   Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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15-DEC-1998
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MUTAGEN 487 487
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                                                                                                                                                                                                                                                                       X.E.
                                                                                                                                                                                                                                                                                                                                                 complete genome sequence of 
nce 277:1453-1474(1997).
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KDA PROTEIN IN WRBA-PUTA INTERGENIC REGION
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. 37, Last sequence. 37, Last annotations.
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Pred. No. 43;
1; Mismatches
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Hypothetical protein
SEQUENCE 57 Aa.
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Pfam; PF00075; rnaseH; 1.
Pydrolase; Nuclease; Endonuclease; Magnesium.
Hydrolase; Nuclease; Endonuclease; Magnesium.
METAL 10 10 MAGNESIUM (BY SIMILARITY).
METAL 50 50 MAGNESIUM (BY SIMILARITY).
METAL 72 72 MAGNESIUM (BY SIMILARITY).
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30-MAY-2000 (Rel. 39
RIBONUCLEASE H (EC 3
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Q9X7R6;
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                                                                                                                                                                                                                                                                                                                                                                                                                         Oliver K., Harris D., James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: THIS ENZYME IS AN ENDONUCLEASE THAT DEGRADES THE RNA-DNA HYBRIDS SPECIFICALLY (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: ENDONUCLEOLYTIC CLEAVAGE TO 5'-PHOSPHO-
                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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Actinomycetales; Streptomycineae;
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88 KRNGWKT
                                                               Local
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SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
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RESULT 13 GRK4_HUMAN

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p32298; Q13293; Q13294; Q15313; Q15314; Q15315; Q15
000641; 000642; Q14453; Q14725;
01-OCT-1993 (Rel. 27, Created)
15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
G PROTEIN-COUPLED RECEPTOR KINASE GRK4 (EC 2.7.1.-) (ITI1).
GPRK2L OR GPRK4 OR GRK4.
                                                                                                                        This
                                                                                                                                                                                                                                                                 Gardner A.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: SPECIFICALLY PHOSPHORYLATES THE ACTIVATED FORMS OF G
-!- PROTEIN-COUPLED RECEPTORS. GRK4-ALPHA CAN PHOSPHORYLATE RHODOPSIN
AND ITS ACTIVITY IS INHIBITED BY CALMODULIN; THE OTHER THREE
ISOFORMS DO NOT PHOSPHORYLATE RHODOPSIN AND DO NOT INTERACT WITH
                                                                use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                 molecular
                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94183267; PubMed=8135832; Sallese M., Lombardi M.S., de Blasi A.;
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Premont R.T.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ambrose C., James M., Barnes G., Lin C., Bates G., Altherr M., Duyao M., Groot N., Church D., Wasmuth J.J., Lehrach H., Housman D., Buckler A.J., Gusella J.F., McDonald M.E.;
"A novel G protein-coupled receptor kinase gene cloned from 4p16.3.";
Hum. Mol. Genet. 1:697-703(1992).
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MEDLINE=97248580;
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                                                                                                                                                                                                                                                                                                                                                                                                            "Two isoforms of G protein-coupled
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Characterization of the G protein-coupled receptor kinase GRK4. Identification of four splice variants.";
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                                                                                                                                                                          ALTERNATIVE PRODUCTS: 4 ISOFORMS; GRK4-ALPHA/GRK4D (SHOWN HERE), GRK4-BETA/GRK4C, GR4K-GAMMA/GRK4A AND GR4K-DELTA/GR4KB; ARE PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: TESTIS, AND IN A LOWER EXTENT IN OTHER TISSUES INCLUDING BRAIN CORTEX AND STRIATUM.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                            European
                                                                                                                                               GPRK SUBFAMILY.
SIMILARITY: CONTAINS 1 RGS DOMAIN.
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                                                                           SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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X97879;
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 CAA66468
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PubMed=1338872;
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MEDLING-20445173; PubMed-10993077;

Shigenobu S., Wattanabe H., Hattori M., Sakaki Y., Ishikawa H.;

Shigenobu S., Wattanabe H., Hattori M., Sakaki Y., Ishikawa H.;

"Genome sequence of the endocellular bacterial symbiont of aphids

Buchnera sp. APS.";

Nature 407:81-86(2000)

-: FUNCTION: THE REACTION CATALYZED BY TOPOISOMERASES LEADS TO THE

CONVERSION OF ONE TOPOLOGICAL ISOMER OF DNA TO ANOTHER.

-:- CATALYTIC ACTIVITY: ATP-INDEPENDENT BREAKAGE OF SINGLE-STRANDED

DNA, FOLLOWED BY PASSAGE AND REJOINING.

1. MISCRITANEOUS MENN A TOPOLOGICAL SUBBULLATIVE.
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01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DNA TOPOISOMERASE I (EC 5.99.1.2) (OMEGA-PROTEIN) (RELAXING ENZYME)
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PRINTS; PR00717; GPCRKINASE.

PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

PROSITE; PS50011; PROTEIN_KINASE_DOM; 1.

PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                     MISCELLANEOUS: WHEN A TOPOISOMERASE TRANSIENTLY BREAKS A DNA BACKBONE BOND, IT SIMULTANEOUSLY FORMS A PROTEIN-DNA LINK, I WHICH A TYROSYL OXYGEN IN THE ENZYME IS JOINED TO A DNA PHOS AT ONE END OF THE ENZYME. SEVERED DNA STRAND.

SIMILARITY: BELONGS TO PROKARYOTIC TYPE I/III TOPOISOMERASE
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Ouery Match 51.4%; Score 38; DB 1; Length 1534;
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Q91953 gallus gall	Q9neu2 caenorhabdi	Q9wuz0 rattus norv	Q9rvx2 deinococcus		Q54222 streptomyce	Q54388 streptomyce	Q9r302 escherichia	Q78509 human immun	Q78507 human immun	Q9ukh9 homo sapien	Q25766 plasmodium	Q9ukh5 homo sapien	Q9ukh6 homo sapien	Q14273 homo sapien	Q9up31 homo sapien	Ģ	human	Q9wjr4 human endog	Q49182 mycobacteri	Q9w526 drosophila	ď	7	Q9n8j0 trypanosoma	Q23541 caenorhabdi	P78810 schizosacch

# ALIGNMENTS

RESULT Q9S2U7

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Best Local Similarity
Matches 7; Conser
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Q9S2U7;
Q9S2U7);
01-MAY-2000 (TrEMBLrel. 13, C-01-MAY-2000 (TrEMBLrel. 13, L-01-MAY-2000 (TrEMBLrel. 13, L
                                                                                                                                                                                                                                                                                    Redenbach M., Kieser H.M., Denapaite D., Eichner A., Cullum J., Kinashi H., Hopwood D.A.; Kinashi H., Hopwood D.A.; "A set of ordered cosmids and a detailed genetic and physical matches and by Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; ALO96884; CAB51427.1: "SEQUENCE 275 AA; 29424 MW; B46AF89DCA186591 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-A3(2);
Bentley S.D., Parkhill
Submitted (JUL-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=A3(2);
Seeger K.J., Harris D.;
Submitted (JUL-1999) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycesae; Streptomyces; CTaxID-1902;
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3 KNGKHNGW 10
                                                                                                              Conservative
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e EMBL/GenBank/DDBJ databases.
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                                                                                                          Score 47; DB Pred. No. 3; 0; Mismatches
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PRELIMINARY;

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Best Local S
Matches 7
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01-0CT-2000 (TremBLrel. 1:
01-0CT-2000 (TremBLrel. 1:
01-MAR-2001 (TremBLrel. 1:
RAD57 RELATED PROTEIN.
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01-NOV-1996
01-MAR-2001
                                                                                                                                                                                                                        Neurospora crassa.

Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Sordariales; Sordariaceae; Neurospora.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3270
German Neurospora gen
Submitted (MAY-2000)
                                                                                                                  SEQUENCE FROM N.A. Schulte U., Aign V., Nyakatura G., Mewes
                                                                                                                                                                                                                                                                                                         B17C10.30.
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ATP-binding; Helicase; Polyprotein.
SEQUENCE 3898 AA; 438268 MW; D167BF5E48B11747 CRC64;
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InterPro; IPR001568; ...
InterPro; IPR001650; ...
Pfam; PF00271; helicase_C; 1.
PRINTS; PR00729; CDVENDOPTASE.
PROSITE; PS00037; MYB_1; UNKNOWN_1.
PROSITE; PS00031; RNASE T2_2; UNKNOWN_1.
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"Comparison of the entire nucleotide and deduced of the attenuated hog cholera vaccine strain GPE-
                                                  SEQUENCE FROM N.A.
                                                                                               Submitted
                                                                                                                                                                                                            NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       parental strain ALD.";
Arch. Virol. 140:1385-1391(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tshikawa K., Nagai H., Kata
Takeuchi K., Hishiyama M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Classical swine fever virus
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EMBL; D49533; BAA08477.1; -.
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InterPro; IPR001005; -.
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IBLrel. 01, Last sequence update)
IBLrel. 16, Last annotation update)
POLYPROTEIN.
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M., Saitoh
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  e project;
the EMBL/GenBank/DDBJ databases
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pt G.;
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., Takagi M., Gotoh K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                            516
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97;
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Query Match

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Q9DRT6;
Q1-MAR-2001
01-MAR-2001
01-MAR-2001
STRAIN-LTS 21E;
Ashton L., Rhodes D., Solomon A., Deacon N., Satchell C., C
Cooper D., Biti R., Stewart G., Kaldor J.;
"Viral diversity in the nef/LTR region of the HIV-1 genome:
associations with long-term nonprogression.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF219695; AAG44172.1:
EMBL; AF219695 AA, 23370 MW; 63BB87C97291ABZD CRC64;
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Q9UTT3;
Q1-MAY-2000
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                                                                                                               Human immunodeficiency vi:
Viruses; Retroid viruses;
NCBI_TaxID=11676;
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                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                             "S. pombe unknown protein.";
Submitted (SEP-1999) to the
EMBL; AB032716; BAA84655.1;
NON_TER 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces.
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Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
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InterPro: IPR003593; -.
SMART; SMO0382; AAA; 1.
SEQUENCE 516 AA; 55456 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4896;
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                                                                                                                                                                                                                                                                              11 KLNGKHKGTKT
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72.7%;
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                                                                                                                             virus type, 1.
es; Retroviridae; Lentivirus
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16,
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                                                                    Deacon N., Satchell C., Carr A.,
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                                                    Thomas C.E., Olsen B., Elkins C.; "Cloning and characterization of tdhA, a dependent heme receptor from Haemophilus Infect. Immun. 66:4254-4262(1998).
EMBL; AF052977; AAC35765.1; -.
                                                                                                                                                                                                    01-NOV-1998
01-MAY-2000
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01-NOV-1998
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NON_TER 294 294
SEQUENCE 294 AA; 32050 MW
                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
MCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1999 (TREMBLIEG: 12, 01-NOV-1999 (TREMBLIEG: 12, 01-MAY-2000 (TREMBLIEG: 13,
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SEQUENCE
                 Signal; Plasmid
SIGNAL 1
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                                   InterPro; IPR000531;
Pfam; PF00593; TonB_
                                                                                                            STRAIN=35000;
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Plasmid pUNCH1204.
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                                                                                                 MEDLINE=98380372; PubMed=9712775;
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                                                                                                                                    NCBI_TaxID=730;
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Pred. No. 22;
1; Mismatches
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POTENTIAL.
TON-DEPENDENT HEME
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                                                                                                                                                      subdivision; Pasteurellaceae;
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Pfam; PF00651; BTB; 1.

PROSITE; PS50088; ANK_REPEAT; 3.

PROSITE; PS50297; ANK_REP_REGION; 1.

PROSITE; PS50097; BTB; 1.

PROSITE; PS00018; EF_HAND; UNKNOWN_1.

SMARF; SM00225; BTB; 1.

SEQUENCE 1009 AA; 111602 MW; E25CE5
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Q9JYE5;
01-OCT-2000
01-OCT-2000
01-MAR-2001
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01-JUL-1997
01-JUL-1997
01-MAR-2001
SEQUENCE FROM N.A.

STRAIN-MC58 / SEROGROUP B;

MEDLINE=20175755; PubMed=10710307;

MEDLINE=20175755; PubMed=10710307;

Tettelin H., Saunders N.J., Heidelberg J., Jeffries A.C., N.

Eisen J.A., Ketchum K.A., Hood D.W., Peden J.F., Dodson R.J.

Nelson W.C., Gwinn M.L., DeBoy R., Peterson J.D., Hickey E.I.

Nelson W.C., Gwinn M.L., DeBoy R., Pieischmann R.D., Dough

Haft D.H., Salzberg S.L., White O., Fleischmann R.D., Dough

Mason T., Ciecko A., Parksey D.S., Blair E., Cittone H., Cli
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MEDINE-97263491; PubMed-9109406;
"Coa3, the mRNA level of which transiently decreases of DNA synthesis in regenerating rat liver cells.";
FEBS Lett. 406:147-150(1997).
EMBL; AB000116; BAA19969.1; -
                                                                                                                   Neisseria meningitidis
Bacteria; Proteobacteri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae
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                                                                                                                   meningitidis (serogroup B).
Proteobacteria; beta subdivision;
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Pred. No.
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H., Clark E.B.,
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AC Q5
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01-MAR-2001
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InterPro; ir.
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                                   01-MAR-2001
01-MAR-2001
                                                                                                                                                                                                                                                                                                Whitehead S., Spratt B.G., Barrell B.G. "Complete DNA sequence of a serogroup menigitidis Z2491.";
                                                                                                                                                                                                                                                                                                                             Parkhill J., Achtman M., James K.D., Bentley S.D., Churche Klee S.R., Morelli G., Basham D., Brown D., Chillingworth Davies R.M., Davis P., Devlin K., Feltwell T., Hamlin N., Jagels K., Leather S., Moule S., Mungall K., Quail M.A., Rutherford K.M., Simmonds M., Skelton J., Whitehood M.A., Rutherford K.M., Simmonds M., Skelton J.,
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   Human
                          NEF
                                                                              Q9DRT9
                                                                                                                                                                                                                                 Hydrolase.
SEQUENCE
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Bacteria; Proteobacteria; beta subdivision;
NCBI_TaxID=65699;
              NEF
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MEDLINE=20222556; PubMed=10761919;
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STRAIN=Z2491 / SEF
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EMBL; AE002512; AAF41970.1;
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                                                                                                                                                                                                                                                    Nature 404:502-506(2000).
EMBL; AL162757; CAB85042.1;
InterPro; IPRO02156; -
Pfam; PF00075; rnaseH; 1.
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STRAINLIS 21C;
STRAINLIS 21C;
Ashton L., Rhodes D., Solomon A., Deacon N., Satt Cooper D., Biti R., Stewart G., Kaldor J.;

"Viral diversity in the nef/LTR region of the HII associations with long-term nonprogression.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ dai EMBL; AF21993; AGG441T0.1;
SEQUENCE 208 AA; 23738 MW; 5B9560E7D4AB85D7 (
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STRAIN=A3(2);
Oliver K., Ha
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Bacteria; Firmicutes; Actinobacteria; Actinobacterid.
Actinomycetales; Streptomycineae; Streptomycetaceae;
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                                                                   SEQUENCE FROM
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Viruses; Retroid viruses; Retroviridae; Lentivirus
NCBI_TaxID=11676;
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"Viral diversity in the nef/LTR region of the associations with long-term nonprogression.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ EMBL; AF219692; AAG44169.1; -
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NCBI_TaxID=11676;
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the EMBL/GenBank/DDBJ databases.

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                  01-FEB-1997
01-FEB-1997
01-NOV-1998
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
SIMILARITY TO MAPSK-LIKE PROTEIN KINASE.
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
Brassicales; Brassicaceae; Arabidopsis.
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P71232;
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  NICKASE
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  features of clones.";
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Redenbach M., Kieser H.M., Denapaite D., Eichner A Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).
EMBL; AL136534; CAB66426.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. STRAIN=A3(2);
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AB020742; BAB10947.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. x. Sequence features of the regions of 3,076,755 bp covered by sixty P1 and TAC
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Last sequence update)
Last annotation update)
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Search completed: July Job time: 990 sec
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J. Mol. Biol. 261:135-143(1996).
EMBL; X95535; CAA64780.1; -.
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Escherichia
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                                                                                                                                                 SEQUENCE
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                                                                                                                                                                                                                                                                                         Plasmid R6K.
                                                                                                                                                                                                                                                                                                   Escherichia coli.
                                                                                                                                                                                                                                                        NCBI_TaxID=562;
                                                    312 KNGIQQGWKT 321
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           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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| HGHEQQHGLGHGHKFKLDDDLEHQGGH<br>    : :             :  :  <br>HDHDHKHEHKHDHKHDHDHDHRHEH | h 34.<br>Similarity 37.<br>10; Conservative | APPLICATION US/08686528A 6054134 6054134 FORMATION: ILINGWOOD, Clifford A. INVENTION: HAEMOPHILUS P SEQUENCES: 1737 King Street, Swit Alexandria Virginia Vi |            | 20202020202020202020202020202020202020                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
| FKLDDI<br> <br> <br>HDHDHI                                                             | 34.:<br>37.(<br>ative                       | cation US/086865 ION: ION: ION: US/WOOD, Clifford PION: HAEMOPHIL ENCES: 4 ADDRESS: USINGS Street, S daria Inia Ited States 1756 3LE FORM: Floppy disk Floppy disk Floppy disk Floppy disk Floppy disk Floppy disk Floppy disk Floppy disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk Flopps disk 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| iQGGH<br>:                                                                             | Score<br>Pred.<br>4; Mi                     | US/08686528A  Clifford A. HAEMOPHILUS AD 4  S: Doane, Swecker Street, Suite  M: M: M: M: M: M: M: M: M: M: M: M: M:                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Þ          | US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08<br>US-08                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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|                                                                                        | gth 313;<br>Indels                          |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 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RESULT 2 US-09-456-287-3 ; Sequence 3, Application US/09456287

GENERAL INFORMATION:

TITLE OF INVENTION: CORRESPONDENCE ADDRESS: NUMBER OF SEQUENCES:

LINGWOOD,

), Clifford A.
HAEMOPHILUS ADHESIN PROTEIN

ADDRESSEE:

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Best Local
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                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                               CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/686,528A
                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION: NAME: Rea, Teresa Stanek
                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS LENGTH: 313 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION: NAME: Rea, Teresa Stanek
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 НДНДНКНЕНКИДНКИДИДНДНКИЕН 127
                              FILING DATE: 20 CLASSIFICATION:
                                                                                                                                                                                           COUNTRY: United States ZIP: 22314-2756
                                                                                                     SOFTWARE:
                                                                                                                                                                                                                              CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRANDEDNESS: single TOPOLOGY: linear
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                                                                                                PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                  LINGWOOD, Clifford A.
VENTION: HAEMOPHILUS ADHESIN PROTEIN
                                  26-JUL-1996
N: 424
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RESULT 5 US-07-945-283-2

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                                                           Matches
                                                                                     Query Match
                                                                       Best Local Similarity
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Best Local
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REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2:
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                                                                                                                                                                                                 FORMATION FOR SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TRINGTH: 337 amino acids
                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
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LENGTH: 337 amino acid
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125 НДНДНКНЕНКИДНКИДНДНДНКИЕН 151
                                                                                                                                                                                             TYPE: a
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                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release 1.
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                                                                                                                                                                                                                                                                                                              FILING DATE:
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TOPOLOGY: li
                           1 HGHEQQHGLGHGHKFKLDDDLEHQGGH 27
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10; Conservative
                                                                                                                                                                                          amino acid
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                                                         Conservative
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linear
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                                                                       Score 57; DB Pred. No. 1.5;
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Pred. No.
                                                         Mismatches
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                                                                                     DB 4;
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                                                                                     Length 337;
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Sequence 2, Application US/07945283 Patent No. 5352596

GENERAL INFORMATION:

APPLICANT: Cheung, APPLICANT: Wesley,

Ronald D.

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Sequence 36, Appr-
Sequence 36, Appr-
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APPLICATION NUMBER: US/07,
FILING DATE: 19920911
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Ribando, Curtis P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: 309-685-4011 ex
TELEFAX: 309-685-4128
(INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1958 amino acids
             SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                               COMPUTER READABLE FORM:
MEDLIM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0.
                                                                                                                                                                                                                                                                        APPLICANT: Ullrich, Axel
APPLICANT: Moller, Niels P.H.
APPLICANT: Moller, Karin B.
TITLE OF INVENTION: NOVEL PRO:
TITLE OF INVENTION: PHOSPHATA:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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                                                                                                                           COUNTRY: U.S.A. ZIP: 10036-2711
                                                                                                                                                               CITY: New York STATE: N.Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                y Match 31.18;
Local Similarity 46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 1958 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Ribando, Curtis P
REGISTRATION NUMBER: 27976
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                                                                                                                                                                                                                 ADDRESSEE:
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                                                                                                                                                                                                  1155 Avenue of the Americas
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US/08/446,345
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Pred. No. 52;
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TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-446-345-36
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Best Local Similarity
Matches 12; Conserv
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                                                               TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
LENGTH: 1174 amino acids
TYPE: amino acid
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REGISTRATION NUMBER: 30742
REFERENCE/DOCKET NUMBER: 76
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)790-9090
TELEPHONE: (212)790-9090
                                                                                                                                     REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA: APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Xu, Tian
TITLE OF INVENTION: KUZ: A No. 5935792el Family of Metalloproteases
NUMBER OF SEQUENCES: 10
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                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                          CLASSIFICATION:
                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94104
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TELEX: 66141 PENNIE
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              STRANDEDNESS:
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                                                CENGTH:
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                              amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                     CALIFORNIA
                                               1239 amino acids
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Pan, Duojia
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Yavari, Reza
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                                                                                                                       (415) 343-4341
linear
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            single
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30.8%;
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Pred. No.
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RESULT 9
US-08-255-457-1
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Sequence 1,
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                                                                                                                                                      Query Match
Best Local
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 2:
                                                                            1004 HGGSRSHHQQHPHDWD----RHQGGH 1025
                                                                                                                                                                                                                                                                                                                                                          NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Xu, Tian TITLE OF INVENTION: KUZ: A No. 6190876el Family of Metalloproteases NUMBER OF SEQUENCES: 10 CORRESPONDENCE ADDRESS:
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ATTORNEY/AGENT INFORMATION:
NAME: OSMAN, RICHARD A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                     Local Similarity
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                                                                                                       1 HGHEQQHGLGHGHKFKLDDDLEHQGGH 27
                                                                                                                                                                                                                                                                                                LENGTH:
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Application US/08255457
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Yavari, Reza
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37.0%;
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                                                                                                                                    Score 48.5; I Pred. No. 94; 2; Mismatches
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Pred. No. 94;
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                                                                                                                                                                  DB 4;
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Best Local Similarity 40.0
                                                                                                                                                                                                                                                                                                                    Sequence 1, Application US/09115032 Patent No. 5972348
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APPLICANT:
                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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TITLE OF INVENTION:
NUMBER OF SEQUENCES:
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                 COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                    STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY: U.S.A. ZIP: 02110-2804
                                                                                                                                               STREET:
                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET:
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                                                                                                                                  Boston
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                                                                                                                                                 225 Franklin Street
                                                                                                                                                                                                                                                                                     Plaut, Andrew G
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                                                                                                                                                                                                                                                  Wright, Andrew
                                                                                                                                                                                                                                                                  Gilbert-Rothstein, Joanne V.
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                                                                                                                                                                 Fish & Richardson
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1; Mismatches
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Pred. No. 3
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Best Local Similarity
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                                                                                     TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 0039
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Wright, Andrew TITLE OF INVENTION: HELICO TITLE OF INVENTION: BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Plaut, Andrew G. APPLICANT: Gilbert-Rothstei APPLICANT: Wright, Andrew
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                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 02110-2804
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                                                 LENGTH:
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                amino acid
)GY: linear
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                                                   60 amino acids
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                                                                                                                      (617) 542-8906
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3.8;
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; Sequence 8, Application US/08584031A
; Patent No. 6030945
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US-08-780-496-8
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Best Local Similarity
"hes 9; Conserve
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US-08-584-031-8
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Best Local Similarity
Matches 10; Conserv
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APPLICANT: Avi Ashkenazi, Anan (
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SEQ ID NO 8
LENGTH: 24
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APPLICANT: Ashkenazi, Avi J.
TITLE OF INVENTION: APO-2 LIGAND
FILE REFERENCE: 11669.22USO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/08/584,031A CURRENT FILING DATE: 1996-01-09 NUMBER OF SEQ ID NOS: 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch. 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/780,496
                                 ATTORNEY/AGENT INFORMATION: NAME: Marschang, Diane L
                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Avi Ashkenazi, Anan Chuntharapai, Kyung Jin TITLE OF INVENTION: Apo-2 Ligand
                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                         STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
NAME: Marschang, Diane I REGISTRATION NUMBER: 35 REFERENCE/DOCKET NUMBER:
                                                                 FILING DATE: 08
CLASSIFICATION:
                                                                                                                                                                                                                           ZIP: 94080
                                                                                                                                                                                                                                         COUNTRY:
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                                                                       08-Jan-1997
N: 435
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39.1%;
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Pred. No. 2.
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Pred. No. 3.
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3.8;
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TELECOMMUNICATION INFORMATION: TELEPHONE: 415/225-5416

TELEFAX:

415/952-9881

TELEPHONE:

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Best Local Similarity 39.1
Conservative
                                                                  Query Match
Best Local Similarity
                                                           Matches
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                                                                                                                                                                                                                        TELEFAX: (716)263-160
NFORMATION FOR SEQ ID NO:
                                                                                                                                                TYPE: amino acids
TOPOLOGY: lines...
VOLECHIE TO
                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Timian, Susan J.
REGISTRATION UNMBER: 34,103
REFERENCE/DOCKET NUMBER: 19
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Knipple, Do APPLICANT: Henderson,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
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432 GMGPEHGHGHH-----AHSHGH 450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Rochester
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                           2 GHEQQHGLGHGHKFKLDDDLEHQGGH 27
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                                                                                                                                                                                                                                     (716)263-1600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      USA
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                                                           Conservative
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N: 435
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Gamma-Aminobutyric Acid
                                                                       27.8%;
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                                                                       Score 46.5;
Pred. No. 8
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Pred. No. 2
                                                         Mismatches
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Search completed: July Job time: 188 sec
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US-08-072-064-1
                                                                                                                                                         Best Loc
Matches
                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: 415/397-8338 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 770,881
FILING DATE: 04-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: OPHD-00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                           ORGANISM: Drosop
POSITION IN GENOME:
                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: |
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 637 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELECOMMUNICATION INFORMATION: TELEPHONE: 415/705-8410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FFRENCH-CONSTANT, RICHARD H. APPLICANT: JACKSON, MEYER B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                    453 GMGPEHGHGHGHH-----AHSHGH 471
                                                                                                                                                         Local Similarity hes 10; Conser
                                                                                                                                                                                                                                                                                                                                                                     TYPE: AMINO ACID
                                                                                                                                                                                                                                                          CHROMOSOME/SEGMENT: III; polytene subregion 66F MAP POSITION: approximately map unit 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UPFILING DATE: 19930602
                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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                                                                                                                       2 GHEQQHGLGHGHKFKLDDDLEHQGGH 27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JACKSON, MEYER B.
                                                                                                                                                         Conservative
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                2001, 09:10:22
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Pred. No. 84;
1; Mismatches
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                                                                                                                                                                                        DB 3; Length 637;
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GenCore version Copyright (c) 1993 - 2000 4.5 Compugen Ltd.

OM protein - protein search, using sw model

Run on: 6, 2001, 09:18:00; Search time 73.59 Seconds (without alignments) 28.983 Million cell updates/sec

US-09-437-912-5

Perfect score: **HGHEQQHGLGHGHKFKLDDDLEHQGGHV** 

Sequence:

Scoring table: BLOSUM62

28

Gapop 10.0 , Gapext 0.5

219241 seqs, 76174552 residues

Total number of hits satisfying chosen parameters:

Minimum DB Maximum DB seq length: 2000000000 length:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 s

summaries

Database PIR\_68:\* pir1:\*
pir2:\*
pir3:\*
pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

| 29                 | 28     | 27     | 26     | 25     | 24     | 23     | 22     | 21                 | 20     | 19                 | 18                 | 17                 | 16                 | 15     | 14     | 13                 | 12        | 11                 | 10                 | 9      | œ      | 7      | O                 | 5      | 4      | w      | 2      | <b></b>      | NO.         | Result     |
|--------------------|--------|--------|--------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------------------|--------------------|--------|--------|--------------------|-----------|--------------------|--------------------|--------|--------|--------|-------------------|--------|--------|--------|--------|--------------|-------------|------------|
| 56.5               | 56.5   | 57     | 57     | 57     | 57     | 58     | 58     | 59                 | 59     | 59.5               | 60                 | 60.5               | 60.5               | 61     | 61.5   | 62                 | 62.5      | 62.5               | 63.5               | 64     | 65     | 85     | 85                |        |        | 98.5   | 98.5   | 167          | Score       |            |
| 33.8               | 33.8   | ٠      | 34.1   | 34.1   | 34.1   |        | 4.     | 5                  | 5      | 5                  | 5                  | 6.                 | 6.                 | 36.5   | 6.     | 7.                 | 37.4      | 7.                 | 8                  | 8      | 38.9   | 0      | 0                 | 4.     | ٠      | 9      | 59.0   | 100.0        | Match       | %<br>Query |
| 313                | 254    | 670    | 337    | 335    | 213    | 549    | 378    | 457                | 110    | 201                | 191                | 515                | 398                | 735    | 199    | 314                | 1085      | 535                | 436                | 776    | 2038   | 621    | 619               | 315    | 290    | 639    | 264    | 644          | Length      |            |
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| A28444             | A31488 | F36791 | D64049 | D38532 | T36345 | T15506 | T49164 | S39079             | T07618 | н82055             | D96701             | T23089             | T02681             | T45059 | T48099 | T35241             | S66149    | S66148             | I49714             | T02702 | A43742 | KGBOH1 | KGBOH2            | A27115 | C27115 | A25486 | C25486 | KGHUH1       | Ħ           |            |
| filaggrin precurso | _      | 0      |        | _      |        | ¢      | tran   | puff C-8 protein - | 4      | peptidyl-prolyl ci | unknown protein, 9 | hypothetical prote | probable zinc tran |        |        | hypothetical prote | pipsqueak | gene pipsqueak pro | MHC H-2K/t-w5-link |        |        | MMH    | kininogen, HMW II | hase   |        | E      | n, HMW | nogen, HMW p | Description |            |

| 4.4<br>4.5                               | 42<br>43                                 | 40<br>41                                 | 39                 | 38     | 37                 | 36                 | 3<br>5             | 34                 | ω<br>ω             | 32                 | 31                 | 30                 |
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| 53<br>53                                 | 53<br>53                                 | 53                                       | 53.5               | 54     | 54.5               | 55                 | 55                 | 55.5               | 55.5               | 55.5               | 55.5               | 56                 |
| 31.7<br>31.7                             | 31.7<br>31.7                             | 31.7<br>31.7                             | 32.0               | 32.3   | 32.6               | 32.9               | 32.9               | 33.2               | 33.2               | 33.2               | 33.2               | 33.5               |
| 529<br>1061                              | 245<br>409                               | 18<br>85                                 | 258                | 389    | 410                | 283                | 189                | 255                | 250                | 242                | 102                | 439                |
| 22                                       | NN                                       | N N                                      | 2                  | N      | Ν                  | N                  | Ν                  | N                  | N                  | N                  | N                  | N                  |
| T08684<br>S37667                         | T23844<br>E83992                         | B32473<br>A45969                         | A48820             | в96635 | T26757             | C85838             | C81428             | A35026             | в35026             | н82061             | T30119             | S58327             |
| hypothetical prote<br>traC-1 protein - E | hypothetical prote<br>ATP/GTP-binding pr | histidine-rich pro<br>hemolymph antifung | homeobox protein ( |        | hypothetical prote | hypothetical prote | peptidyl-prolyl ci | filaggrin A - mous | filaggrin B - mous | hypothetical prote | hypothetical prote | cobalt accumulatio |

kininogen, HMW precursor [validated] - human

prokininogen low molecular

N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen N;Contains: bradykinin (kallidin I); HMW Kininogen I; HMW kininogen II; low molecula C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 08-Dec-2000 C;Date: 28-May-1986 #sequence\_revision 28-May-1986 #text\_change 08-Dec-2000 C;Accession: Ad1279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;

R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.
Biochemistry 23, 5691-5697, 1984
A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide A;Reference number: A90490; MUID:85122621
A;Accession: A01279

A; Molecule type: mRNA A; Residues: 1-389 < OHK>

A;Cross-references: GB:K02566; NID:g177889
R;Takagaki, Y.; Kitamura, N.; Nakanishi, S.
J. Biol. Chem. 260, 8601-8609, 1985
A;Title: Cloning and sequence analysis of cDNAs
A;Reference number: A92544; MUID:85234582
A;Accession: A25276 for human high molecular weight and

A;Molecule type: mRNA
A;Residues: 1-592,'I',594-644 <TAK>
A;Residues: 1-592,'I',594-644 <TAK>
A;Cross-references: GB:M11437; NID:g186751; PIDN:AAB59550.1; PID:g386852
R;Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I.
FEBS Lett 321, 93-97, 1993

FEBS Lett. 321, 93-97, 1993
A;Title: Cloning, expression and characterization of human kininogen domain 3.
A;Reference number: \$32422; MUID:93223854

A; Accession: S32422

A; Molecule type: mRNA A; Residues: 'ANSM', 253-377 < AUE>

A;Note: differences are due to known cloning artifacts
R;Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W.
Eur. J. Biochem. 152, 307-314, 1985
A;Title: The amino acid sequence of the light chain of human high-molecular-mass kini
A;Reference number: A91153; MUID:86030270
A;Accession: A91153

A; Molecule type: protein A; Residues: 379-644 <LOT>

not determined

A;Note: the bradykinin sequence preceding the light chain sequence was not determine R;Kellermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. Eur. J. Biochem. 154, 471-478, 1986
A;Title: Completion of the primary structure of human high-molecular-mass kininogen A;Reference number: A24871; MUID:86108361

A; Accession: A24871

A; Molecule type: protein A; Residues: 'Z', 20-380 <KEL1>

R;Kellermann, J.; Lottspeich, F.; Henschen, A.; in Kinins IV, Greenbaum, L.M., and Margolius, H Mueller-Esterl, W. .S., ed., pp.85-89, Plenum Press, New of human high molecular mass kininog

light chain

kininoge

A; Title: Amino acid sequence of the A; Reference number: A27899

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A; Molecule type: protein
A; Residues: 379-389, 'K', 390-407,'Q',409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; Scic. Biochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin molety in human plasma kininogens. A; Reference number: A27699; MUID:88209021
A; Accession: A27699
A; Molecule type: protein
A; Residues: 380-389 <MIN>
R; Maeda, H; Matsumura, Y.; Kato, H.
J. Biol. Chem. 263, 16051-16054, 1988
A; Title: Purification and identification of [hydroxyprolyl A; Reference number: A31905; MUID:89034061
A; Reference number: A31905; MUID:89034061
A; Molecule type: protein
A; Molecule type: protein
A; Molecule type: protein
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A; Mesidues: 381-389 < KAT2>
A; Experimental source: urine
A; Note: this peptide had Pro-383 modified to
A; Accession: C61495
A; Molecule type: protein
A; Residues: 380-389 < KAT3>
R; Lenarcic, B.; Krasovec, M.; Ritonja, A.; O
FEBS Lett. 280, 211-215, 1991
A; Title: inactivation of human cystatin C an
A; Reference number: S14303; MUID:91192133
A; Accession: S14447
A: Coloration of Coloration of All Proteins of Accession: S14447
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A; Residues: 381-389 < MAE>
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Blochem. Blophys. Res.; Commun. 150, 511-516, 1988
A; Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released from human A; Reference number: A34030; MUID:88106632
A; Accession: A34030
A; Molecule type: protein
                                                                                                                                                                                                                                                                                                                  A;Title: Purification from human plasma of a A;Reference number: S68059; MUID:96033974 A;Accession: S68059
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: protein
A; Residues: 450-452,'X',454,'X',456 <LIT>
R; Straczek, J: Maachi, F; le Nguyen, D.;
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: protein
A; Residues: 264-359, N., 361-375 < LEN2>
R; Little, S.S.; Johnson, D.A.
Biochem, J. 307, 341-346, 1995
A; Title: Human mast cell tryptase isoforms: A; Reference number: S55239; MUID:95251593
A; Accession: S55239
                                               A; Title: Structural organization of the human A; Reference number: A92545; MUID:85234583
                                                                                                                                   A; Molecule type: protein A; Residues: 431-434 <STR> R; Kitamura, N.; Kitagawa, J. Biol. Chem. 260, 8610-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues of A;Reference number: A61495; MUID:88211869
A;Accession: A61495
A;Accession: A61495
A;Molecule type: protein
A;Residues: 380-389 <KAT1>
A;Experimental source: urine
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A;Residues: 380-389 <SAS>
R;Lenarcic, B; Gabrijelcic, D; Rozman, B; Drobnic-Kosorok,
Biol. Chem. Hoppe-Seyler 369, 257-261, 1988
A;Title: Human cathepsin B and cysteine proteinase inhibitors
A;Reference number: S02482; MUID:89076517
A;Recession: S02482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Note: this peptide had Pro-383 modified to 4-hydroxyproline A; Accession: B61495
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-19;189-192;310-314;381-389 <LEN1>
                                                                                                                                        Kitagawa, H.; Fukushima, D.;
260, 8610-8617, 1985
gene
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                                                                                                                                                                                                                                                                                                                                                                                                                tetrapeptide that
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                                                                                                                                                                                  Y.; Miyata,
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HGHQKPHGLGHGHQLKLDDLKQQREDGYDHRHPVGH

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A; Generic Survey.

A; Cross-references: GDB:125256; OMIM:228960

A; Map position: 3q27-3q27

A; Introns: 65/3; 102/3; 131/1; 188/3; 224/3; 253/1; 310/3; 346/3; 375/3

C; Superfamily: kininogen; cystatin homology
C; Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
E; 1-944/Product: HMW kininogen I (prokininogen) # status experimental <MAT1>
F; 19-379, Domain: cystatin homology <CY1>
F; 19-379, Domain: cystatin homology <CY1>
F; 19-379, Domain: cystatin homology <CY2>
F; 264-375, Domain: cystatin homology <CY2>
F; 264-375, Domain: cystatin homology <CY3>
F; 380-389, Product: LMW kininogen I (skilidin II) # status experimental <HCH>
F; 381-389, Product: bradykinin (kallidin II) # status experimental <HCH>
F; 391-380, Product: low molecular weight growth promoting factor # status experimental
F; 28-614, 83-94, 107-126, 142-145, 206-218, 229-248, 264-257, 328-340, 351-370, Disulfide Site: pyrrolidone carboxylic acid (Gln) (in mature form) # status experimental
F; 28-614, 83-94, 107-126, 142-145, 206-218, 229-248, 264-267, 328-340, 351-370, Disulfide bond
F; 48, Binding site: carbohydrate (Asn) (covalent) # status experimental
F; 383, Modified site: Met-Lys (kallikrein) # status experimental
F; 389, 390, Cleavage site: Ang Carboxylic (Pro) (partial) # status experimental
F; 389, 390, Cleavage site: Ang Ser (kallikrein) # status experimental
F; 381, 532, 546, 557, 571, 593, 628, Binding site: carbohydrate (Asn)
F; 577, Binding site: carbohydrate (Ser) (covalent) # status experimental
F; 389, 3354, 546, 557, 571, 593, 628, Binding site: carbohydrate (Asn)
F; 577, Binding site: carbohydrate (Ser) (covalent) # status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT
C25486
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Qy
                                                                                                                                                                                       A; Residues: 1-264 <KIT>
C; Comment: The nucleotide
C; Superfamily: kininogen;
                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-264 <KIT>
                                                                                                                                                                                                                                                                                            A; Title: Differing expression A; Reference number: A92625; Mt A; Accession: C25486
                                                                                                                                                                                                                                                                                                                                                                     R; Kitagawa, H.; Kitamura, N.; I
J. Biol. Chem. 262, 2190-2198,
                                                                                                                                                                                                                                                                                                                                                                                                                            C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Mar-1989 #sequence_revision 08
C:Accession: C25486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         K-kininogen,
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A;Contents: annotation; bradykinin
C;Comment: The HMW biring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Gene: GDB: KNG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fed. Proc. 27, 52-57
A; Title: Structural
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                                                                                    Query Match
Best Local
                                                            Matches
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Best Local
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                                                         Local Similarity 50.00 to 18; Conservative
     1 HGHEQQHGLGHGHKFKLDD---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HGHEQQHGLGHGHKFKLDDDLEHQGGHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HMW precursor - rat (fragment) attus norvegicus (Norway rat)
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                                                                                 59.0%;
                                                                                                                                                                                       cystatin
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2198, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.
                                                                                                                                                                                                                                                                                                                            on patterns and MUID:87137443
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     ----DLEHQGGH
                                                         Score 98.5; D
Pred. No. 4.4e
3; Mismatches
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Pred. No. 5.
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                                                                         4.4e-06;
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15;
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                                                            6;
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                                                                                                                                                                                                                  GenBank,
                                                            Indels
                                                                                                                                                                                                                                                                                                                                                the rat kininogen gene family
                                                                                                                                                                                                                  release
                                                         9;
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RESULT
A27115
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J. Biol. Chem. 262, 2345-2351, 1987
A;Title: Differing utilization of homologous transcription initiation sites of A;Reference number: A25488; MUID:87137465
A;Accession: A25488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 20-Aug-1999
C;Accession: C27115; A25488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: the authors translated the codon CAA C; Superfamily: kininogen; cystatin homology C; Keywords: alternative splicing F;1-18/Domain: signal sequence #status predic F;19-639/Product: kininogen, HMW I #status profile
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution A;Reference number: A92625; MUID:87137443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N;Contains: bradykinin
C;Species: Rattus norvegicus (Norway rat)
C;Date: 08-Mar-1989 #sequence_revision 08
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A25486
major
                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-48 < KAG>
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A; Residues: 1-290 <FU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Fung, W.P.; Schreiber, G.
T Biol. Chem. 262, 9298-9308, 1987
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                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary
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Best Local
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acute phase alpha-1 protein 1 -
                                                                                           124
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nes 18; Conserv
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                                                                                                            1 HGHEQQHGLGHGHKFKLDD------DLEHQGGH 27
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                                                                                                                                                                   1 Similarity
17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1-639 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -290 <FUN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LMW precursor - rat (fragments)
                                                                                                                                                                     Conservative
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                                                                                                                                                                                     54.8%;
47.2%;
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                                                                                                                                                                 Score 91.5; D
Pred. No. 4.3e
4; Mismatches
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Pred. No. 1.1e-05;
3; Mismatches 6
rat (fragments)
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J. Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine A;Reference number: A91923; MUID:70180420
A;Molecnia ****
                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein A; Molecule type: protein A; Residues: 'Z',20-104,'E',106-256,'XX',257-376 A; Residues: 'Z', 20-104, E', 106-256, 'XX', 257-376 A;
                                                                                       A;Title: Bovine high molecular weight kininogen. A;Reference number: A92627; MUID:87137530 A;Accession: B29559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokinin C;Species: Bos primigenius taurus (cattle) C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun C;Accession: A01282; A91923; A91941; A91938; B29559
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the A;Reference number: 892653; MUID:87250580
A;Accession: A27115
                                                                                                                                                                                      A; Molecule type: protein
A; Residues: 456-496 <HA2>
R; Sueyoshi, T.; Miyata, T
                                                                                                                                                                                                                                                        A;Title: Studies on the primary structure of bovine high-molecular-weight kininogen A;Reference number: A91938; MUID:75170265 A;Accession: A91938
                                                                                                                                                                                                                                                                                                                               R; Han, Y.N.; Komiya, M.; Iw:
J. Biochem. 77, 55-68, 1975
                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Accession: A91941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Han, Y.N.; Kato, H.; Iwanaga, S.; Suzuki, T.
J. Biochem. 79, 1201-1222, 192
A;Title: Primary structure of bovine plasma high-molecular-weight kininogen.
A;Reference number: A91941; MUID:76260155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 376-391 < KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:V01492; GB:K01758; NID:g493; R;Kato, H.; Nagasawa, S.; Suzuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
A; Residues: 1-619 <KIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Kitamura, N.; Takagaki, Y.; Furuto, Nature 305, 545-549, 1983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: kininogen; cystatin homology F;19-65/Domain: cystatin homology (fragment) <CYS>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Gene: MAP1
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A; Residues: 1-315 <FUN>
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C; Date: 31-Mar-1989 #sequence_revision 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local S
Matches 17
                                                                                                                                                              Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, Biol. Chem. 262, 2768-2779, 1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           148 NGHQKPHGLGHGHKHKLDDLKQQRDDGYNYRHPMGH 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity nes 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A single gene for bovine high molecular weight nce number: A93317; MUID:84014106
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Kellermann,
152, 307-314,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.88;
    J.; Henschen,
, 1985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 91.5; DB 2;
Pred. No. 4.7e-05;
4; Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S.; Tanaka,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -DLEHQGGH 27
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                                              <SUE>
                     Foertsch,
                                                                                                                                          The
                                                                                                                                                                                      H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PIDN:CAA24736.1;
                                                                                                                                        amino acid sequence,
                                                                                                                                                                                      Hayashida, H.; Miyata, T.; Iwana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 315;
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                     В.;
                     Muller-Esterl,
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xyproline residue is present in the kininogen by wallingth, is a potent varyordine residue is present in the kininogen by wallingth. It is a potent varyordine residue is present in the kininogen prior to the release of bradykinin. C;Superfamily: kininogen; cystatin homology C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-619/Product: HMW kininogen II heavy chain #status experimental <HCH>
F;19-130/Domain: cystatin homology <CY2>
F;141-252/Domain: cystatin homology <CY2>
F;261-372/Domain: cystatin homology <CY3>
F;377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F;378-386/Product: lysyl-bradykinin (kallidin II) #status experimental <CH>
F;378-386/Product: HMW kininogen II light chain #status experimental <LCH>
F;418-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experiment F;27-589,82-93,106-125,141-144,205-217,228-247,261-264,325-337,348-367/Disulfide bonds:
F;87,168,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status experimental F;36/Binding site: carbohydrate (Asn) (covalent) #status experimental F;36/Binding site: carbohydrate (Asn) (covalent) (partial) #status experimental F;36/Binding site: anbohydrate (Asn) (covalent) (partial) #status experimental F;36/Binding site: Anydroxyproline (pro) #status experimental F;36/Anydrate (Asn) (covalent) (partial) #status experimental F;36/Anydrate (Asn) (covalent) (covale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  kininogen, HMW I precursor - bovine

N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokinino
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-
C;Accession: A01281; A91932; A91938; A29559
R;Kitamura, N: Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanis
Nature 305, 545-549, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Note: article in Japanese
A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form a C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of the C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is important in the glycine/histidine/lysine-rich region of HMW kininogen light chain is important: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, casidne is present in the kininogen prior to the release of bradykinin.
                                                                                                                                    A; Reference number: A91923; A; Accession: A91923
                                                                                                                                                                             A; Title: Studies on the structure of bovine kininogen: A; Reference number: A91923; MUID: 70180420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Reference number: A; Accession: A01281
                                             A; Molecule type: protein A; Residues: 378-393 < KAT
                                                                                                                                                                                                                                                                                                         A;Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1; PID:g492 R;Kato, H.; Nagasawa, S.; Suzuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
A; Residues: 1-621 <KIT>
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Seikagaku 56, 808, 1984
A;Title: Disulfide bonds
                                                                                                                                                                                                                                                                    Kato, H.; Nagasawa, S.; Suz
Biochem. 67, 313-323, 1970
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Best Local
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Iwanaga,
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    Suzuki,
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n as
                                                                                                             C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
                                    C; Accession: A43742; B43742
R; Haynes, S.R.; Mozer, B.A.
                                                                                                                                                                                                             N; Alternate names: membrane protein N; Contains: female sterile homeotic
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R; Sueyoshi, T.; Miyata, T
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Best Local
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Mozer, B
246-257,
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                                    Bhatia-Dey,
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ein fsh, 205K
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N.; Dawid,

20-Sep-1999

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A; Nother article in Japanese
A; Nother article in Japanese
A; Note: article in Japanese
C; Comment: The HMW kininogen procursor is produced from the same gene as the LMW form
C; Comment: The HMW kininogen procursor is produced from the same gene as the LMW form
C; Comment: The glyclne/histidine/lysine-rich region of HMW kininogen light chain is i
C; Comment: The glyclne/histidine/lysine-rich region of HMW kininogen light chain is i
C; Comment: The glyclne/histidine/lysine-rich region of HMW kininogen light chain is i
C; Comment: The glyclne/histidine/lysine-rich
C; Comment: The glyclne/histidine/lysine-rich
C; Comment: The glyclne/histidine/lysine-rich
C; Comment: The glyclne/histidine/lysine-rich
F; 19-379/Product: HMW prokininogen I heavy chain #status experimental <HCH>
F; 19-379/Product: HMW kininogen I heavy chain #status experimental <HCH>
F; 19-379/Product: Cystatin homology <CY2>
F; 19-379/Product: Lysyl-bradykinin (kallidin I) #status experimental <KBDY>
F; 380-389/Product: Dyrolidone carboxylic acid (Gln) (in mature form) #status experimental
F; 19/Modified site: carbohydrate (Thr) (covalent) #status experimental
F; 197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F; 379-379/Cleavage site: Met Lys (kallikrein) #status predited
F; 381-379/Cleavage site: Met Lys (kallikrein) #status predited
F; 381-379/Cleavage site: Met Lys (kallikrein) #status predited
F; 381-379/Cleavage site: A-vdroxvoroline (Pro) #status predited
F; 382-379/Cleavage site: Met Cys (kallikrein) #status experimental
F; 382-379/Cleavage site: Met Cys (kallikrein) #status experimental
F; 382-379/Cleavage site: Met Cys (kallikrein) #status experimental
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A; Title: Studies on 1
A; Reference number: 2
A; Accession: A91938
                                                                                                                                                                                                                                                                                                                                                 F;382/Modified site: 4-hydroxyproline (Pro) **status predicted F;388-389/Cleavage site: Arg-Ser (kallikrein) **status experimental F;398,406,512/Binding site: carbohydrate (Ser) (covalent) **status experimental F;399,400,520,524,536,548,553,570/Binding site: carbohydrate (Thr) (covalent) F;498-499/Cleavage site: Arg-Thr (kallikrein) **status experimental
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A;Contents: annotation; bovine cleavage sites; bovine carbohydrate binding sites R;Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
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A;Accession: A29559
A;Molecule type: protein
A;Residues: 'Z',20-123, 'I',125-127,'I',129-378 <
R;Lottspeich, F.; Kellermann, J.; Henschen, A.;
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A;Title: Bovine high molecular weight kininogen.
A:Beference number: A92627; MUID:87137530
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                                                                              1 HGHEQQHGLGHGHKFKLDDDLEHQGGH
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38; MUID:75170265
нснсн 481
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Pred. No. 0.
                                                                                                                                                            Mismatches
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J.00073;
J.2;
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76 HGHGGGHGGGHQIGHFSDSDDDIEEGIKHV 105

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A;Gene: fsh
A;Gene: fsh
A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Keywords: alternative splicing; transmembrane protein
F;1-2038/product: female sterile homeotic protein, 205K #status predicted
F;1-1106/product: female sterile homeotic protein, 110K #status predicted
F;59-116/pomain: bromodomain homology <BRO1>
                                                                                                                                                                                                                                                                                                                                                                                                          Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of A;Reference number: A84420; MUID:20083487
A;Accession: A84446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:AC005313; NID:g3548797; PID:g3548806
A;Experimental source: cultivar Columbia
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon,
euss, D.; Mierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: Arabidopsis thaliana chromosome II BAC T18E12 genomic sequence A;Reference number: Z14702 A;Accession: T02702
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                                                                                                                                                                                             A; Map position: 2
A; Introns: 219/1; 340/2; 387/1; 417/2; 503/3; 538/3; 603/3; 698/3;
A; Note: T18812.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Accession: T02702; A84446
R;Rounsley, S.D.; Lin, X.; Kaul, S.;
submitted to the EMBL Data Library,
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                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-776 <STO>
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A; Residues: 1-776 < RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein At2g03240 [imported] - Arabidopsis thaliana hypothetical protein T18E12.9 N;Alternate names: hypothetical protein T18E12.9 C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 02-Feb-2001
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A;Residues: 1-1106 <HA2>
A;Cross-references: EMBL:M23222
                                                                                                                                                                                                                                                                    A; Gene: At2g03240
                                                                                                                                                                                                                                                                                                               A;Cross-references: GB:AE002093; NID:g3548806; PIDN:AAC34478.1; GSPDB:GN00139
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A;Accession: B43742
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Best Local S
Matches 11
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HGHEQQHGLGH--GHKFKLDDDLEHQGGHV
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                                                                                                Similarity
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                                                                                             38.3%;
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                                                                      1;
                                                                                           Score 64; DB 2
Pred. No. 0.65;
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Pred. No. 1.
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1.3;
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S66149
                                                                                      gene pipsqueak protein A long form - fruit fly (Dro C;Species: Drosophila melanogaster C;Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 C;Accession: S66149; S66150; T45461 R;Weber, U.; Siegel, V.; Mlodzik, M. EmBO J. 14, 6247-6257, 1995
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Best Local Similarity
"~+~hes 12; Conserv
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C;Superfamily: POZ domain homology
F;21-123/Domain: POZ domain homology <POZ>
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R;Weber, U.; Siegel, V.; Mlodzik, M.
EMBO J. 14, 6247-6257, 1995
               A; Status: preliminary
                                     A; Reference number: A; Accession: S66149
                                                                          A; Title:
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A; Residues: 1-535 <WEB>
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A; Molecule
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A; Residues: 1-436 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MHC H-2K/t-w5-linked ORF precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                    332 HEHEHNHGHGHGH------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity hes 13; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
                                                                                                                                                                                                                            12
                                                                                                                                                                                                                                                                                                                     1 HGHEQQHGLGHGHKFKLDDDLEHQGGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 HGHEQQHG-----LGHGHKFKLDDDLEHQGGH 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10
                                                     pipsqueak encodes a novel nuclear
ace number: S66148; MUID:96134923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HAHSHDHGHSREELHHGHSHGHSHDSLHHGGH 113
                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transmembrane protein with histidine-rich charge clusters encoded I49714; \mbox{\sc MUID}:90097821
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 38.0%;
                                                                                                                                                                                                                                                                                                                                                                             37.48;
                                                                                                                                                                                                                                                                                                                                                           0;
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                                                                                                                                                                                                                                                                                                                                                                           Score 62.5;
Pred. No. 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 63.5; DB Pred. No. 0.42;
                                                                                                                                                                                                                                                                                    -GGH 347
                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                       27
                                                                       protein
                                                                                                                                                                                 fly (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PIDN:CAA62473.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                                                                                                                            BG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (Drosophila melanogaster)
                                                                                                                                                                                                                                                                                                                                                                                              2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14;
                                                                       required
                                                                                                                                                  #text_change 01-Dec-2000
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                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 436;
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                                                                         downstream of
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R; Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A. submitted to the EMBL Data Library, September 1998

A; Reference number: Z21572

A; Accession: T35241

A; Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: DNA

A; Residues: 1-314 <SEE>

A; Cross-references: EMBL:AL031515; PIDN:CAA20646.1; GSPDB:GN00070; SCOEDB:SC5C7.34

A; Genetics:
A; Genetics: SCOEDB:SC5C7.34
                                                                                                  hypothetical protein T20010.200 - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
                                        R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; Zeitler, submitted to the Protein Sequence Database, April 2000
                                                                                                                                                                       RESULT
T48099
                                                                                  C; Accession:
                                                                                                                                                                                                                                                                                                         Q
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Introns: 427/3
C;Function:
C;Function:
A;Description: required for establishing polarity
C;Superfamily: POZ domain homology
E;21-123/Domain: POZ domain homology <POZ>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 1-355,'E',357-1005,'H',1007-1020,'Q',1021-1061,'ERS'
A; Residues: 1-355,'E',357-1005,'H',1007-1020,'Q',1021-1061,'ERS'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: DNA  
A;Residues: 'MQ',428-1085 <WE2>  
A;Residues: 'MQ',428-1085 <WE2>  
A;Cross-references: EMBL:X90986; NID:g1149498; PIDN:CAA62475.1; PID:g1149501  
R;HOTOWitz, H.; Berg, C.A.  
Development 122, 1859-1871, 1996
A; Accession:
                      A; Reference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: The Drosophila pipsqueak gene encodes a nuclear BTB-domain-containing protein A; Reference number: Z22972; MUID:96232300 A; Accession: T45461
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A;Accession: S66150
A;Status: preliminary
A;Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                                    Matches
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Best Local :
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                      number:
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                                                                                                                                                                                                                                                                                                                                                    Conservative
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                        Z24484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              37.4%;
                                                                                                                                                                                                                                                                                                                                                                          37.1%;
76.9%;
                                                                                                                                                                                                                                                                                                                                                  0;
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                                                                                                                                                                                                                                                                                                                                                                      Score 62; DB 2; Pred. No. 0.47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 62.5;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                          Length 314;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1085;
                                                            K.; Mewes, H.W.; Rudd,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11;
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Search completed: July Job time: 647 sec

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A;Authors: Shownkeen, R.; Sims, M.; Smaldon, N.; Smith, A.; Smith, M.; Sonnhammer, E. tock, L.; Wilkinson-Sproat, J.; Wohldman, P. A;Title: 2.2 Mb of contiguous nucleotide sequence from chromosome III of C. elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              hypothetical protein Y3986B gg [imported] - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jul-2000 C;Accession: T45059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
A; Introns: 163/2
A; Note: T20010.200
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A;Experimental source:
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <OBE>
                                                                                                                                                                                                                                                          A; Experimental source: clone Y39B6B C; Genetics:
                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-735 <WIL>
                                                                                                                                                                                                                                                                                                                                                                                     A;Reference number: S43531; MUID:94150718
A;Accession: T45059 .
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Best Local
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    516
                                                                                  Local Similarity
mes 11; Conserv
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                                          HGHEQQHGLGHGHKFKLDDDLEHQGGH 27
НСИНСЕНСТИНСИНСЕНИНАРАНИСИИ 542
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                                                                                  Conservative
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ce: cultivar Columbia; BAC
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                                                                                                    36.5%;
                                                                                                    Score 61;
Pred. No.
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                                                                                                                          DB 2;
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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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                                                                                                                                                                                                                                                               No
   33228754331115432133222223233333222354333333228
                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                             Score
 Match
                                                                                                                                                                                                                                                                                                                                                                                                                                BLOSUM62
Gapop 10.0 , Gapext 0.5
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                                                                                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries
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167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGHEQQHGLGHGHKFKLDDDLEHQGGHV 28
                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                         644
639
661
619
621
693
2038
 DB
                                                                                                                                                                                                       KNG_MOUSE
KNH2_BOVIN
KNH1_BOVIN
CAUP_DROME
       SLYD_AERHY
HSF8_LYCPE
CH38_DROME
BAF1_KLUMA
PO3A_XENLA
Z255_HUMAN
                                                   TRC5_ECOLI
D29B_ARATH
ZNT1_MOUSE
ZNT1_RAT
                                                                                 ANTF_SARPE
TRC4_ECOLI
                                                                                                KE4_BRARE
BOX5_NOTVI
                                                                                                               S109_RABIT
KE4_HUMAN
HYPB_BARAJA
HYPB_RHOCA
ZNUA_HAEIN
VG50_HSV11
COT1_YEAST
FILA_MOUSE
                                                                                                                                                                          CSUP_DROME
KE4L_CAEEL
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KE4_MOUSE
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                                                                                                                                                                                                                                                                                     SUMMARIES
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P01045 bos taurus
P01044 bos taurus
P04269 drosophila
P13709 droson***
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Q9uid9
Q16825
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Q06737
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P41153
P07183
                                                                                 P11088
Q9pub8
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Q00130
P32798
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Q92504
Q45257
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                                                                                                                                                                                                                                      P08934 rattus norv
                                                                                                                                                                                                                                             P01042 homo sapien
                                                                                                                                                                                                                                                             Description
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4 drosophila
7 caenorhabdi
                     7 sarcophaga
9 escherichia
0 escherichia
10 escherichia
11 arabidopsis
12 mus musculu
12 rattus norv
13 aeromonas h
13 copersico
13 drosophila
14 kluyveromyc
                                                                                                8 saccharomyc
8 mus musculu
8 brachydanio
1 notophthalm
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4 homo sapien
7 bradyrhizob
0 rhodobacter
6 haemophilus
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               xenopus lae
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| \$                 | 44                | 43         | 42        | 41         | 40         | 39         | 38                | 37        | 36                | 35         | 34         |
|--------------------|-------------------|------------|-----------|------------|------------|------------|-------------------|-----------|-------------------|------------|------------|
| 40                 | 48                | 48         | 48        | 48         | 48         | 48         | 48                | 48        | 49                | 49         | 49.5       |
| 28.7               | 28.7              | 28.7       | 28.7      | 28.7       | 28.7       | 28.7       | 28.7 .            | 28.7      | 29.3              | 29.3       | 29.6       |
| 0/87               | 601               | 562        | 510       | 382        | 142        | 142        | 139               | 59        | 419               | 108        | 414        |
| -                  | ىر د              | μ.         | ٠         | $\vdash$   | ш          | μ.         | _                 | μ.        | Н                 | Ъ          | ഥ          |
| NUVBLAHLME         | PDM1_DROME        | TPP1_MOUSE | FKH_DROME | YHH6_YEAST | SALA_DROOR | SALA_DROME | SALA_DROSI        | HPN_HELPY | GSC_DROME         | AGN3_APLCA | Y288_MYCGE |
| P204/1 Inizobium m | P31368 drosophila | _          |           | _          |            | _          | P21749 drosophila | •         | P54366 drosophila | .,         | _          |

# ALIGNMENTS

| RA<br>RT                                                                                  | RR  | R.                                      | R 3                                                     |                                   | RP                   | RN  | RL | RT | RT                                                                   | RA | RA                                                      | RX                                | RP                   | RN  | RE.                             | D T                                     | 8 F                                                         | RX          | RP | RN | RL | RT | RT                                                                   | RA | RA | RX                                | RP.             | R  | R.                                    | 1 50 | N F                | A E           | RX            | RC            | RP                                         | RN | ox :    | 200                              | 3 6 | 0 2 |                                         | D<br>E         | DT                                            | D DI                                                                       | AC   | ID                               | RES      |
|-------------------------------------------------------------------------------------------|-----|-----------------------------------------|---------------------------------------------------------|-----------------------------------|----------------------|-----|----|----|----------------------------------------------------------------------|----|---------------------------------------------------------|-----------------------------------|----------------------|-----|---------------------------------|-----------------------------------------|-------------------------------------------------------------|-------------|----|----|----|----|----------------------------------------------------------------------|----|----|-----------------------------------|-----------------|----|---------------------------------------|------|--------------------|---------------|---------------|---------------|--------------------------------------------|----|---------|----------------------------------|-----|-----|-----------------------------------------|----------------|-----------------------------------------------|----------------------------------------------------------------------------|------|----------------------------------|----------|
| Sueyoshi T., Miyata T., Kato H., Iwanaga S.; "Disulfide bonds in bovine HMW kininogens."; | [6] | 3 2 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 3 | "Structural features of plasma kining and kininggens ". | MEDITINE=9020062; PubMed=4902632; | SEQUENCE OF 381-389. | [5] | •  |    | "The amino acid sequence of the light chain of human high-molecular- |    | Lottspeich F., Kellermann J., Henschen A., Foertsch B., | MEDLINE=86030270; PubMed=4054110; | SEQUENCE OF 379-644. | [4] | Biochemistry 73:5691-5697(1984) | 111111111111111111111111111111111111111 | TISOLATION OF A NUMBER CHARLES ALL SHICKGWG H., SGESGKI H.; | ed=6441591; |    |    |    |    | "Structural organization of the human kininogen gene and a model for |    |    | MEDLINE≈85234583; PubMed=2989294; | GENE STRUCTURE. | ٠. | J. Biol. Chem. 260:38601-88609(1985). |      | man nigh molecular | for home ties | 4582; PubMed= | TISSUE=Liver; | SEQUENCE FROM N.A. (ISOFORMS HMW AND LMW). |    | D=9606; | Primates: Catarrhini: Hominidae: |     |     | S NO S TO | ECURSOR (ALPHA | 01-OCT-2000 (Rel. 40, Last annotation update) | 21-JUL-1986 (Rel. 01, Created) 01-FEB-1996 (Rel. 33, Last sequence update) | 043; | KNG_HUMAN STANDARD; PRT; 644 AA. | RESULT 1 |

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                                                                                        Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSTIE; PS00287; CYSTATIN; 2.
Glycoprotein; Plasma; Repeat; T
Bradykinin; Blood coagulation;
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between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FACTOR XII; (3) HAW-KININGGEN INHIBITS THE THROMBIN-AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HAW-KININGGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION OF OAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA EMDOTHELIUM-DERIVED RELAXING FACTOR ACTION), INDIRECTLY VIA EMDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5) LMW-KININOGEN IS IN CONTRAST TO HMW-KININOGEN NOT INVOLVED IN BLOOD
                                                             SIGNAL
                                                                              Alternative
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                                                                                                                                                                                                                                       MIM; 228960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                             InterPro; IPR000010; -. InterPro; IPR002395; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOW PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININGGEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLOTTING.
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M11437;
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KININOGEN HEAVY CHAIN
BRADYKININ.
                                                                                            Thiol protease inhibitor; Vasodilator;
; Inflammatory response; Signal;
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                                                             SEQUENCE FROM N.A. (ISOFORMS HMW MEDLINE=87137443; PubMed=3029068;
                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10116;
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gene family.";
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CYSTATIN-LIKE 3.
CYSTATIN-LIKE 3.
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Pred. No. 2.9e-15;
; Mismatches 0;
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DR EMBL; M14369; AAA41485.1; ALT_SEQ.
DR EMBL; M14369; AAA41485.1; ALT_SEQ.
DR EMBL; M16455; AAA41485.1; -.
DR PIR; A28486; A25486.
DR PIR; A28055; A28055.
DR InterPro; IPR000010; -.
DR InterPro; IPR002395; -.
DR InterPro; IPR002395; -.
DR PIR; PR00331; Cystatin; 3.
DR PRINTS; PR00331; Cystatin; 3.
DR PRINTS; PR00337; CYSTAPIN; 2.
DR PROSITE; PS00287; CYSTAPIN; 2.
DR PRINTS;                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TO ITELEMENT IN CONTRACT

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"Structure and expression of the genes for major acute phase alpha 1-
protein (thiostatin) and kininogen in the rat.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
TISSUE SPECIFICITY: PLASMA.
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DOMAIN
HMW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PERKALLKERIN AND FACTOR XI MAD PATION OPTIMALLY PERKALLKERIN AND FACTOR XI NEXT TO
FACTOR XII, (3) HMW-KININGEN INHERITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION ACAUSES (4E1) INCREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTACIANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION); (5)
LMM-KININGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMM-
                                                                                                                                                                                                                            STRAIN-C57BL/6 x CBA; TISSUE=Liver; Takano M., Kondoh J., Yayama K., Okamo Molecular cloning of cDNAs for mouse
                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                             KNG.
                                                                                                                                                                                    Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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PRINTS; PR00334; KININOGEN.
PROSITE; PS00287; CYSTATIN; 1.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS; HMW (SHOWN HERE) AND LMW
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IPR003243; -
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                                                           STANDARD;
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73102
                                                                                                                                                                                                                                                 58.4%;
Created)
Last sequence update)
                                                                                                                                                                                                                                                                                                                          WW;
                                                                                                                                                                                                                                               Score 97.5; DB 1;
Pred. No. 7.3e-06;
                                                                                                                                                                                                                                                                                                                          MISSING (IN ISOFORM LMW). 774460258D58796E CRC64;
                                                                                                                                                                                                                                                                                                                                                                        N-LINKED (GLCNAC. . .) (POTENTIAL).

"-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

N-LINKED (GLCNAC. . .) (POTENTIAL).

VSPPYIAREQEERDAETEQGPTHGHGWLHEKQ ->
CEYKGRLSKAGAEPAPERQAESSQVKQ (IN ISO)
                                                                                                                                                                                                                                                                                                                                                               (MM)
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MBL outstation -
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HUNCTION: (1) KININGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
HWA-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HWW-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE
PETTIDE BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS; (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STINULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ

OCTION INDUCEDITY OF AND CREASE OF AND CAUSES (4E3)
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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MEDILINE=84014106; PubMed=6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T.,
"A single gene for bovine high molecular weight
weight kininogens.";
Nature 305:545-549(1983).
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J. Biochem. 77:55-68(1975).
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Mammalia; Eutheria;
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KININOGEN, HMW II PRECURSOR (THIOL PROTEINASE INHIBITOR) [CONTAINS:
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 Biochem.

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Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
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SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HMW II AND LMW II KININOGEN PRECURSORS
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                                                                                      PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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                                                                                                                                                                                   TO RESIDUE 398
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PubMed=1169237;
Suzuki T.;
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Mammalia; Eutheria;
Bovidae; Bovinae; Bc
NCBI_TaxID=9913;
                                                                                 21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
KININOGEN, HMW I PRECURSOR (THIOL PROTEINASE INHIBITOR) [CONTAINS:
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Eukaryota; Metazoa;
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EMBL; V01492;
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                                                                         BRADYKININ]
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                                                                                                                                                      BOVIN
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B29559; B29559.
                                                                                                                                                                                                                          HGHQKQHGLGHGHK-----HGHGH 479
                                                                                                                                                                                                                                                    HGHEQQHGLGHGHKFKLDDDLEHQGGH 27
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                  454
619
                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAA24736.1; -.
CAA24737.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                  AA;
                                                                                                                                                        STANDARD;
                  Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cetartiodactyla;
                                           Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                  68710 MW;
                                                                                                                                                                                                                                                                                            50.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIGHT CHAIN.

CYSTATIN-LIKE 1.

CYSTATIN-LIKE 2.

CYSTATIN-LIKE 3.

PYRROLIDONE CARBOXYLIC A

N-LINKED (GLCNAC...).
                                                                                                                                                                                                                                                                             Score 85; DB Pred. No. 0.00 2; Mismatches
                                                                                                                                                                                                                                                                                2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-LINKED (GLCNAC. . N-LINKED (GLCNAC. . N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        OR 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PARTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BRADYKININ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INTERCHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            KININOGEN,
                                                                                                                                                                                                                                                                                                                                                 -> P.
-> V.
-> K.
F04320A8EB0EE0DA CRC64;
                               Ruminantia; Pecora; Bovoidea;
                                                                                                                                                      621
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MMH
                                                                                                                                                      A
                                                                                                                                                                                                                                                                                             .00033
                                                                                                                                                                                                                                                                                                       Length 619;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (PARTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACID
                                                                                                                                                                                                                                                                             8
                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                             1:
    PIR;
PIR;
                         Pfam; PF00031; Cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN;
                                                                                                                                                                                                                                                                                                                                                 - -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sueyoshi T., Miyata T., Miyata T., Miyata T., Iwanaga S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 19-378. MEDLINE-87137530; F
                                                                                PIR; A01281; KGBOH1
PIR; A29559; A29559
InterPro; IPR000010
                                                                                                                           EMBL; V01491; CAA24735.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-75170265;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 458-498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=70180420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 378-393.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "A single gene for bovine weight kininogens.";
Nature 305:545-549(1983).
[2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=84014106; PubMed=6571699;
                                                                    InterPro; IPR002395;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kitamura N., Takagaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Biochem. 67:313-323(1970).
                                                                                                                                                                                                                                                                                          TO RESIDUE 400
TISSUE SPECIFIC
                                                                                                                                                                                                                                                                                                                                                                            ACTION)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           portion."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem.
                                                                                                                                                                                                                                                                                            SPECIFICITY: PLASMA
                                                                                                           KGBOH1.
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HIGHTON: (1) KININGÉNIS ARE INHIBITORS OF THIOL PROTEASES; (2)

HMW-KININGEN. PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT
TO FACTOR XII; (3) HMW-KININGEN INHIBITS THE THROMBIN- AND
PLASMIN-INDUCED AGGREGATION OF THROMBOLYTES; (4) THE ACTIVE
PEPPIDE BRADYKININ THAT IS RELEASED FROM HWW-KININGEN SHOWS
A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH
MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)
NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL,
(4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE
IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3)
RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS),
(4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ
ACCTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                               between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Han Y.N., Komiya M., Iwanaga S., Suzuki T.;
"Studies on the primary structure of bovine high-molecular-weight kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
Glycoprotein; Plasma; Duplication; Vasodilator; Alternative Thiol protease inhibitor; Bradykinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Bovine high molecular weight kininogen. The amino acid positions of carbohydrate chains and disulfide bridges i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               kato H., Nagasawa S., Suzuki T.;
"Studies on the structure of bovine kininogen:
ponds and of methionyl bonds in kininogen-II.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN. SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: EXTRACELLULAR.
ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS A PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    262:2768-2779(1987)
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bovine high molecular weight
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hashimoto N.,
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RESULT 6
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Matches 15
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CHAIN
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                                                                                                                                                                                                                                                                                                             Gomez-Skarmeta J.-L., del Corral R.D., de la Ferres-Marco D., Modolell J.; "Araucan and caupolican, two members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-1996
01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P54269;
01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HOMEOBOX PROTEIN CAUPOLICAN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CAUP_DROME
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=96180722; PubMed=8620542;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CARBOHYD
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SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly)
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                                                                                                                                                              FUNCTION: CONTROLS PRONEURAL AND VEIN FORMING GENES. POST TRANSCRIPTIONAL CONTROLER OF AC-SC (ACHAETE-SCUTE). MAY AVACTIVATOR THAT INTERACTS WITH THE TRANSCRIPTIONAL COMPLEX ASSEMBLED ON THE AC AND SC PROMOTERS AND PARTICIPATES IN TRANSCRIPTION INITIATION.

SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
                                                                                                                                                 SIMILARITY: BELONGS TO THE TALE/IRO FAMILY OF HOMEOBOX PROTEINS
                                                                                                                                                                                                                                                                         de homeoproteins that control 85:95-110(1996).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 Similarity
15; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (Rel. 34,
(Rel. 34,
(Rel. 40,
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Best Local
                                    EMBL; M23221; AAA28540.1; -
EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; -
EMBL; M15763; AAA70423.1; -
EMBL; M15763; AAA70422.1; -
EMBL; M15764; AAA70422.1; -
PIR; A43742; A43742
HSSP; P04002; 1WFA.
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P13709; P13710;
O1-JAN-1990 (Rel. 13, Created)
O1-JAN-1990 (Rel. 13, Last sequence update)
O1-OCT-1996 (Rel. 34, Last annotation update)
FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE PROTEIN).
FS(1)H OR FSH.
                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                  between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a
                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: REQUIRED MATERNALLY FOR PROPER EXPRESSION OF HOMEOTIC GENES INVOLVED IN PATTERN FORMATION, SUCH AS -!- SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN.
-!- SIMILARITY: CONTAINS 2 BROMODOMAINS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           apparent membrane proteins.";
Dev. Biol. 134:246-257(1989).
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MEDLINE=89276730; PubMed=2567251;
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Q31125; Q9Z1W1;
01-NOV-1997 (Rel
                                                    the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-2000 (Rel. 40, Last sequence update)
01-CCT-2000 (Rel. 40, Last annotation update)
HISTIDINE-RICH MEMBRANE PROTEIN KE4.
                                                                                                                                                                                                                                  Rowen L., Qin S., Madan A., Loretz C., James R., Dors Hall J., Lasky S., Hood L.; "Sequence of the mouse major histocomaptibility locus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                    EMBL; M32010; AAA37767.1;
                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL
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"A putative transmembrane protein with histidine-rich charge clusters encoded in the H-X/tw5 region of mice.";
Mol. Cell. Biol. 10:138-145(1990).
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11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS00633; BROMODOMAIN_1;
PS50014; BROMODOMAIN_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51
495
945
330
451
750
790
816
874
1731
1939
909
1022
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1106
350
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810
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1959
1959
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Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         09 G -
22 H -
205332 MW;
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BROMODOMAIN
ET DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciurognathi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Craniata; Vertebrata; Euteleostomi;
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* RKPYY.
849E0706D50A0098 CRC64;
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0.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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                                                                                                                                                         EMBL outstation
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                                                                                                                                                         collaboration
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     RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barandon R.C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Barandon R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beesson K.Y., Benos P.V., Berman B.P., Bhandari D., Bottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenportt L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Evangelista C.C., Ferraz C., Ferristra S., Fleischmann W.,
RA Hortin R., Gary N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Hortin D. Huston K.A Howland T.J. Hernandez J.R., Houck J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 13
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TRANSMEM
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TRANSMEM
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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=99403013; PubMed=10471719; Stathakis D.G., Burton D.Y., McIvor W.E., Krishnakumar S., Wright T.R., O'Donnell J.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CSUP_DROME STANDARD; PRT; 4
09V3A4;
01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence up
01-OCT-2000 (Rel. 40, Last annotation
CATECHOLAMINES UP PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TRANSMEM
TRANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata;
Pterygota; Neoptera; Endopterygota; Diptera
                                                                                                                                                                                                                                                                                                                       MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                   STRAIN-BERKELEY;
                                                                                                                                                                                                                                                                                                                                                                                                "The catecholamines up (Catsup) protein of Drosophila melanogaster functions as a negative regulator of tyrosine hydroxylase activity."; Genetics 153:361-382(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CATSUP OR CG10449
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                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Drosophilidae; Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MGI:95909;
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13; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 476
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197
197
242
413
437
136
274
274
476
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Pred. No. 0.2;
0; Mismatches
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V -> L (IN REF. 1).
ACALITEGRAVDSDVAGGAGPGWVLPTTAGGFIYVATVSVL
PELLREASPLQSLLEVLGLLGGVAMMVLIAHLE -> RVPF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HIS-RICH.
HIS-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SPREGQWTVTWQVVQVLAGSCHSLQADLST (IN REF.
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a; Brachycera; Musc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
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RESULT 10
KE4L_CAEEL
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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Llang Y., Lin X.,

RA Lu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D. L.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Spier E., Spradling A.C., Simpson M., Skupski M.P., Smith T.,

RA Syliskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Wassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Wang Z.-Y., Nassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Nassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Wang Z.-Y., Nassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Wang Z.-Y., Nassaaman D.A., Weinstock G.M., Weissenbach J.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou S., Zhu S., Zhu X., Smith H.O.,

RA Zheng X.H., Zhong F.N., Robin G.M., Venter J.C.;

"The genome sequence of Drosophila melanogaster.";

RI SUBCELULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).

C. -: SIMILARITY: BELLONGS TO THE KE4/CATSUP FAMILY.

C. -: SIMILARITY: BELLONGS TO THE KE4/CATSUP FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                             01-OCT-2000
                                                                                                                                                                                                                                                                01-OCT-2000
                                                                                                                                                                                                                                                                                  Q9XTQ7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TRANSMEM CARBOHYD
   Submitted -!- SUBCE
                                                 (1)
SEQUENCE FROM N.A.
PRISTOL N2;
                                                                                                                            Eukaryota; Metazoa; Nemata
Rhabditidae; Peloderinae;
                                                                                                                                                                  Caenorhabditis elegans
                                                                                                                                                                                        H13N06.5
                                                                                                                                                                                                         HYPOTHETICAL
                                                                                                                                                                                                                            01-OCT-2000
                                                                                                                                                                                                                                                                                                   KE4L_CAEEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the European Bioinformatics Institute.
                                      Lennard N.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FlyBase;
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                                                                                                                                                                                                                                                                                                                                                                                               83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                1 HGHEQQHGLGHGHKFK-LDDDLEHQGGH 27
nitted (OCT-1997) to the EMBL/GenBank/DDBJ databases.
SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                                                                                                                                             НDHDHGHDHGHHHHGHDHDHDHDHGH 110
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0 (Rel. 40, Last sequ
0 (Rel. 40, Last anno
AL KE4-LIKE PROTEIN H
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167
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                                                                                                                                                                                                                                                                                                   STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39
155
187
242
391
415
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                                                                                                                              Nematoda; Chromadorea; Rhabditida; Rhabditoidea; rinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                48658
                                                                                                                                                                                                     Last sequence update)
Last annotation update)
PROTEIN H13N06.5 IN CHROMOSOME
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POTENTIAL.
N-LINKED (GLCNAC. . .) (POTENTIAL)
F7111A254C07AB4C CRC64;
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RESULT 11
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ID S109_RABIT
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01-OCT-1996
15-JUL-1999
01-OCT-2000
                      MORI S., GOTO K., GOTO F., MUTAKAMI K., Ohkawara S., YOShir "Dynamic changes in mRNA expression of neutrophils during to facute inflammation in rabbits.";
Int. Immunol. 6:149-156(1994).
-!- SIMILARITY: BELONGS TO THE S-100 FAMILY.
-!- SIMILARITY: CONTAINS 2 EF-HAND CALCIUM-BINDING DOMAINS.
                                                                                                                                                                                                                                                                                                                                           15-JUL-1999 (Rel. 38, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
CALGRANULIN B (MIGRATION INHIBITORY FACTOR-RELATED PROTEIN 14)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CARBOHYD
CARBOHYD
                                                                                               SEQUENCE OF 45-82 FROM N.A. STRAIN-NEW ZEALAND WHITE; MEDLINE=94198229; PubMed=8148323;
                                                                                                                                                  "Rabbit polymorphonuclear neutrophils form 35S-labeled S-sulfo-calgranulin C when incubated with inorganic [35S]sulfate.";
J. Biol. Chem. 271:19802-19809(1996).
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CARBOHYD
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TRANSMEM
This SWISS-PROT entry
                                                                                                                                                                                                   MEDLINE=96355278; PubMed=8702688;
Yang Z., de Veer M.J., Gardiner E.E.,
                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=NEW ZEALAND
                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vej
Mammalia; Eutheria; Lagomorpha; Leporidae;
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Oryctolagus cuniculus (Rabbit).

Oryctolagus cuniculus (Rabbit).

Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                    S100A9 OR MRP-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                         Underwood J.R., Robinson H.C.;
                                                                                                                                                                                                                                                                NCBI_TaxID=9986;
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                                                                         K., Ohkawara S., Yoshinaga M.;
of neutrophils during the cour;
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is produced through a collaboration
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European Bioinformatics Institute.

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SEQUENCE
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Q92504; Q9UIQ0;
Q1-CCT-2000 (Rel. 40, Created)
Q1-CCT-2000 (Rel. 40, Last seq
Q1-CCT-2000 (Rel. 40, Last ann
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DOMAIN
       Tubby B.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
                                                                                                    [2]
SEQUENCE FROM N.A.
Lana I.,
                                                                                                                                           Chen L., Ikemura T., Abe K., Kimura M., Inoko H.; "cDNA cloning of the human homologues of the mouse at the centromeric end of the human MHC region.";
                                                                                                                                                                          Ando
                                                                                                                                                                                 SEQUENCE FROM N.A. TISSUE=Kidney; MEDLINE=97001166;
                                                                   Submitted
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                                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                            "Molecular cloning flanking region.";
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SUBCELLULAR LOCATION TISSUE SPECIFICITY: AND PANCREAS.
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3; PS00018; EF_HAND; 1.
5; PS00303; S100_CABP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                           Similarity 9; Conserv
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                                                                                                                                                                        Kikuti Y.Y.,
                                                                  (DEC-1998)
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01-NOV-1997
15-JUL-1999
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TRANSMEM 138
TRANSMEM 139
TRANSMEM 169
TRANSMEM 214
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CONFLICT
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                                                                                                                                                                       Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group; Bradyrhizobium group; Bradyrhizobium.
NCBI_TaxID=375;
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                                                                                                                                                                                                        Bradyrhizobium japonicum.
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by non-profit institutions as long
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                                       Acta 1184:135-138(1994).

WORK IN THE MOBILIZATION OF N.
9 NICKEL IONS PER MOLECULE.

ELONGS TO THE HYPB/HUPM FAMILY
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Pred. No. 0.93
1; Mismatches
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ELLREASPLQSLLEVLGLLGGVIMMVLIAHLE -> VPFSL
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                                                           OF NICKEL INTO HYDROGENASE
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01-AUG-1992
01-NOV-1997
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P26410;
             Nickel.
                                                    PIR; D38532; D38532.
PIR; S21903; S21903.
                                                                            EMBL; X61007; CAA43326.1; -. EMBL; M55089; AAA72926.1; -.
                                                                                                              entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                       the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                     Colbeau A., Richaud P., Toussaint B., Caballero F.J., Elster C., Delphin C., Smith R.L., Chabert J., Vignais P.M.;
"Organization of the genes necessary for hydrogenase expression Rhodobacter capsulatus. Sequence analysis and identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhodobacter capsulatus (Rhodopseudomonas capsulata)
Bacteria; Proteobacteria; alpha subdivision; Rhodob
                        Pfam; PF01495; HypB_UreG;
                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                     Xu H.W., Wall J.D.;
"Clustering of genes necessary for hydrogen oxidation in Rhodobacter
                                                                                                                                                                                                                                                                                            MEDLINE-91177833;
                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                          Rhodobacter capsulatus. Sequence hyp regulatory mutants.";
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                                        InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=93268090; PubMed=8497190;
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                                                                                                                                                                                                                             Bacteriol. 173:2401-2405(1991 FUNCTION: COULD BE INVOLVED
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                                                                                                                                                                                                                                                                               H.W., Wall J.D.;
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                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE HYPB/HUPM FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OR HUPM.
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                                                                                                                                                                           the Swiss Institute of Bioinformatics and the
                                        IPR002894;
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(Rel. 23, Last sequence update)
(Rel. 35, Last annotation update)
EXPRESSION/FORMATION PROTEIN HYPB
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THE THYOLVED IN NICKEL BINDING AND
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32737 MW;
  35342 MW;
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B7276C3E1AA0FD02 CRC64;
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P44526;
01-NOV-1995 (Rel. 3
01-NOV-1995 (Rel. 3
15-DEC-1998 (Rel. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F. Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M. McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                                                                              Zinc; Transport.
DOMAIN 115
                                                                                                                                                                        InterPro; IPR001987; -.
Pfam; PF01297; Lipoprotein_4; 1.
                                                                                                                                                                                                    EMBL; U32698; AAC21794.1; TIGR; HI0119; -.
                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for con
                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                           Science 269:496-512(1995).
-!- FUNCTION: INVOLVED IN THE HIGH-AFFINITY ZINC SYSTEM (BY SIMILARITY).
                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                              SYSTEM (BY SIMILARITY).
-!- SIMILARITY: BELONGS TO THE FIMA/PSAA/SSAB/SCAA FAMILY.
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MEDLINE-95350630;
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                                                                                                                                                                                                                                                                                                                                                                                                                        "Whole-genome random sequencing and influenzae Rd.";
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C UPTAKE SYSTEM PROTEIN ZNUA
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PubMed=7542800;
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37.0%;
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40.7%;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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09v5n1 drosophila
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086731 streptomyce
091yb2 arabidopsis
09nes7 caenorhabdi
081036 arabidopsis
027920 bradysia hy
                                                                               Q9nnv9 plasmodium
Q9w3l3 drosophila
                                                                                                Q9jkn1 mus musculu
Q9gtn0 drosophila
Q9vwx5 drosophila
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Q9v3p9 drosophila
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09vu00 drosophila
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| HGHEQQH<br>   :: <br> HGHQKPH                                 | ch<br>1 Simi<br>18;                                                  | 6 0 0 0 0 1 · 6 1 0 6                                                                                                                                     | 01-JUL 1997 (Tr<br>01-JUL 1997 (Tr<br>01-CCT-2000 (Tr<br>K-KININOGEN (FR<br>KNGK.<br>Rattus norvegic<br>Eukaryota; Meta<br>Mammalia; Euthe<br>NCBL TaxID-1011<br>[1] | 16.          |            | 55 55 55 55 55 55 55 55 55 55 55 55 55                                                                    | 15 7                                                                               | ហ ហ ហ ហ ហ ហ<br>យ យ យ យ យ យ                                                                                                    | 5<br>8<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>5<br>6<br>6<br>7<br>7<br>7<br>7<br>7<br>7<br>7                                                           | 59.5<br>59                 |
| HGHEQQHGLGHGHKFKLDD<br>   ::      :   <br>HGHQKPHGLGHGHQLKLDD | larity<br>Conserva                                                   | N.A.<br>88;<br>11c d<br>11c d<br>1239<br>10239<br>14; K<br>11                                                                                             | (Trembli<br>(Trembli<br>(Trembli<br>(FRAGME)<br>)<br>jicus ()<br>jicus ()<br>jicus ()<br>jicus ()<br>jicus ()                                                        | PRELIMINARY  |            |                                                                                                           | ω 4 4 4                                                                            | 44444                                                                                                                         |                                                                                                                                                                      | л (л (л                    |
| KLDD-<br>KLDDI                                                | 59.<br>50.<br>tive                                                   | A.  By Pubmed-9321484  Igor M.R., Innes  deletions in ex allow mapping of 791-792(1997). AAC09070.1; - 2395; - 2395; - KININGEN. 1126 126 128             | de C                                                                                                                                                                 | VARY;        |            | 24<br>250<br>255<br>366<br>189                                                                            | 168<br>213<br>554<br>102                                                           | 119<br>378<br>398<br>494<br>495                                                                                               | 245<br>245<br>348<br>457<br>457<br>457<br>511<br>505                                                                                                                 | 201<br>79                  |
| KQQ                                                           |                                                                      | =932<br>In<br>In<br>Spin<br>Spin<br>Spin<br>1;<br>1;                                                                                                      | 04,<br>04,<br>15,<br>15,                                                                                                                                             |              |            |                                                                                                           |                                                                                    |                                                                                                                               | 555555555                                                                                                                                                            | 10                         |
| HGHEQQHGLGHGHKFKLDDDLEHQGGH 27                                | Score 98.5; DB 11; Length Pred. No. 2.4e-06; 3; Mismatches 6; Indels | B.A., Harrap S.B., on 10 of rat.K-kini both genes to rat                                                                                                  | Treated)  Last sequence update)  Last annotation update)  Craniata; Vertebrata;  Sciurognathi; Muridae;                                                              | PRT; 126 AA. | ALIGNMENTS |                                                                                                           |                                                                                    |                                                                                                                               |                                                                                                                                                                      | Q9KNX6<br>Q9M435<br>Q6A306 |
|                                                               | th 126;<br>ls 9; Gaps 1;                                             | Koike G., nogen and T1- chromosome 11.";                                                                                                                  | Euteleostomi;<br>Murinae; Rattus.                                                                                                                                    |              |            | Q9Kp2/ Vibrio choi<br>Q61571 mus musculu<br>Q61570 mus musculu<br>Q9vgs1 drosophila<br>Q9pj12 campylobact | Q9vwm5 drosophila<br>Q9x8j8 streptomyce<br>Q9w4c1 drosophila<br>Q94189 caenorhabdi | Q9vyp3 drosophila<br>Q9lxs1 arabidopsis<br>Q9zt63 arabidopsis<br>Q9zt63 drosophila<br>Q9vex1 drosophila<br>Q18009 caenorhabdi | 054396 plsum sativ O9xel3 picea glauc O9w2x1 drosophila Q26227 rhynchoscia O9w416 drosophila O9vxg3 drosophila O9vxg3 drosophila O9v2s4 drosophila O9w2s4 drosophila | ~                          |

PRELIMINARY;

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RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibeywam C.,
RA Liu X., Mattei B., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Syradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Skupski M.P., Wang X.,
RA Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhon S., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
CC -!- SUBCELLUAR LOCATION: NUCLEAR (BY STMILARTY).
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A Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
A George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
A Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
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A Barandon R.C., Rogers Y.-H.C., Blazej R.G., Miklos G.L.G.,
A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.G.,
Baldwin D., Baxendale J., Bayakataroglu L., Beasley E.M.,
A Beleson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Bentova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Burtis K.C., Busan D.A., Butler H., Cadieu E., Center A., Chandra I.,
A Gersty J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
A Gerbios B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
                                                                                                                 Query Match
Best Local
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SEQUENCE 693
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InterPro; IPR001356; -
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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                                                                                                                                                                                                                                                                        PROSITE; PS00027; HOMEOBOX_1; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                          Pfam; PF00046; homeobox; 1.
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RC STRAIN=BERKELEY;

RX MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

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RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

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Q9V3P9;
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Q9GTN1;
01-MAR-2001
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda;
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
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Schmid K.J., Aquadro C.F.;
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NCBI_TaxID=7240;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.28;
46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              13,
13,
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70.5; DB Pred. No. 0.029;
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RAILMMEI B.E., Kodira C.D., Kraft C., Kennison J.A., Ketchum K.A., Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X., RA Liu X., Mattei B., McIntosh T.C., McIeod M.P., McPherson D., RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., RA Mount S.M., Moy M., Murphy B., Murphy L., Muzphy D.M., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syiskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q.A., Ra Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu X., Smith H.O., RA Zhence 287:2185-2195(2000).
Q9VWS0
ID Q9
AC Q9
DT 00
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Best Local S
Matches 14
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InterPro; IPR002395; -.
Pfam; PF00379; insect_cuticle; 1
PRINTS; PR00947; CUTICLE
PRINTS; PR00334; KININOGEN.
PROSITE; PS00233; CUTICLE; 1.
01-MAY-2000 (Tri
01-MAR-2001 (Tri
CG6632 PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S.E., Agbayani A., Arcaina T.T., Baxter E., Blazej R.G., Butenhoff C., Champe M., Chavez C., Chew M., Ciesiolka L., Doyle (Farfan D.E., Galle R., George R.A., Harris N.L., Hoskins R.A., Houston K.A., Hummasti S.R., Karra K., Kearney L., Kim E., Lee B. Lewis S., Li P., Lomotan M.A., Mazda P., Moshrefi A.R., Moshrefi Nixon K., Pacleb J.M., Park S., Pfeiffer B., Poon L., Sequeira A. Sethi H., Shir E., Svirskas R.R., Wan K.H., Weinburg T., Zhang R. Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.

EMBL; AE003643; AAF5339.1; -
EMBL; AE003409; AAF44875.1; -
ENBL; AE003409; AAF44875.1; -
ENBL; FBGN0028071; BG:DS06238.4.
                                                    Q9VWS0;
01-MAY-2000
                                                                                          OSWV60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Celniker S., Rubin G.M.;
"An exploration of the sequence of a 2.9-Mb region of the genome of Drosophila melanogaster: the Adh region.";
Genetics 153:179-219(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ashburner M., Misra S., Roote J., Lewis S.E., Blazej R., Davis T., Doyle C., Galle R., George R., Harris N., Hartzell G., Harvey D., Hong L., Houston K., Hoskins R., Johnson G., Martin C., Moskrefi A., Palazzolo M., Reese M.G., Spradling A., Tsang G., Wan K., Whitelaw K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN-Y, AND CN BW SP;
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                                                                                                                                                                                                                                                                                                                                             Hypothetical protein.
SEQUENCE 218 AA; 24371 MW;
                                                                                                                                                                                 182
                                                                                                                                                                                                                                                        Local Similarity
nes 14; Conser
                                                                                                                                                                                                                     1 HGH-----EQQHGLGHGHKFKLDDDLEHQGGH 27
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                                                                                                                                                                                 HGHGSSSHSYSLKQEHGHGHGHSHGQDHGFEHGHGY 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FROM N.A.
AND CN BW SP;
                (TrEMBLrel. (TrEMBLrel.
                                                    (TrEMBLrel.
                                                                                          PRELIMINARY
                                                                                                                                                                                                                                                                       42.2%;
                13,
13,
16,
                                                                                                                                                                                                                                                     ; Score 70.5; D; Pred. No. 0.03
3; Mismatches
                Last sequence update)
Last annotation updat
                                                  Created)
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                                                                                          686
                                                                                                                                                                                                                                                                       DB 5;
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                                                                      Query Match
Best Local Similarity
Watches 13; Conserv
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C. Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L. B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Gerbalos B., Deltcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Devishake C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Mount S.M., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Mand T., Welson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Spier E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Spier E., Spradling A.C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wand Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbah J.,
RA Wand Z.-Y. Wassarman D.A., Weinstock G.M., Weissenbah J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).

BMBL, AE003509; AAF48868.1; "Thubbsc. FERENCOSONS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeilfer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                            PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR00334; KININOGEN.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                           Pfam; PF00628; PHD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE003509; AAF48868.1; -
FlyBase; FBgn0030945; CG6632.
InterPro; IPR000104; -.
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                                                                                                                                                                                                                                                                                                                                                                                        InterPro;
466
                                                1 HGHEQQHGLGHGHKFKLDDDLEHQGGH 27
HGHGHGHGHGHGHGHHSSSGHGGGH 492
                                                                                                                                                                                                                                             SM00249; PHD;
                                                                                                                                                                                                                                                                                                                                                                                      IPR000169; -. IPR001965; -.
                                                                                                                                                                                                                    686 AA;
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PubMed=10731132;
                                                                                                                      41.98;
48.18;
                                                                                                                                                                                                                    70647 MW;
                                                                                                0;
                                                                                                                         Pred. No.
                                                                                                                                             Score 70;
                                                                                                                                                                                                                    17C56F19B5D2B901 CRC64;
                                                                                                Mismatches
                                                                                                                                             DB 5; Length 686;
                                                                                                0;
                                                                                                Gaps
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RESULT Q9JKN1

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                                                                                                                                               Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Cloning of new mammalian zinc tr
Submitted (FEB-2000) to the EMBL/
EMBL; AF233322; AAF43423.1; -.
InterPro: IPR002524; -
Pfam; PF01545; Cation_efflux; 1.
SEQUENCE 378 AA; 41790 MW; B!
Q9VWX5;
01-MAY-2000 (Tr
01-MAY-2000 (Tr
01-MAR-2001 (Tr
CG5936 PROTEIN.
                                                                                                                                                                                                         "The evolutionary analysis of 'orphans' from the Drosophila identifies incorrectly annotated and rapidly evolving genes. Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AF264920; AAG10259.1; -...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2000
01-OCT-2000
01-MAR-2001
                                                   Q9VWX5
                                                                                                                                                                                                                                                                                                                                                       Q9GTNO;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                    Drosophila yakuba (Fruit fly)
                                                                                                                                                                                                                                                                                                                                               DS06238.4-LIKE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                  Q9GTN0
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                Schmid
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                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zhu W., Mager S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE-BRAIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=10090;
                                                                                                      179
                                                                                                                                                                                                                                                                                                                                                                                                                                                     163
                                                                                                                                                         Local
                                                                                                                        1 HGHEQQHGLGHG---HKFKLDDDLEHQGGH
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                                                                                                     HGHGHAHGHGSSSHSYSLKQEHGHGHGH
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                                                                                                                                              l Similarity
13; Conser
                                                                                                                                                                                                                                                             K.J., Aquadro C.F.;
                                                                                                                                                                                                   213 AA;
                   (TrEMBLrel.
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                                                                                                                                              Conservative
          (TrEMBLrel.
                                                   PRELIMINARY
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
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Rodentia;
                                                                                                                                                                                                 23731 MW;
                                                                                                                                                        40.48;
43.38;
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48.1%;
         13,
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16, Last sequence update)
16, Last annotation update)
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        Created)
Last sequence update)
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                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation updat
                                                                                                                                             Pred. No. 0.0
2; Mismatches
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                                                                                                                                                                  Score
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B98AC19C9A045006 CRC64;
                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                CRC64;
                                                                                                                                                                Length 213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length
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Q9NNV9

Q9NNV9

Q9NNV9; 01-OCT-2000

PRELIMINARY; (TremBLrel. 15,

Created)

198

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RESULT

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"The genome sequence of Drosophila melanogaster."
                                                                                                                     Query Match
Best Local S
                                                                                                   Matches
                                                                                                                                                                                                            Pfam; PF00001; 7tm_1; 2.

Pfam; PF00001; 7tm_1; 2.

PROSITE; PS00237; G_PROTEIN_RECEPTOR; 1.

G-protein coupled receptor; Glycoprotein; Transm SEQUENCE 385 AA; 43204 MW; ECAC1B1AA9AFFABE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D., Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F., George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N., Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D., Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G., Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0030901; CG5936.
InterPro; IPR000276; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M., Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolishakov S., Borkova D., Bottchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Pterygota; Neoptera;
                                                                                                                                                                                                                                                                                                                                                                           -!- SUBCELLULAR LOCATION: INTEGRAI-!- SIMILARITY: BELONGS TO FAMILY EMBL; AE003508; AAF48812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=20196006; PubMed=10731132;
  217
                               HGHEQQHGLGHGHKFKLDDD
HGHGHGHAHGHGYLKDDD
                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                            IPR000276;
                                                                                                Conservative
                                                                                                                     39.5%;
55.0%;
236
                                            20
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                                                                                                                        Score 66;
Pred. No.
                                                                                                Mismatches
                                                                                                                           0
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                                                                                                                                                                                                                                                Transmembrane
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                                                                                                                                               Length 385;
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Q9W3
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RRA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,
RRA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RRA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RRA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RRA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RRA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RRA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RRA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RRA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RRA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RRA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RRA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RRA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RRA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RRA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Dietz S.M.,
RRA Glodon K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RRA Glodon K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RRA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RRA Hostin D., Houston K.A., Howland T.J., Hernandez J.R., Houck J.,
RRA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RRA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RRA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             В
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Best Local S
Matches 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TAR-2001 (TrEMBLrel. 13, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
FEMALE STERILE (1) HOMOEOTIC PROTEIN
FS(1)H OR CG2252.
Drosophila ---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spielmann T., Beck H.;
"Analysis of stage specific transcription in reveals a set of genes exclusively transcribe parasites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tirsecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR002395; -. PRINTS; PR00334; KININOGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (JUN-2000) to the EMBL/GenBank/DDBJ databases
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01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NON_TER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    198 AA;
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16,
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Last annotation updat
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Pred. No. 0.14
1; Mismatches
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RESULT
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Best Local S
Matches 11
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Q9ZRC7;
Q1-MAY-1999
Q1-MAY-1999
Q1-MAY-2000
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EMBL; AB003442; AAF46312.2; -. E1yBase; EBgn000456; fs(1)h.
                                                                                                                                                                                                                                               TISSUE-ROOT NODULES;
Dobrita S.V., Mullin B.C.;
Dobrita S.V., Mullin B.C.;
"In vitro expression of actinorhizal nodulin AgNOD-GHRP and demonstration of its toxicity ot Escherichia coli.";
(In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);
the Biology of Plant-Microbe Interactions:
Proceedings of the 8th International Symposium on Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L. Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M. Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M. Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Syirska R., Tector C., Turner R., Venter E., Wang A.H., Wang X., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
SEQUENCE FROM
                                             protein from Alnus
Thesis (1993), The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embr. Magnoliophyta; eudicotyledons;
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PRINTS; PR00308; ANTIFREEZEI.
PRINTS; PR00503; BROMODOMAIN.
PRINTS; PR00334; KININOGEN.
                                                                                                                             Twigg P.G.;
                                                                                                                                                                                                                                  Plant-Microbe
                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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PROSITE; PS00104; BROMODOMAIN_2;
PROSITE; PS00583; PFKB KINASES_1;
SEQUENCE 1937 AA; 195339 MW;
                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=3517;
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                                                                                             'Isolation of
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                                                                               a nodule-specific cDNA encoding Alnus glutinosa.";
                                                                                                                                                                                                                                  Interactions,
                                               glutinosa.";
University of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AGNOD-GHRP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Embryophyta; Trachedons; core eudicots;
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                                                  Tennessee,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tracheophyta; Spermatophyta; dicots; Rosidae; eurosids I;
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                                                  Knoxville,
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Horowitz H., Berg C.A.;

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RESULT ID POSSILT OF POSSILT OCC POSSIC RN RN RN RR RN RX
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Best Local (
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01-NOV-1998 (TremB
01-JUN-2000 (TremB
T18E12.9 PROTEIN.
T18E12.9.
                                                                                                                        Drosophila melanogaster (Fruit fly).

Drosophila melanogaster (Fruit fly).

Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                          PSQ
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01-MAY-2000 (TrEMBLrel.
01-MAY-2000 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                         Q9V5N1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A nodule-specific gene family from Alnus glutinosa encodes gland histidine-rich proteins expressed in the early stages of actinorhizal nodule development.";

Submitted (SEP-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; US9156; AAD00171.1;
EMBL; US9156; AAD00171.1;
InterPro: JPR002395;
PRINTS; PR00334; KININOGEN.
SEQUENCE 99 AA; 10567 MW; 2ACBE4D57C070E83 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-CV. COLUMBIA;
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., M
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Ven
"Arabidopsis thaliana chromosome II BAC T18E12 genomic s
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005313; AAC34478.1: -
SEQUENCE 776 AA; 89775 MW; BE30603ACFADD14E CRC64;
                              TISSUE-OVARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Magnoliophyta; eudicotyledo
Brassicales; Brassicaceae;
NCBI_TaxID=3702;
                                                  SEQUENCE FROM N.A.
                                                                                                 NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana (Mouse-ear cress).
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                                                  (ISOFORM A).
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Pred. No. 0.93
1; Mismatches
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Pred. No. 0.11;
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                                                                                                                                                 Brachycera; Muscomorpha;
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Kashurner M., Henderson S.N.,
RA Sutton R.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
RA Ballew R.C., Rogers Y.H.C., Blaze'R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarcoglu L., Beasley E.M.,
RA Abril J.F., Agbayani A., An H.-J., Andrews Pfennkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktarcoglu L., Beasley E.M.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchen A., Deng Z., Mays A.D., Dev I., Dietz S. M.,
Dodson K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Conpeleian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guna P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Krapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Harris N.L., Harvey D., Krapt C., Kraptiz S., Kulp D., Lai Z.,
RA Harris N.L., Harvey D., Krapt C., Kraptiz S., Kulp D., Lai Z.,
RA Hostin D., Kalpen K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melsch P., Venter B., Winner R., Nush R., Nelson D.L.,
RA Melsch P., Venter B., Winner R., Delabri M., Nelson D.L.,
RA Spier E., Spradling A.C., Stapleton M., 
VARSPLIC
CONFLICT
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Horowitz H., Berg C.A.;
"The Drosophila pipsqueak gene encodes protein required early in oogenesis.";
Development 122:1859-1871(1996).
[3]
                                                                                                                                                                                                                                                  EMBL; U48358; AAC47153.1; EMBL; U48402; AAC47154.1;
                                                       VARSPLIC
                                                                                              SMART; SM00225;
                                                                                                                                 InterPro; IPR002197; -.
Pfam; PF00651; BTB; 1.
                                                                                                                                                                                        FlyBase; FBgn0004399; psq.
                                                                                                                                                                                                              EMBL; AE003829; AAF58769.1; EMBL; AE003829; AAF58770.1;
                                                                            Alternative splicing.
                                                                                                                  PROSITE
                                                                                                                                                                       InterPro; IPR000210; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Aberrant splicing and transcription termination caused insertion into the intron of a Drosophila gene.";
                                                                                                                                                                                                                                                                                         ALTERNATIVE PRODUCTS: 3 ISOFORMS; A/1 (SHOWN HERE), PRODUCED BY ALTERNATIVE SPLICING.
                                                                                                                  PS50097;
                                                                                              BTB; 1.
                                                                                                                  BTB;
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MISSING (IN ISOFORM E MISSING (IN ISOFORM 2 Q -> QQ (IN REF. 1 AN MW; 77420C782DE6ECA5
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086731;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SMART; STUDE:
Alternative splicing.
428 535
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PROSITE; PS50097; BTB; 1.
SMART; SM00225; BTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (LONG AND SHORT ISOFORMS).
MEDLINE=96134923; PubMed=8557044;
Weber U., Siegel V., Mlodzik M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interpro; IPR000210; -. Interpro; IPR002197; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "pipsqueak encodes a novel nuclear protein required downstream seven-up for the development of photoreceptors R3 and R4.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FlyBase; FBgn0004399; psq.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 8-105 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBO J. 14:6247-6257(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly).
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Pred. No. 2
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TRDLSNTTEPLDIDNHLAQQIHRLDQSPMHSISHHHTGDES
NSNLVQHIKEBVIEAKHLAQOHHLS -> VSWLASFGLVS
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SC5C7.34.
SC5C7.34.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacterida Actinomycetales; Streptomycineae; Streptomycetaceae; NCBI_TaxID=1902;
                                                                                                                        the 8 Mb Streptomyces coelicolor A3(2) chromosome."; Mol. Microbiol. 21:77-96(1996).
EMBL; AL031515; CAA20646.1; -.
                                                                                           Hypothetical protein. SEQUENCE 314 AA; 3
                                                                                                                                                                  Redenbach M., Kieser H.M., Denapaite
Kinashi H., Hopwood D.A.;
                                                                                                                                                                                                                                   Submitted
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Seeger K.J.,
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| Arabidopsis thalia | AAG22955     | 21 | 309  | •    | 62   | ٠,     |
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|                    | AAR24393     | 13 | 351  | •    | 63   | -      |
| Arabidopsis thalia | AAG43478     | 21 | 398  | •    | 4.   | ~      |
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| Arabidopsis thalia | AAG43479     | 21 | 344  | •    |      |        |
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| g prot             | AAW25029     | 18 | 1213 | •    | 67   | 01     |
| Drosophila TATA-bi | AAW06086     | 17 | 1213 | ٠    | 67   | -      |
| Light chain of hum | AAY93352     | 21 | 11   | ٠    | 68   | w      |
| Arabidopsis thalia | AAG46905     | 21 | 179  | •    | 69   | $\sim$ |
| Arabidopsis thalia | AAG24334     | 21 | 179  | •    | 69   | _      |
| š                  | AAW72390     | 19 | 180  | •    | 72.5 | _      |
| Arabidopsis thalia | AAG42194     | 21 | 177  | •    | ۶    | •      |
| Human high molecul | AAY81995     | 21 | 12   | •    | 74   | w      |
| high molec         | AAY81994     | 21 | 12   | •    | 79   | 7      |
| two-chain          | AAY81999     | 21 | 16   |      | 98   | ٠ı     |
| two-chain          | AAB06337     | 21 | 16   | •    | 98   | 01     |
| Human HKH20 peptid | AAY71879     | 21 | 19   |      |      |        |
| n high polyme      | AAW07625     | 17 | 20   | 70.6 | 125  | w      |
| Partial peptide of | $\mathbf{L}$ | 16 | 110  | •    | 4    | $\sim$ |
|                    |              |    |      |      |      |        |

## ALIGNMENTS

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PF XX PR PA PA XX
                                                                                                                                                           AAY81997
                                                                                                                                                                                                                                             Human; high molecular weight kininogen; HK;
two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition, tumour; cancer; ocular disorder;
rheumatoid arthritis; endothelial cell apoptosis.
A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                    WPI; 2000-376483/32.
                                                                                                                        10-NOV-1998;
                                                                                                                                                05-NOV-1999;
                                                                                                                                                                        18-MAY-2000
                                                                                                                                                                                               WO200027866-A1
                                                                                                                                                                                                                        Homo sapiens.
                                                                                                                                                                                                                                                                                                       Human high molecular weight kininogen domain 5 fragment #6
                                                                                                                                                                                                                                                                                                                                 16-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                           AAY81997;
                                                                                                                                                                                                                                                                                                                                                                                 AAY81997 standard; peptide;
                                                                                   (MCCR/) MCCRAE R K.
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                                                                                                                        98US-0107833
                                                                                                                                                99WO-US26419
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is derived from human high molecular weight kininogen (HK) domain 5. HK is a 120 kD glycoprotein which binds with high affinity to endothelial cells, where it is cleaved to two-chain high molecular weight kininogen (HKa) by plasma kallikrein. Hka or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting angiogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by
The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a
                                       Claim
                                                                 that
                                                                                                        WPI; 2000-376306/32
                                                                                                                                                                          (UTEM )
(DUPO )
(COLM/)
                                                                                                                                                                                                                                                         09-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                           Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              04-SEP-2000
                                                                                 Method
                                                                                                                                 Colman WR, Mousa AS
                                                                                                                                                                                                                                                                                                               WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                    Light chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY93351 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 13;
                                                                                                                                                                                                                                10-NOV-1998;
                                                                                                                                                                                                                                                                                    18-MAY-2000
                                                                                                                                                                                                                                                                                                                                         HOMO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inhibiting endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the compostion may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GHKHKHGHGHGKHKNKGKKNGKHNGWKT 28
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                                                                                                                                                                                                                                                                                                                                        sapiens.
                                        8
                                                                                                                                                            DUPONT PHARM CO. COLMAN W R. MOUSA A S.
                                                                                                                                                                                                      UNIV TEMPLE
                                        Page 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 of human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                                                                                                                               proliferation;
                                       41pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               peptide;
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                                                                endothelial cell
ial cell migration
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 177;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                              proliferation, using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
.8e-15;
                                                                                                                                                                                                                                                                                                                                                                             ; analogue; angiogenesis;
cell migration; vitronectin
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Best Local (
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The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kbm glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used to used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                                                                                                                                             Method for inhibiting endothelial cell proliferation, using
                                                                                                                                                                                                                                                                               WPI; 2000-376306/32.
                                                                                                                                                                                                                                                                                                             Colman WR,
                                                                                                                                                                                                                              that inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                           (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          09-NOV-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Light chain
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY93353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY93353 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          inhibit migration of endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GHKHKHGHGHGKHKNKGKKNGKHNGWKT 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 high molecular weight kininogen; glycoprotein; endothelial cell; kallikrein; heavy chain; light chain; analogue; angiogenesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                             Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of
                                                                                                                                                                                                                                                                                                             Mousa AS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                40-41;
                                                                                                                                                                                                                                                                                                                                                                                                                          98US-0107844.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human high molecular weight kininogen analogue
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    proliferation; endothelial
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                                                                                                                                                                                             41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                179
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A
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                                                                                                                                                                                                                                               compound
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  Query Match
Best Local Similarity
Matches 28; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                         The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                        Claim 9;
                                                                                                                                                                                                                                                                                                              Method
                                                                                                                                                                                                                                                                                                                                                                 Colman WR, Mousa AS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-SEP-2000
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                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                         WPI; 2000-376306/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                                                       (UTEM ) UNIV TEMPLE
(DUPO ) DUPONT PHARI
(COLM/) COLMAN W R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    HOMO
                                                                                                                                                                                                                                                                                                                                                                                            (MOUS/) MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
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                                                                                                                                                                                                                                                                                               inhibit endothelial cell migration
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sapiens.
                                                                                                                                                                                                                                                                                                          for inhibiting endothelial cell proliferation, using compound
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                                                                                                                                                                                                                                                                     Page 38; 41pp; English.
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                                                                     186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
    Conservative
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               100.0%;
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Score 177; DB 21;
Pred. No. 1.3e-14;
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Pred. No. 1.
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AAY93345 ID AAYS

AAY93345 standard;

peptide; 47

ΑA

AAY93345;

RESULT

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RESULT AAY93342 ID AAY9
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XX AAY9
XX Ligh
XX Ligh
XX Huma
KW Plass
KW Plass
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence represents the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kba glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains.
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                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Page 3; 41pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Method for inhibiting endothelial cell proliferation, using compound
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-376306/32.
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                                                                                                                                                                                                                                                                                                                                 inhibit migration of endothelial cells
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
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   105
                                                                                                                                                 Local Similarity
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                              1 GHKHKHGHGHGKHKNKGKKNGKHNGWKT 28
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ghkhkhghghgkhknkgkkngkhngwkt 132
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                                                                                                                     Conservative
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                                                                                                                                                 Score 177; DB 21; Pred. No. 1.8e-14;
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                                                                                                                                                                                                                                                                                                                                 to vitronectin.
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Matches 27
Human; high molecular weight kininogen; glycoprotein; endothelial cell; plasma kallikrein; heavy chain; light chain; analogue; angiogenesis; endothelial cell proliferation; endothelial cell migration; vitronectin
                                                             Light chain
                                                                                              04-SEP-2000
                                                                                                                                                         AAY93348 standard;
                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a fragment of the light chain of huma high molecular weight kininogen. It is used to produce compounds of the invention. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 3; Page 36; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Colman WR, Mousa AS
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(DUPO ) DUPONT PHARM CO.
(COLM/) COLMAN W R.
(MOUS/) MOUSA A S.
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                                                                                                                                                                                                                                                                                               Similarity 27; Conserv
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kallikrein; heavy chain; light chain; analogue; angio
elial cell proliferation; endothelial cell migration;
                                                                                                                                                                                                                                                                                                                                                                         47
                                                          of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                             Conservative
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                                                                                                                                                         peptide;
                                                                                                                                                                                                                                                                                                           97.2%;
                                                                                                                                                                                                                                                                                                          Score 172; DB 21; Pred. No. 1.3e-14;
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                                                                                                                                                                                                                                                                                    high molecular weight; kininogen; fragment; 1.2; wound treating agent; bovine; growth promotion;
                                                                                                               28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                      Partial peptide of human HMW kininogen fragment
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COLMAN W R.
MOUSA A S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard; peptide;
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17-SEP-1993; 17-SEP-1993;

93JP-0230616 93JP-0230616.

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RESULT
AAY93347
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Best Local Similarity
Matches 27; Conserv
The present sequence represents an analogue of the light chain of human high molecular weight kininogen. High molecular weight kininogen is a 120 kDa glycoprotein which binds with high affinity to endothelial cells, where it is cleaved by plasma kallikrein into heavy and light chains. Analogues of high molecular weight kininogen are used in the method
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim
                                                                                                                                                                                                                                                                                                                                                                                          endothelial cell
                                                                                                                                                                                                                                                                                                                                                                                                                                         Light chain of human high molecular weight kininogen analogue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY93347 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A wound treating agent contq. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                           Claim
                                                                                                               Method
                                                                                                                                                                Colman WR,
                                                                                                                                                                                                                                                                             09-NOV-1999;
                                                                                                                                                                                                                                                                                                                               WO200027415-A2
                                                                                                                                                                                                                                                                                                                                                                                                        plasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY93347;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       on fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               agent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human
                                                                                                                                                                                                                (UTEM ) UNIV TEMPLE.
(DUPO ) DUPONT PHARN
                                                                                                                                                                                                                                                     10-NOV-1998;
                                                                                                                                                                                                                                                                                                     18-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        rragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR75186 is a partial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (FARH ) HOECHST JAPAN
                                                                                                                                                                                                    (COLM/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
                                                                                                 od for inhibiting endothelial cell proliferation, using compound
inhibit endothelial cell migration -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GHKHKHGHGHGKHKNKGKKNGKHNGWK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ghkhkhghghgkhknkgkkngkhngwk 63
                                                                                                                                       2000-376306/32.
                                                                            5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ent 1, amino acids 458-520. Partial peptides of bovine and kininogen fragments 1.2, 1 and 2, are used in wound treating compsns. and act as the active component. The fragments are 1 in wound treating because they have growth promotion activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8;
                                                                                                                                                                                                                                                                                                                                                                                        high molecular weight kininogen; glycoprotein; endothelial cell; kallikrein; heavy chain; light chain; analogue; anglogenesis; elial cell proliferation; endothelial cell migration; vitronectin.
                                                                                                                                                                                     ) DUPONT PHARM CO.
) COLMAN W R.
) MOUSA A S.
                                                                         Page 37; 41pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page 8; 8pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 AA;
                                                                                                                                                                Mousa AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                     98US-0107844.
                                                                                                                                                                                                                                                                              99WO-US26377.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                즛
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 172; 1
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  corresponding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .7e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ng to human kininogen peptides of bovine a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nts are
activity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RESULT 1

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RESULT
AAR75181
ID AAR7
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                                                 Matches
                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention. The specification describes a method of inhibiting endothelial cell proliferation. The method comprises contacting endothelial cells with a compound containing high molecular weight kininogen analogues. The method and the compounds can be used for inhibiting endothelial cell proliferation. The compounds can also be used for inhibiting angiogenesis. The compounds can also be used to
                                                                                                                                                      AAR75181 is a partial peptide corresponding to human kininogen fragment 1.2, amino acids 390-520. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compsns, and act as the active component. The fragments are
                                                                                                         Sequence
                                                                                                                                            useful in wound treating because they have growth promotion activity
                                                                                                                                                                                                                    Claim
                                                                                                                                                                                                                                                                               WPI; 1995-158909/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75181;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                            have
                                                                                                                                                                                                                                                       A wound
                                                                                                                                                                                                                                                                                                                              17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                     17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                            28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                   JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                 wound treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                            high molecular weight; kininogen; fragment; 1.2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Partial peptide of human HMW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAR75181 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inhibit migration of endothelial cells to vitronectin.
                                                                                                                                                                                                                                                                                                    (FARH ) HOECHST JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                        1 GHKHKHGHGHGKHKNKGKKNGKHNGWK 27
                                                                                                                                  tibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GHKHKHGHGHGKHKNKGKKNGKHNGWK 27
und treating agent contg. a partial peptide of kininogen growth promotion activity of fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7;
                                               Similarity
27; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                 Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              83
                                                                                                           131 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AA;
                                                                                                                                                                                                                                                                                                                             93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                 agent; human;
                                                                                                                                                                                                                                                                                                                                                     93JP-0230616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         peptide;
                                                          97.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.2%;
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                                                0;
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                                                           Score 172;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kininogen fragment 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 172;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2.3e-14;
                                                             ω
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                                                                     DB 16;
                                                           .7e-14;
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                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; 2; partial;
                                                                      Length 131;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                0,
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                                                Gaps
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RESULT 1
AAR75178
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                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                       Query Match
 JP07082172-A
                             Misc-difference
                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                            AAR75179 is a partial peptide corresponding to bovine kininogen fragment 2, amino acids 456-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent componens and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                                  Bos taurus
                                                                   Misc-difference
                                                                                                                  high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
                                                                                                                                                Partial peptide of HMW kininogen fragment 1.2.
                                                                                                                                                                      05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                                                                                                                                         AAR75178;
                                                                                                                                                                                                            AAR75178 standard;
                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (FARH ) HOECHST JAPAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JP07082172-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                high molecular weight; kininogen; fragment; 1.2; 1; 2; partial; wound treating agent; bovine; growth promotion; fibroblast.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Partial peptide of HMW kininogen fragment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-DEC-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR75180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28-MAR-1995
                                                                                                                                                                                                                                                       12
                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                       1 GHKHKHGHGHGKHKNKGKKNGKHNGWK 27
                                                                                                                                                                                                                                                                                                                                                                        fibroblasts.
                                                                                                                                                                                                                                                                                                   l Similarity
22; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                        Page 7; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard;
                                                                                                                                                                                                                                                                                                                                                    41
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                    Ã,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .93Jb-0530616
                                              /label= Pro,
                           /label= Val or Leu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93JP-0230616
                                                                   Location/Qualifiers
                 /label= Lys or Arg
                                                                                                                                                                                                            peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide; 41
                                                                                                                                                                                                                                                                                                           80.2%;
81.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              χ.
                                                                                                                                                                                                            110
                                                                                                                                                                                                                                                                                                 Score 142; DB Pred. No. 5.2e 1; Mismatches
                                                                                                                                                                                                                                                                                                   1;
                                                          Thr
                                                                                                                                                                                                            ₽Ã
                                                                                                                                                                                                                                                                                                           DB 16;
.2e-11;
                                                                                                                                                                                                                                                                                                                    Length 41;
                                                                                                                                                                                                                                                                                                   Indels
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RESULT :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
Cell adhesion inhibiting peptide(s), used as cancer metastasis inhibitor – comprises partial amino acid sequence of human high polymer quininogen {\bf L} chain
                                               WPI; 1996-421988/42
                                                                                                                                                                                                                                                                                          Human; high polymer; quininogen; L-chain; cell adhesion; cancer metastasis; platelet aggregation; inhibition; wound; inflammatory disease; arteriosclerosis; glomerular nephritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR75178 is a partial peptide corresponding to bovine kininogen fragment 1.2, amino acids 387-496. Partial peptides of bovine and human kininogen fragments 1.2, 1 and 2, are used in wound treating agent compones. and act as the active component. The fragments are useful in wound treating because they have growth promotion activity
                                                                                             28-SEP-1994;
                                                                                                                                           13-AUG-1996.
                                                                                                                                                                                                                                     Key
                                                                                                                    28-SEP-1995;
                                                                                                                                                                  JP08208692-A.
                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                            Homo sapiens.
                                                                                                                                                                                                                                                                                                                                          Human high polymer quininogen L-chain derived peptide
                                                                                                                                                                                                                                                                                                                                                                  04-FEB-1997
                                                                                                                                                                                                                                                                                                                                                                                         AAW07625;
                                                                                                                                                                                                                                                                                                                                                                                                             AAW07625 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 6; 8pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A wound treating agent contg. a partial peptide of kininogen have growth promotion activity of fibroblasts.
                                                                     (SUMU ) SUMITOMO SEIYAKU KK
                                                                                                                                                                                                                         Peptide
                                                                                                                                                                                                                                                                                   treatment.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1995-158909/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (FARH ) HOECHST JAPAN KK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-SEP-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-MAR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                     13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GHKHKHGHGHGKHKNKGKKNGKHNGWK 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  fibroblasts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ghghkhghghgkhknkgknngkhydwr 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 81.5
22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            110 AA;
                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                            94JP-0259451
                                                                                                                   95JP-0276418
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                                                                                                                                                                                                   /note=
13..20
                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                              peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80.2%;
                                                                                                                                                                                       "claimed peptide (claim 6)"
                                                                                                                                                                                                             "claimed peptide (claim 1)"
                                                                                                                                                                                                                                                                                                                                                                                                              20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 142; DB Pred. No. 1.4e 1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 110;
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RESULT 1
AAY71879
ID AAY7
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                                                                                                                                                                                                                                                                                                                 29-APR-1999;
06-MAY-1999;
01-OCT-1999;
           The patent discloses a method for preventing or treating a disorder resulting from the release of bradykinin in a mammal which produces a heparin-binding protein (HBP) that binds to a HBP antagonist This method involves administration of a mammalian HBP antagonist (especially aprottinin) and/or monoclonal antibodies that bind to prekallikrein-H-kininogen complexes in the HBP, to decrease the release of bradykinin in the mammal. The antagonists of HBP (e.g. aprottinin) decrease the permeability of the endothelial cells and are used to prevent or treat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; heparin binding protein; HBP; antiinflammatory; cardiovascular; immunosuppressive; vasotropic; prevention; treatment; bradykinin; aprotinin; H-kininoqen; HK; systemic inflammatory response syndrome; pre-kallikrein; ischaemia reperfusion; anaphylaxis; allograft rejection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     are useful in cell adhesion, cancer metastasis or platelet aggregation inhibitors, and in wound, inflammatory disease, arteriosclerosis or glomerular nephritis treating agents. The present peptide was synthesised using a solid phase method, and purified using a YMC-DOS-120A-S15/13 column.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim
 disorders
                                                                                                                                                                                                                                                                                                                                                                                                    09-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                        28-APR-2000; 2000WO-DK00213
                                                                                                                                                                                                                                                                                                                                                                                                                              WO200066151-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY71879;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAY71879 standard;
                                                                                                                                       Example
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                                                                                                                                                                                                                      2000-687445/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   respiratory distress syndrome; HKH20 peptide.
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                                                                                                                                                                            systemic inflammatory response syndrome, xis and allograft rejection by modulating
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 resulting
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99DK-0000613.
99DK-0001402.
99US-0157384.
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endothelial cells and are used to from the release of bradykinin suc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           the human high polymer quininogen L-chain.
                                                                                                                                    75pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  derived from domain 5 of H-Kininogen (479-498 aa).
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s 0;
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such as
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Best Local
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            or a synthetic compound comprising the present sequence may be used in a pharmaceutical composition for inhibiting anglogenesis. Angiogenesis occurs in a number of disease states, such as tumour formation and expansion, and certain ocular disorders. It can also occur in a rheumatoid joint, hastening joint destruction by allowing an influx of leukocytes. The composition may inhibit angiogenesis by inhibiting endothelial cell proliferation or by inducing endothelial cell proliferation or by inducing endothelial cell apoptosis. Peptides used in the composition may be recombinant peptides, natural peptides, or synthetic peptides. They may also be chemically synthesised, using, for example, solid phase synthesis methods.
                                                                                                                                                                             The present sequence is derived from human two-chain high molecular weight kininogen (HKa) domain 5. HKa is product of high molecular weight kininogen (HK) cleavage by plasma kallikrein. HK is a 120 key glycoprotein which binds with high affinity to endothelial cells.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    respiratory distress syndrome. The present sequence is HKH20 peptide which is derived from the domain 5 of human H-Kininogen (HK) protein (479-498 residues). HKH20 treatment of endothelial cells inhibits or prevents the HBP-induced increase in permeability of the endothelial cells.
                                                                                                                                                                                                                                                                Claim
                                                                                                                                                                                                                                                                                                               A pharmaceutical composition used to inhibit angiogenesis, inhibit endothelial cell proliferation, and induce endothelial cell apoptosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   angiogenesis inhibition; tumour; cancer; ocular d
rheumatoid arthritis; endothelial cell apoptosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  two-chain high molecular weight kininogen; HKa;
angiogenesis inhibition; tumour; cancer; ocular disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory response syndrome, ischaemia reperfusion, anaphylaxis and/or allograft rejection. They are also used to treat adult
                                                                                                                                                                                                                                                                                                                                                                 WPI; 2000-376483/32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human; high molecular weight kininogen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human two-chain high molecular weight kininogen domain 5 fragment
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les 18; Conser
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90.0%;
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Query Match

Query Match

Best Local Similarity 100.0%; Pred. No. 4.7e-06;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 13 HKNKGKKNGKHNGWKT 28

||||||||||||||||
Db 1 hknkgkkngkhngwkt 16

Search completed: July 6, 2001, 09:09:18

Job time: 124 sec
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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Total number of hits satisfying chosen parameters: Minimum DB seq length: 0

193259

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database: Issued\_Patents\_AA:\*

1: /cgn2\_6/ptodata/2/iaa/5A\_COMB.pep:\*
2: /cgn2\_6/ptodata/2/iaa/5B\_COMB.pep:\*
3: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
4: /cgn2\_6/ptodata/2/iaa/6B\_COMB.pep:\*
5: /cgn2\_6/ptodata/2/iaa/ACTUS\_COMB.pep:\*
6: /cgn2\_6/ptodata/2/iaa/backfiles1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 27                | 26              | 25              | 24                | 23               | 22                | 21              | 20                | 19                | 18              | 17              | 16                | 15               | 14              | 13                | 12                | 11                | 10              | 9    | 8               | 7       | 6           | ر.<br>ت      | 4                | ω                | N                 | 1                 | NO.         | Result |
|-------------------|-----------------|-----------------|-------------------|------------------|-------------------|-----------------|-------------------|-------------------|-----------------|-----------------|-------------------|------------------|-----------------|-------------------|-------------------|-------------------|-----------------|------|-----------------|---------|-------------|--------------|------------------|------------------|-------------------|-------------------|-------------|--------|
| G                 | 53              | 53              | 53                | 53               | 53                | 53              | 53                | 54                | 54              | 54              | 54.5              | 55               | 55              | 55                | 56.5              | 56.5              | 56.5            | 56.5 | 56.5            | 56.5    | 59          | 59           | 61.5             | 61.5             | 67                | 67                | score       | 1      |
| 29.9              | 29.9            |                 |                   | 29.9             |                   | •               | •                 | 30.5              | 0.              | •               | 0.                |                  | 31.1            | 31.1              | 31.9              | 31.9              | 31.9            | 31.9 | 31.9            | 31.9    | ω<br>ω<br>ω | 33.3         | 34.7             | 34.7             | 37.9              | 37.9              | Match       | Query  |
| 637               | 637             | 637             | 617               | 28               | 28                | 28              | 28                | 834               | 834             | 834             | 1261              | 60               | 60              | 60                | 376               | 376               | 337             | 337  | 313             | 313     | 1199        | 515          | 1085             | 1085             | 1213              | 1213              | Length      |        |
| w                 | w               | ω               | L                 | N                | <u>_</u>          | μ.              | _                 | 4                 | N               | Ν               | 4                 | υ                | N               | 1                 | L                 |                   | 4               | ω    | 4               | w       | 4           | 4            | N                | ш                | -                 | <u> </u>          | - 58        |        |
| US-08-072-064-6   | US-08-072-064-4 | US-08-072-064-1 | US-08-137-614A-26 | US-08-436-703B-7 | -677-304-         | US-08-303-025-2 | -152-488-         | US-09-323-433A-4  | US-08-396-001-4 | US-08-861-464-4 | US-09-208-742-4   | PCT-US95-05772-1 | US-09-115-032-1 | US-08-255-457-1   | US-08-594-031-102 | US-08-594-031-100 | US-09-456-287-2 | -08  | US-09-456-287-3 | -08-686 | -208        | -08-942-012E | US-08-938-534-28 | US-08-431-080-28 | US-08-646-715-20  | US-08-188-582-20  | 11          | 1      |
| Sequence 6, Appli | 4,              | 1, 2            | 26,               | 7,               | Sequence 2, Appli | 2,              | Sequence 2, Appli | Sequence 4, Appli | 4,              | 4,              | Sequence 4, Appli | Ļ                | 1,              | Sequence 1, Appli | 103               | Sequence 100, App | ν,              | 'n   | ω               | ω       | 2,<br>A     | 32,          | •                | 28,              | Sequence 20, Appl | Sequence 20, Appl | Description |        |

Query Match

37.9%; Score 67;

DB 1; Length 1213;

## ALIGNMENTS

| Q.,                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | , , , , , , , , , , , , , R |
|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------|
| : Hoey, Timothy : Ruppert, Siegfr : Tanese, Naoko : Wang, Edith : Weinzierl, Robe INVENTION: TATA-I INVENTION: TATA-I INVENTION: NUCLEI SEQUENCES: 36 DENCE ADDRESS: EE: FLEHR, HOHBAC 4 Embarcadero Ce San Francisco California : USA 4111-4187 READABLE FORM: TYPE: Floppy disk TYPE: Floppy disk R: IBM PC compati NG SYSTEM: PC-DOS E: Patentin Relee PHICATION DATA: TION NUMBER: US/ DATE: 28-JAN-1999 ICATION INFORMATION: OSMMAN, Richard 36, ATION NUMBER: 36, ATION INFORMATION OSMMAN AID NO CE/DOCKET NUMBER: 36, ATION JOHNATION OSMMAN AID NO CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET NUMBER: 36, CE/DOCKET | 20<br>Ap<br>534<br>ORM<br>: |

Best Local Similarity

57.9%;

Pred. No. 1.7;

GENERAL INFORMATION:

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RESULT 3
US-08-431-080-28
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INFORMATION FOR SEQ ID NO:
                                                                                                1160 HKHKHKHRHSKDKDKERKD 1178
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                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 1213 amino acids
                                                                                                                                                                                                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: OSMAN, RICHARD A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: A-57650-2/AJT/RAO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 435
PRIOR APPLICATION UNDER: US 08/188,582
FILING DATE: 28-JAN-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 09-MAY-199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: TATA-BINDING PROTEIN ASSOCIATED FACTORS, TITLE OF INVENTION: NUCLEIC ACIDS ENCODING TAFS AND METHODS OF USE NUMBER OF SEQUENCES: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 4 L....
CITY: San Francisco
                                                                                                                                                                                                                                                                              TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                2 HKHKHGHGHGKHKNKGKKN 20
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                Application US/08431080
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                                                                                                                                                                Conservative
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Weinzierl, Robert O.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hoey, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Dynlact, Brian D.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
                                                                                                                                                                                                                                                                 protein
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                                                                                                                                                                                37.9%;
57:9%;
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Pred. No. 1
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                                                                                                                                                                       APPLICANT: Gottscniin, ...
APPLICANT: Singer, Miriam S.
TITLE OF INVENTION: Telomerase Composit
NUMBER OF SEQUENCES: 32
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
                                                                                                                                                                                                                                                                                                                     Patent No. 5916752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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                                                            ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Parker, David L.
REGISTRATION NUMBER: 32,165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: ARCD:155/PAR TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: SN 08/326,781
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                                                                                                     COUNTRY: UN
ZIP: 77210
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TELEFAX: 79-0924
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CITY: F
                                                                                                                                                                                                                                                                                                                                                                                                                                          512 GHKSKKGRHKSGKSHIEHKNKGSNLIKSN 540
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             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: PatentIn Release #1.0, Vers
                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: sin
TOPOLOGY: linear
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ZIP: 77210
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TELEFAX: (713) 789-2679
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GHK-----HKHGHGHGKHKNKGKKNGKHN 24
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                                                                                                                                                              Houston
                                                                                                                                               TEXAS
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                                                                                                                          UNITED STATES OF AMERICA
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Pred. No. 6.9;
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                Version #1.30
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CLASSIFICATION: 536 PRIOR APPLICATION DATA:

08/431,080

APPLICATION NUMBER: US/0 FILING DATE: 26-SEP-1997

US/08/938,534

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US-09-208-742-2
Sequence 2, Application US/09208742
Patent No. 6174679
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                        SEQ ID NO 32
LENGTH: 515
TYPE: PRT
ORGANISM: Spodoptera littoralis nuclear polyhedrosis virus
US-08-942-012B-32
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Best Local Similarity
Matches 8; Conserv
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APPLICANT: Miller,
APPLICANT: Lu, Albe
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/08/942,012B CURRENT FILING DATE: 1997-10-01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Biological Insect Control Agents Expressing TITLE OF INVENTION: Insect-Specific Toxin Genes, Methods and ComFILE REFERENCE: 28-96a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: PAIKER, DAVID L.
REGISTRATION NUMBER: 32,165
REFERENCE/DOCKET NUMBER: ARCI
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS:
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LENGTH: 1085 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: SN 08/326,781 FILING DATE: October 20, 1994 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                512 GHKSKKGRHKSGKSHIEHKNKGSNLIKSN 540
                                                                                                                          58 HNHNHGHRHHRHEN 71
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE:
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Black, Bruce
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lu, Albert
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                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                Score 59;
Pred. No.
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Pred. No. 6.
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RESULT 8 US-09-456-287-3

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US-08-686-528A-3
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                                                                                                                                                       US-08-686-528A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 3, Application US/08686528A Patent No. 6054134 GENERAL INFORMATION:
                                                                  Matches
                                                                                                 Query Match
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Best Local Similarity 50.0%;
Matches 11; Conservative
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CURRENT FILING DATE: 1998-12-10
NUMBER OF SEO ID NOS: 6
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TITLE OF INVENTION: CIF150/hTAF11150 is Necessary for Cell
TITLE OF INVENTION: Cycle progression
FILE REFERENCE: 1453.002
                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: INFORMATION FOR SEQ ID NO: 3:
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                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Rea, Teresa Stanek
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                      MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Burns, Do
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
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113 НКИДИНДИ-ДИКИЕНКИДИЕНИ 134
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: US/08/686,528A FILING DATE: 26-JUL-1996 CLASSIFICATION: 424
                                                                                 Local Similarity
                                                                                                                                                                                                      STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: United States ZIP: 22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                            TOPOLOGY:
                              2 HKHKHGHGHGKHKNKGKKNGKHN 24
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                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LINGWOOD, Clifford A.
ZENTION: HAEMOPHILUS ADHESIN PROTEIN
                                                                                                                                                                                            linear
                                                                           31.9%;
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Pred. No.
                                                                                 Score 56.5;
Pred. No. 8
                                                                  Mismatches
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15;
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Sequence 3, Application US/09456287 Patent No. 6218147

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                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-686-528A-2
                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08686528A Patent No. 6054134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/456,287
                                                                                                                                                                                                                                                                                                         APPLICANT: LINGWOOD, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Rea, Teresa Stanek
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         113 НКИДИДИН-ДИКИЕНКИДИЕНИ 134
                                 APPLICATION NUMBER: FILING DATE: 26-JUI
                CLASSIFICATION:
                                                                                                                                                                                                                                 CITY: Alexandria
                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 1737 King
CITY: Alexandria
STATE: Virginia
                                                                                                                                                                                  ZIP:
                                                                                                                                                                                                 COUNTRY: United States
                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 HKHKHGHGHGKHKNKGKKNGKHN 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              rRY: United States
22314-2756
                                                                                                                                                                                  22314-2756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           f: 313 amino acids amino acid
                                                                                                                                                                                                                    Virginia
                                                                                                                                                                                                                                                    E: Burns, Doane, Swecker & Mathis, L.L.P. 1737 King Street, Suite 500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                          LINGWOOD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LINGWOOD, Clifford A. VENTION: HAEMOPHILUS ADHESIN PROTEIN
INFORMATION
                                 26-JUL-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  31.9%;
                                                                                                                                                                                                                                                                                                                           HAEMOPHILUS ADHESIN PROTEIN
                                                                                                                                                                                                                                                                                                                                          Clifford A.
                                                    US/08/686,5282
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Pred. No. 8;
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; MOLECULE TYPE: protein
US-08-686-528A-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-456-287-2
                                                               Matches
                                                                              Best Local Similarity
                                                                                            Query Match
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Best Local Similarity 43.5%;
                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 30,4
REFERENCE/DOCKET NUMBER:
INFORMATION FOR SEQ ID NO: 2:
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: LINGWOOD, Clifford A.
TITLE OF INVENTION: HAEMOPHILUS ADHESIN PROTEIN
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: 1737 Kind
CITY: Alexandria
STATE: Virginia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LENGTH: 337 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                             TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                            2 HKHKHGHGHGKHKNKGKKNGKHN 24
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                                                                                                                                                                                                                                                                                                          NAME:
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НКНОНОН-ОНКНЕНКНОНЕНН 158
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                                                                                                                                                                                                          amino acid
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                                                               Conservative
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linear
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43.5%;
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                                                                              Score 56.5;
Pred. No. 8
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Pred. No. 8
                                                             Mismatches
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                                                                                             DB 4;
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; FRAGMENT TYPE: I
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US-08-594-031-100
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Patent No.
                                                                                                                                                                                             Patent No. 5783182
GENERAL INFORMATION:
                                                                                                                                                                                                                     Sequence 102, Application US/08594031 Patent No. 5783182
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 31.9%; Score 56.5; Best Local Similarity 47.6%; Pred. No. 9 Matches 10; Conservative 4; Mismatche
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APPLICATION NUMBER: 60/006,838
FILING DATE: 16 NOV-1995
ATTORNEY/AGENT INFORMATION:
NAME: Remenick, James
REGISTRATION NUMBER: 36,902
REFERENCE/DOCKET NUMBER: 0A146-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
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COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:
                                                                                                                                     APPLICANT: THOMPSON, Timothy C.
TITLE OF INVENTION: METHOD FOR IDENTIFYING METASTATIC SEQUENCES: 175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: THOMPSON, TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL: NO ANTI-SENSE: NO
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                                                                                                                          CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                104 GNGTGSHHN---VDGKHHGWR 121
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OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
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ZIP: 20004-2400
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CITY: Washington
                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/594,031 FILING DATE: 30-JAN-1996
                                                           STATE:
                                                                      CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid
                                                                                                              ADDRESSEE:
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3. 5783182
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                                                                                         E: BAKER & BOTTS,
1299 Pennsylvania
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1299 Pennsylvania Avenue, N.W.
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Nenue,
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US-08-255-457-1
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Best Local Similarity 47.6%;
Matches 10; Conservative 4
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APPLICATION NUMBER: 60/006,838

FILING DATE: 16-NOV-1995

ATTORNEY/AGENT INFORMATION:

NAME: Remenick, James

REGISTRATION NUMBER: 36,902

REFERENCE/DOCKET NUMBER: 0A146-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/090001
                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
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SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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104 GNGTGSHHN---VDGKHHGWR 121
                                                                                                                                                                                                                                         STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
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                                                                            CLASSIFICATION: 530
                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                CITY: Boston
                                                                                                                                                                                                                                                                                                                 STREET:
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TELEFAX: 202-639-7890
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STRANDEDNESS: sir
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                                                                                                                                                                                                                                                                                                                   225 Franklin Street
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Pred. No. 9
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                                                                                                                                                 Version
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; MOLECULE TYPE: US-09-115-032-1
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TELEFAX: (01.7
TELEFAX: 200154
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 60 amino acids
TYPE: amino acid
TYPE: 1inear
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US-09-115-032-1
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   Query Match
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Matches 9; Conserv
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                                                                                                                                                                    TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul C.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00398/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELLEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Plaut, Andrew G.
APPLICANT: Gilbert-Rothstein, Joanne V.
APPLICANT: Wright, Andrew
TITLE OF INVENTION: HELICOBACTER PYLORI NICKEL BINDING
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/255,457
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
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CITY: Boston
STATE: Massac
                                                                                                                                     TYPE:
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                                                                                                                       TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                           FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
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(617) 542-8906
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                                                                                                      protein
                    31.1%;
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   4; Mismatches
                   Score 55; DB 2; Length 60; Pred. No. 2.4;
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   11; Indels
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Search completed: July Job time: 189 sec

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СНИНИНИТИНИНУНССЕНИНИНИ 33

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                                                                                                   ; TOPOLOGY: linear; MOLECULE TYPE: protein PCT-US95-05772-1
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PCT-US95-05772-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Дb
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                                                                                                                                                                         INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Plaut, Andrew G.
APPLICANT: Gilbert-Rothstein, Joanne V.
APPLICANT: Wright, Andrew
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Wright, Andrew TITLE OF INVENTION: HELICO BINDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                       TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY: U.S.A.
ZIP: 02110-2804
                                                                                                                                                                                                                                                                                                                        CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
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                              4; Mismatches
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                                          Score 55; I
Pred. No. 2.
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Title:
Perfect score:
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seq length: 0-
seq length: 2000000000
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1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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July 6, 2001, 09:18:01; Search time 73.59 Seconds (without alignments) 28.983 Million cell updates/sec
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177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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kininogen, HMW II
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| 62                 | 62                 | 62.5               | 62.5               | 63                 | 63                 | 63                 | 63                 | . 63.5             | 63.5               | 63.5               | 63.5                                   | 64                 | 64                 | 64.5               | 64.5               |
| 35.0               | 35.0               | 35.3               | 35.3               | 35.6               | 35.6               | 35.6               | 35.6               | 35.9               | 35.9               | 35.9               | 35.9                                   | 36.2               | 36.2               | 36.4               | 36.4               |
| 389                | 189                | 980                | 306                | 735                | 351                | 286                | 208                | 226                | 196                | 196                | 110                                    | 375                | 207                | 549                | 398                |
| N                  | Ν                  | Ц                  | N                  | N                  | Ц                  | N                  | ĸ                  | N                  | N                  | N                  | N                                      | N                  | N                  | ν                  | N                  |
| в96635             | C81428             | S45444             | S08607             | T45059             | KGZQHL             | S07193             | T08132             | T27843             | A49987             | D85999             | T07618                                 | T08134             | T08109             | T15506             | T02681             |
| hypothetical prote | peptidyl-prolyl ci | BEM1 protein-bindi | chorion protein s3 | hypothetical prote | histidine-rich gly | chorion protein s3 | oleosin-like prote | hypothetical prote | probable fkbP-type | hypothetical prote | <ul> <li>cold stress protei</li> </ul> | oleosin-like prote | oleosin-like prote | hypothetical prote | probable zinc tran |

## ALIGNMENTS

| A; "Itle: Completion of the primary structure of numan high-molecular-mass kininogen. A; Reference number: A24871; MUID:86108361  A; Accession: A24871  A; Molecule type: protein A; Residues: 'Z', 20-380 < KELL> A; Residues: 'Z', 20-380 < KELL> A; Reflermann, J.; Lottspeich, F.; Henschen, A.; Mueller-Esterl, W. in Kinins IV, Greenbaum, L.M., and Margolius, H.S., ed., pp. 85-89, Plenum Press, New A; Title: Amino acid sequence of the light chain of human high molecular mass kininoge A; Reference number: A27899  A; Accession: A27899 | A; Note: differences are due to known cloning artifacts R; Lottspeich, F; Kellermann, J.; Henschen, A.; Foertsch, B.; Muller-Esterl, W. Eur. J. Biochem. 152, 307-314, 1985 A; Title: The amino acid sequence of the light chain of human high-molecular-mass kini A; Reference number: A91153; MUID:86030270 A; Accession: A91153; MUID:86030270 A; Accession: A91153 A; Molecule type: protein A; Residues: 379-644 < LOT> A; Note: the bradykinin sequence preceding the light chain sequence was not determined R; Kellermann, J; Lottspeich, F; Henschen, A; Mueller-Esterl, W. Eur. J. Biochem. 154, 471-478, 1986 | A; Molecule type: mRNA A; Molecule type: mRNA A; Residues: 1-592, /I', 594-644 < TAK> A; Residues: 1-592, /I', 594-644 < TAK> A; Residues: 1-629, /I', 594-644 < TAK> A; Residues: 1-629, /I', 594-644 < TAK> A; Residues: GB: M11437; NID: g186751; PIDN: AAB59550.1; PID: g386852 A; Auerswald, E.A.; Roessler, D.; Mentele, R.; Assfalg-Machleidt, I. FEBS Lett. 321, 93-97, 1993 A; Title: Cloning, expression and characterization of human kininogen domain 3. A; Reference number: S32422; MUID: 93223854 A; Accession: S32422 A; Molecule type: mRNA A; Residues: 'ANSM', 253-377 < AUE> | A;Accession: A01279 A;Molecule type: mRNA A;Residues: 1-389 <ohk> A;Cross-references: GB:K02566; NID:g177889 A;Cross-references: GB:K02566; NID:g177889 R;Takagaki, Y.; Kitamura, N.; Nakanishi, S. J. Biol. Chem. 260, 8601-8609, 1985 A;Title: Cloning and sequence analysis of cDNAs for human high molecular weight and l A;Reference number: A92544; MUID:85234582 A;Accession: A25276</ohk> | RESULT 1  KCHUH1  Kininogen, HMW precursor [validated] - human  kininogen, HMW precursor [validated] - human  N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen; prokininogen  N;Contains: bradykinin (kalildin I); HMW kininogen I; HMW kininogen II; low molecular  C;Species: Homo sapiens (man)  C;Date: 28-May-1986 #text_change 08-Dec-2000  C;Date: 28-May-1986 #text_change 08-Dec-2000  C;Accession: A01279; A25276; S32422; A91153; A24871; A27899; A27699; A31905; A34030;  R;Ohkubo, I.; Kurachi, K.; Takasawa, T.; Shiokawa, H.; Sasaki, M.  B;Ochemistry 23, 5691-5697, 1984  A;Title: Isolation of a human cDNA for alpha-2-thiol proteinase inhibitor and its ide  A;Reference number: A90490; MUID: B5122621 |
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FEBS Lett. 280, 211-215, 1991
A;Title: Inactivation of human cystatin C A;Reference number: S14303; MUID:91192133
A;Accession: S14447
A;Molecule transparence
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A; Molecule type: protein
A; Molecules 381-389 < MAE>
A; Residues: 381-389 < M.E
A; Residues: 381-380 < M.; Ideishi, M.; Arakawa, K.
R; Sasaguri, M.; Ikeda, M.; Ideishi, M.; Arakawa, K.
Biochem. Biophys. Res. Commun. 150, 511-516, 1988
A; Title: Identification of [hydroxyproline(3)]-lysyl-bradykinin released
A; Title: Tdentification of [hydroxyproline(3)]-lysyl-bradykinin released
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 431-434 <57R>
A; Residues: 431-434 <57R>
B; Kitamura, N.; Kitagawa, H.; Fukushima, D.; Takagaki,
J. Biol. Chem. 260, 8610-8617, 1985
A; Title: Structural organization of the human kininoger
                                                                                                                                                                                                                           A; Molecule type: protein
A; Residues: 450-452, 'X', 454, 'X', 456 <LIT>
R; Straczek, J.; Maachi, F.; le Nguyen, D.;
FEBS Lett. 373, 207-211, 1995
                                                                                                                                                                                                                                                                                                                                    A;Molecule type: protein
A;Residues: 264-359,'N',361-375 <LEN2>
A;Rittle, S.S.; Johnson, D.A.
Biochem. J. 307, 341-346, 1995
A;Title: Human mast cell tryptase isoforms:
A;Reference number: S55239; MUID:95251593
A;Accession: S55239
                                                                                                                              A;Title: Purification from human plasma of a A;Reference number: S68059; MUID:96033974 A;Accession: S68059 A;Molecule type: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Molecule type: protein
A;Residues: 1-19;189-192;310-314;381-389 <LEN1>
R;Rato, H.; Matsumura, Y.; Maeda, H.
FEBS Lett. 232, 252-254, 1988
A;Title: Isolation and identification of hydroxyproline analogues of bradykinin
A;Reference number: A61495; MUID:88211869
A;Accession: A61495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Residues: 380-389 < KAT3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Experimental source: urine A; Note: this peptide had Pro-383 modified A; Accession: C61495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: protein
A; Residues: 381-389 < KAT2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: protein A; Residues: 380-389 <SAS>
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A; Molecule type: protein
A; Residues: 379-389, 'K', 390-407, 'Q', 409-644 <KEL2>
R; Mindroiu, T.; Carretero, O.A.; Proud, D.; Walz, D.; S
Blochem. Biophys. Res. Commun. 152, 519-526, 1988
A; Title: A new kinin molety in human plasma kininogens.
A; Reference number: A27699; MUID:88209021
A; Accession: A27699
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number:
  A92545; MUID:85234583
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                        kininogen gene and a model for its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           kininogen by human
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                                                                     Y.; Miyata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Turk,
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                                                                                                                                                                                                                                                         M.H.; Nabet,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cathepsin
                                                                        T.; Nakanishi,
                                                                                                                                                                                                                                                                                                                                                                                          of substrate-spec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 inflammatory
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F;142-253/Domain: Cystatin homology <CY2>
F;264-375/Domain: Cystatin homology <CY2>
F;264-375/Domain: Cystatin homology <CY3>
F;380-389/Product: lysyl-bradykinin (kallidin II) #status experimental <BDY>
F;380-389/Product: bradykinin (kallidin I) #status experimental <CH>
F;381-389/Product: low molecular weight growth promoting factor #status experimental F;431-44/Product: low molecular weight growth promoting factor #status experimental F;431-43/Product: low molecular weight growth promoting factor #status experimental F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental F;28-614,83-94,107-126,142-145,206-218,229-248,264-267,328-340,351-370/Disulfide bond F;48/Binding site: carbohydrate (Asn) (covalent) #status experimental F;169,205,294/Binding site: wet-tys (kallikrein) #status experimental F;389/Modified site: #tydroxyproline (Pro) (partial) #status experimental F;389-390/Cleavage site: Arg-Ser (kallikrein) #status experimental F;401,533,542,446,557,571,593,628/Binding site: carbohydrate (Thr) (covalent) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                           kininogen, HMW II precursor - bovine
N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen
N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen
C;Species: Bos primigenius taurus (cattle)
C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999
C;Accession: A01202; A91923; A91941; A91938; B29559
R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, Sature 305, 545-549, 1983
A;Title: A single gene for bovine high molecular weight and low molecular we
A; Molecule type: protein A; Residues: 376-391 < KAT: R; Han, Y.N.; Kato, H.; Iv
                                                                                                                                   R:Kato, H.; Nagasawa, S.; Suzuki, T.
J. Biochem. 67, 313-323, 1970
A;Title: Studies on the structure of bovine
A;Reference number: A91923; MUID:70180420
                                                                                                                                                                                                                                                                              A; Cross-references: GB: V01492;
                                                                                                                                                                                                                                                                                                       A;Accession: A01282
A;Molecule type: mRNA
A;Residues: 1-619 <KIT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      F;1-18/Domain: signal sequence #status experimental <SIG>
F;19-644/Product: HMW kininogen I (prokininogen) #status experimental <MAT1>
F;19-379,390-644/Product: HMW kininogen II #status experimental <MAT2>
F;19-379/Domain: HMW kininogen heavy chain #status experimental <HCH>
F;19-379/Domain: cystatin homology <CYI>
F;19-131/Domain: cystatin homology <CYI>
F;19-131/Domain: cystatin homology <CYI>
                                                                                                A; Accession: A91923
                                                                                                                                                                                                                                                                                                                                                                                                                     A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A:Title: Structural features of plasma kinins and kininogens.

A:Reference number: A91455; MUID:90255622

A:Contents: annotation; bradykinin

C:Comment: The HMW kininogen precursor and the LMW form are produced from the same ge C:Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of C:Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is i C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   xyproline residue
C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               . Similarity
28; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 es: GDB:125256; OMIM:228960
3q27-3q27
102/3; 131/1; 188/3; 224/3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ST
                                   <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                     ene for bovine high molecular A93317; MUID:84014106
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ki, T.
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Pred. No. 2.7
); Mismatches
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                                                                                                                                                                       kininogen:
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2.7e-13;
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prior to the release of bradykinin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  T.; Nawa, H.; Nakanishi, S.
                                                                                                                                                                                                                                                                          PIDN:CAA24736.1;
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                                                                                                                                                                       disulfide
                                                                                                                                                                                                                                                                          PID: 9494
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Iwanaga,

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Suzuki,

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C:Comment: The HMW kininogen precursor is produced from the same gene as the LMW form as C:Comment: Kininogen is a cysteine precursor is produced from the same gene as the LMW form as C:Comment: Kininogen is a cysteine precursor of HMW kininogen light chain is imposed C:Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator, i xyproline residue is present in the kininogen prior to the release of bradykinin.

C:Superfamily: kininogen; cystatin homology C:Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; dupl F:1-18/Domain: signal sequence #status predicted <SIG>
F:19-619/Product: HMW kininogen II #status predicted <MAT>
F:19-376/Product: HMW kininogen II heavy chain #status experimental <HCH>
F:19-130/Domain: cystatin homology <CY1>
F:261-372/Domain: cystatin homology <CY2>
F:377-386/Product: lysyl-bradykinin (kallidin II) #status experimental <KBDY>
F:388-619/Product: bradykinin (kallidin II) #status experimental <CH>
F:418-488/Region: glycine/histidine/lysine-rich
F:27-589,82-93,106-125_141-144,205-217,228-247,261-264,325-337,348-357/Disulfide bonds:
F:47/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:136,169,204,280/Binding site: carbohydrate (Asn) (covalent) #status experimental
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F;47/Binding site: carbohydrate (Asn) (covalent, Asn) (covalent) **summark (Asn) (covalent) **summark (Asn) (covalent) **summark (Asn) (covalent) **summark (Asn) (covalent) (partial) **status experimental F;186/Binding site: carbohydrate (Asn) (covalent) (partial) **status experimental F;197/Binding site: Met-Lys (Rallikrein) **status experimental F;376-377/Cleavage site: Met-Lys (Rallikrein) **status experimental F;380/Moddfied site: 4-hydroxyproline (Pro) **status experimental F;386-387/Cleavage site: Arg-Ser (Rallikrein) **status experimental F;396,400,404,510/Binding site: carbohydrate (Ser) (covalent) **status experimental F;397,398,518,522,534,546,551,568/Binding site: carbohydrate (Thr) (covalent) **status experimental
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A;Title: Primary stru
A;Reference number: A;
A;Accession: A91941
A;Molecule type: prot
A;Residues: 387-455
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J. Biochem. 77, 55-68, 1975
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A;Residues: 456-496 KHA2>
A;Residues: 456-496 KHA2>
A;Residues: 456-496 KHA2>
A;Residues: 456-2779, 1987

J. Biol. Chem. 262, 2768-2779, 1987
A;Title: Bovine high molecular weight kininogen.
A;Reference number: A92627; MUID:87137530
A;Accession: B29559
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A; Residues: 'Z', 20-104, 'E', 106-256, 'XX', 257-376 <SUE>
R; Lottspeich, F.; Kellermann, J.; Henschen, A.; Foertsch,
Eur. J. Biochem. 152, 307-314, 1985
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Seikagaku 56, 808,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Title: The amino acid sequence of the light chain of human high-molecular-mass A; Reference number: A91153; MUID: 86030270
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470
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                                                                  1 GHKHKHGHGHGKHKNKGKKNGKHNGWKT 28
GHGHKHGHGKHKNKGKNNGKHYDWRT
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mary structure of bo
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iya, M.; Iwanaga, S.; Suzuki, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein
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                                                                                                                                                                                                83.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of bovine plasma high-molecular-weight kininogen. The \ensuremath{\mathtt{MUID}}\xspace:76260155
                                                                                                                                                  Score 147; DB Pred. No. 7.8e

1; Mismatches
                                                                                                                                                                                                                                     DB
                                                                                                                                                                                            .8e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       bovine
S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            found
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The amino acid sequence, positions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         carbohydrate
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                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                (covalent) #status
                                                                                                                                                      0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Iwanaga
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RESULT

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R; Han, Y.N.; Komiya, M.; Iwanaga, S.; Suzuki, T.

J. Biochem. 77, 55-68, 1975

A; Title: Studdles on the primary structure of bovine high-molecular-weight kininogen. A; Title: Studdles on the primary structure of bovine high-molecular-weight kininogen. A; Reference number: A91938

A; Accession: A91938

A; Accession: A91938

A; Molecule type: protein
A; Sueyoshi, T.; Miyata, T.; Hashimoto, N.; Kato, H.; Hayashida, H.; Miyata, T.; Iwana
J. Biol. Chem. 262, 2768-2779, 1987

A; Title: Bovine high molecular weight kininogen. The amino acid sequence, positions of A; Reference number: A92627; MUID:87137530

A; Reference number: A92627; MUID:87137530

A; Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUE>
A; Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUE>
A; Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUE>
A; Residues: 'Z', 20-123, 'I', 125-127, 'I', 129-378 <SUE>
A; Fitte: The amino acid sequence of the light chain of human high-molecular-mass kini A; Reference number: A91153; MUID:86030270

A; Contents: annotation; bovine clavage sites; bovine carbohydrate binding sites
R; Sueyoshi, T.; Miyata, T.; Kato, H.; Iwanaga, S.
Seikagaku 56, 808, 1984

A. Title: Diagnation of human high-molecular-mass sites and the state of the bovine carbohydrate binding sites
Relargatu 56, 808, 1984
                                                                                 F;1-18/Domain: signal sequence #status predicted <SIG>
F;19-621/Product: HMW prokiningen I heavy chain #status experimental <HCH>
F;19-379/Product: HMW kiningen I heavy chain #status experimental <HCH>
F;19-130/Domain: cystatin homology <CYI>
F;141-252/Domain: cystatin homology <CYZ>
F;263-374/Domain: cystatin homology <CYZ>
F;263-374/Domain: cystatin homology <CYZ>
F;379-388/Product: bradykinin (kallidin II) #status experimental <BDY>
F;380-388/Product: bradykinin (kallidin II) #status experimental <BDY>
F;389-521/Product: HMW kininogen I light chain #status experimental <LCH>
F;417-488/Region: glycine/histidine/lysine-rich
F;19/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status experimental
F;27-591,82-93,106-125,141-144,205-217,228-247,263-266,327-339,350-369/Disulfide bond
F;87,168,169,204/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;197/Binding site: carbohydrate (Thr) (covalent) #status experimental
F;197/Binding site: carbohydrate (Asn) (covalent) #status experimental
F;378-379/cleavage site: Met-Lys (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Contents: annotation; disulfide bonds
A;Note: article in Japanese
C;Comment: The HMW kininogen precursor is produced from the same gene as the LMW form
C;Comment: Kininogen is a cysteine proteinase inhibitor, takes part in initiation of
C;Comment: The glycine/histidine/lysine-rich region of HMW kininogen light chain is i
C;Comment: Bradykinin, released from kininogen by kallikrein, is a potent vasodilator
xyproline residue is present in the kininogen prior to the release of bradykinin.
C;Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing; blood coagulation; cysteine proteinase inhibitor; d
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N;Alternate names: alpha-2-thiol proteinase inhibitor; preprokininogen N;Contains: bradykinin (kallidin); kininogen I; kininogen II; prokininogen C;Species: Bos primigenius taurus (cattle) C;Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 22-Jun-1999 C;Accession: A01181; A91923; A91938; A29559 R;Kitamura, N.; Takagaki, Y.; Furuto, S.; Tanaka, T.; Nawa, H.; Nakanishi, Sature 305, 545-549, 1983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Title: Studies on the structure of bovine kininogen: cleavages of disulfide bonds A;Reference number: A31923; MUID:70180420
A;Accession: A91923
A;Molecule type: protein
A;Residues: 378-393 <KAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; MCJecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-621 <KITY
A; Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1;
A; Cross-references: GB:V01491; GB:K01757; NID:g491; PIDN:CAA24735.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Title: A single gene
A;Reference number: A93
A;Accession: A01281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Title: Disulfide bonds in bovine HMW kininogens A; Reference number: A94300
F;382/Modified site: 4-hydroxyproline (Pro) #status predicted F;388-389/Cleavage site: Arg-Ser (kallikrein) #status experimental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         kininogen,
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A93317; MUID:84014106
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for major acute phase alpha-1-protein

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N:Contains: bradykinin
C:Species: Rattus norvegicus (Norway rat)
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 15-Nov-1996
C:Accession: A25486
R;Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S.
J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene f.
A;Reference number: A92625; MUID:87137443
A;Accession: A25486
A;Molecule type: mRNA
A;Residues: 1-639 <KIT>
A;Note: the authors translated the codon CAA for residue 347 as Asn
C:Superfamily: kininogen; cystatin homology
C;Keywords: alternative splicing
F;1-18/Domain: signal sequence #status predicted <MAT>
F;19-639/Product: kininogen, HMW I #status predicted <MAT>
F;19-131/Domain: cystatin homology <CY1>
F;264-375/Domain: cystatin homology <CY3>
F;264-375/Domain: cystatin homology <CY3>
                                                                                                              δÃ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Species: Rattus no
C;Date: 08-Mar-1989
C;Accession: C25486
  RESULT
                                                                    B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Kitagawa, H.; Kitamura, N.; Hayashida, H.; Miyata, T.; Nakanishi, S. J. Biol. Chem. 262, 2190-2198, 1987
A;Title: Differing expression patterns and evolution of the rat kininogen gene family. A;Reference number: A92625; MUID:87137443
A;Accession: C25486
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Comment: The nucleotide sequence was obtained from
C;Superfamily: kininogen; cystatin homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: DNA
A; Residues: 1-264 <KIT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    kininogen, HMW I precursor -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          K-kininogen,
                                                                                                                                                                                       Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -kininogen, HMW precursor - rat (fragment)
Species: Rattus norvegicus (Norway rat)
Spate: 08-Mar_1989 #sequence_revision 08-Mar_1989 #text_change 30-Sep-1993
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Best Local Similarity
                                                                    492
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                                                                                                              1 GHKHKHGHGHGKHKNKGKKNGKH 23
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6
                                                                    GHGHGHGRDKHTNKDKNNVKH
                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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82.1%;
                                                                                                                                                                                  49.78;
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                                                                                                                                                            Score 88; DB
Pred. No. 0.00
0; Mismatches
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                                                                    514
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Pred. No. 0.0026;
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                                                                                                                                                                                     0.0054;
                                                                                                                                                                                                           DB 2;
                                                                                                                                                            8
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                                                                                                                                                                                                           Length 639;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 621;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: Rattus norvegicus (Norway rat)
C;Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #te(),Accession: A27115
                                                                                                                                                                                                                                                                                В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: MAP1
C;Superfamily: kininogen;
F;19-65/Domain: cystatin |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             J. Biol. Chem. 262, 9298-9308, 1987
A;Title: Structure and expression of the genes for major acute phase alpha-1-protein A;Reference number: A92653; MUID:87250580
A;Accession: A27115
A;Status: not compared with conceptual translation
A;Molecule type: DNA
A;Molecule type: DNA
A;Residues: 1-315 <FUN>
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-290 <FUN>
A; Residues: 1-290 <FUN>
R; Kageyama, R.; Kitamura, N.; Ohkubo, H.; Nakanishi, S.
J; Biol. Chem. 262, 2345-2351, 1987
A; Title: Differing utilization of homologous transcription initiation sites A; Reference number: A25488; MUID:87137465
A; Reference number: A25488; MUID:87137465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     K-kininogen, LMW precursor - rat (fragments)
C. Species: Rattus norvegicus (Norway rat)
C. Date: 31-Mar-1989 #sequence_revision 31-Mar-1989 #text_change 20-Aug-1999
C. Accession: C27115; A25488
R. Fung, W.P.; Schreiber, G.
J. Biol. Chem. 262, 9298-9308, 1987
A. Title: Structure and expression of the genes for major acute phase alpha-1
A. Reference number: A92653; MUID:87250580
                 A; Reference number:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: GB:J02662; NID:g205071; PIDN:A C;Superfamily: kininogen; cystatin homology F:19-65/Domain: cystatin homology (fragment) <CYS>
                                                                                                                                                                                  T48099
                                                                                                                                                                                                           RESULT
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A; Residues: 1-48 < KAG>
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Best Local Similarity
Matches 19; Conserv
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19; Conservative
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33.9%;
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31-Mar-1989 #text\_change 16-Jul-1999

0;

---GKHKNKGKKNGKH 23

Score 80.5; DB Pred. No. 0.02; Mismatches

DB

2;

290;

4;

Indels

33;

Gaps

2

PIDN: AAA41483.1;

PID:g205072

0f

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R;Obermaier, B.; Ottenwaelder, B.; Duchemin, D.; submitted to the Protein Sequence Database, Apri
                                                                                                                     hypothetical protein T20010.200 - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000 C:Accession: T48099
   A; Accession:
T48099
                                                          , D.; Zeitler, K.; Mewes, H.W.; Rudd, April 2000
                                                                                           s:
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Score 80.5; DB Pred. No. 0.022; 0; Mismatches

2;

Length 315; Indels

4;

33;

Gaps

2

214

Вþ

140

GHGYGYGHGHGKFKHGKHGKFKHGKH 165

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A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-199 <OBE>
A;Cross-references: EMBL:AL163816
A;Experimental source: cultivar Columbia; BAC clone T20010
C;Genetics:
                                                                                                                                                                                                                                           R;Marty, I.; Monfort, A.; Stiefel, V.; Ludevid, Plant Mol. Biol. 30, 625-636, 1996
A;Title: Molecular characterization of the gene A;Reference number: S65780; MUID:96189273
A;Accession: S65780
                                                                                                                                                                                                                                                                                                                           glycine/proline-rich protein GPRP - Arabidopsis thaliana
C;SpecLes: Arabidopsis thaliana (mouse-ear cress)
C;Date: 28-Oct.1996 #sequence_revision 27-Feb-1997 #text_change 21-Jul-2000
C;Accession: S65780
                                                                                                                                                                                                                                                                                                                                                                                             RESULT
S65780
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Palmiter, R.D.; Findley, S.D.
EMBO J. 14, 639-649, 1995
A;Title: Cloning and functional characterization
A;Reference number: S54302; MUID:95188868
A;Accession: S54303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N:Alternate names: zinc transporter ZnT-1
C:Species: Rattus norvegicus (Norway rat)
C:Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change
C:Accession: S54303
                 Qy
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A;Residues: 1-177 <MAR>
A;Cross-references: EMBL:X84315;
A;Note: mRNA was also sequenced
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A;Residues: 1-507 <PAL>
A;Cross-references: EMBL:U17133; NID:g577842; PIDN:AAA79234.1; PID:g577843
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A; Introns: 163/2
                                                                                                                               A;Gene: GPRP
A;Introns: 99/1
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Best Local
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Best Local Similarity
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GHKHKHGHGHG--KHKNKGK-KNGKH
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                                                                Similarity
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                                                 Conservative
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                                                                41.0%;
57.7%;
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57.7%;
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Pred. No. 0.07
2; Mismatches
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                                                               Score 72.5; DB Pred. No. 0.11;
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                 23
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                                                 Mismatches
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A;Gene: fsh
A;Gene: fsh
A;Cross-references: FlyBase:FBgn0004656
C;Superfamily: unassigned bromodomain proteins; bromodomain homology
C;Superfamily: spicing; transmembrane protein
F;1-2038/Product: female sterile homeotic protein, 205K #status pred
F;1-1106/Product: female sterile homeotic protein, 110K #status pred
F;59-116/Domain: bromodomain homology <BR01>
F;59-1-7/7----/-- bromodomain homology <BR02>
                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-1106 <HA2>
A; Cross-references: EMBL:M23222
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                 A; Cross-references: A; Accession: B43742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Drosophila melanogaster
C;Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change
C;Accession: A43742; B43742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    female sterile homeotic protein, 205K - fruit fly N;Alternate names: membrane protein fsh, 205K N;Contains: female sterile homeotic protein, 110K
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N;Alternate names: protein K10A8_130
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-2038 <HAY>
                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: A; Accession: A43742
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A; Title: The Drosophila fsh
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R;Sato, S.; Nakamura, Y.; Kaneko,
                                                                                                                                                                                                                                                                                                                               A; Status: preliminary
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A; Introns: 97/1
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A; Residues: 1-173 <SAT>
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Best Local Similarity 39...
Conservative
    Matches
                    Query Match
Best Local Similarity
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    Conservative
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ce: cultivar Columbia; BAC
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                  40.1%;
46.2%;
                    Score 71;
Pred. No.
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Database,
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Pred. No. 0
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August 2000
                                        DB 2;
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                                      Length 2038;
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Gaps
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1 GHKHKHGHGHGKHKNKGKKNGKHNGW

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597 GHGHGHGHGHGHGHGHGHGHGY 622

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gene 2C protein - slime mold (Dictyostelium discoideum)
(;Species: Dictyostelium discoideum
C;Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 29-Oct-1999
C;Accession: S08137
R;Ramji, D.P.; Richards, A.J.; Jagger, P.; Bleasby, A.; Hames, B.D.
Mol. Microbiol. 4, 129-135, 1990
A;Title: Two cyclic AMP-regulated genes from Dictyostelium discoideum encode homologous A;Reference number: S08136; MOID:90205618
A;Accession: S08137
A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-515 <WILD
A;Cross-references: EMBL:299942; PIDN:CAB17070.1; GSPDB:GN00028; CESP:H13N06.5
A;Experimental source: clone H13N06
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A; Introns: 118/1; 156/2; 182/2; 306/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, October 1997 A; Reference number: Z19673 A; Accession: T23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     hypothetical protein H13N06.5 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct.1999 #sequence_revision 15-Oct.1999 #text_change 18-Feb-2000 C;Accession: T23089
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 14
T23089
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A;Actarran S54302
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C;Species: Mus musculus (house mouse)
C;Date: 15-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999
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A; Residues: 1-503 < PAL>
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A;Residues: 1-98 <RAM>
A;Residues: 1-98 <RAM>
A;Cross-references: EMBL:X16827; NID:g7161; PIDN:CAA34727.1; PID:g7162
C;Genetics:
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Search completed: July 6, 2001, 09:18:01 Job time: 647 sec

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| SEQUENCE OF 3 SEQUENCE OF 3 SEQUENCE J.V.; Pierce J.V.; Structural i "Structural i Fed. Proc. 27 [6] DISULFIDE BON Sueyoshi T.; "Disulfide bo          | MEDLINE-8<br>Ohkubo I.<br>"Isolatior<br>its identit<br>its identit<br>its identit<br>its identit<br>Biochemist<br>[4]<br>SEQUENCE (<br>MEDLINE-8<br>MEDLINE-8<br>LOTTSPEIC)<br>Mueller-E<br>Mueller-E<br>The amino<br>mass kinii                                      | RP SEQUENCE FROM N. TISSUE-Liver; RX MEDLINE-85234582 RA Takagaki Y., Kit RT Takagaki Y., Kit RT Two human prekin RT Two human prekin RT J. Biol. Chem. 2 RN [2] RP GENE STRUCTURE. RX MEDLINE-85234583 RA Kitamura N., Kit RA Nakanishi S.; RT TSTRUCTURAL Orga RT Its evolution."; RL J. Biol. Chem. 2 RN [3] | SULT 1  L KNG_HUMAN  KNG_HUMAN  P01042; I  21-JUL-1  01-FEB-1: 01-OCT-2  KININOGEB  BRADYKIN.  KNG.  HOMO sap: Eukaryott  Mammalia.  NCBI_Tax.                                                                                | 34 58.5 3 35 58 3 36 58 3 37 58 3 38 58 3 39 58 3 40 57 3 41 56.5 7 42 56.5 3 45 56.5 3                                                                                                                                                                                                                       |
|--------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|---------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 235622; PubMed=4952632;<br>l features of plasma kinins and<br>27:52-57(1968).<br>ONDS.<br>Miyata T., Kato H., Iwanaga<br>bonds in bovine HMW Kininogen | 122621; PubMed=6441591; Kurachi K. Takasawa T. Sh. of a human cDNA for alpha 2: tty with low molecular weight ry 23:5691-5697(1984).  F 379-644. S030270; PubMed=4054110; F Kellermann J., Henschen sterl W.; acid sequence of the light of cohem. 152:307-314(1985). | .A. (ISOFORMS HMW 2; PubMed=2989293 tamura N., Nakani quence analysis o molecular weight ninogens."; 260:8601-8609(198 3; PubMed=2989294 tagawa H., Fukush tagawa H., Fukush an1zation of the 260:8610-8617(198                                                                                                 | STANDARD; PRT; 644 901043; 901043; 986 (Rel. 01, Created) 996 (Rel. 33, Last sequence updat) 900 (Rel. 40, Last annotation upo PRECURSOR (ALPHA-2-THIOL PROTE: IN); 1ens (Human); 1: Eutheria; Primates; Catarrhini; 1D-9606; | 3.1 212 1 SLYD_AERHY 2.8 155 1 KNOB_PLAFD 2.8 277 1 KNOB_PLAFD 2.8 473 1 KNOB_PLAFA 2.8 634 1 KNOB_PLAFN 2.8 657 1 KNOB_PLAFN 2.8 449 1 CSUP_DROME 2.2 476 1 KEND_PLAFN 2.2 1063 1 ELF1_DROME 2.2 176 1 KE4_MOUSE 2.3 1063 1 ELF1_DROME 3.7 1 ZNUA_HAEIN 1.9 337 1 ZNUA_HAEIN 1.6 645 1 CNG3_CHICK ALIGNMENTS |
| and kininogens."; aga S.; gens.";                                                                                                                      | hiokawa H., Sasaki M.;<br>2-thiol proteinase inhibitor and<br>1 kininogen.";<br>2 n A., Foertsch B.,<br>3 chain of human high-molecular-                                                                                                                              | AND LMW).  ; shi S.; shi S.; f CDNAs for human high molecular prekininogens. Primary structures of prekininogens. Primary structures of thima D., Takagaki Y., Miyata T., human kininogen gene and a model for 5).                                                                                              | T; 644 AA.  nce update) ation update) OL PROTEINASE INHIBITOR) [CONTAINS: aniata; Vertebrata; Euteleostomi; tarrhini; Hominidae; Homo.                                                                                        | O07046 aeromonas h Q29175 sus scrofa P05229 plasmodium A P13817 plasmodium G P09346 plasmodium N P06719 plasmodium Q09034 drosophila G Q31125 mus musculu E Q3422 actinobacil N P44526 haemophilus P44526 haemophilus P44526 plasmodium Q09080 gallus gall                                                    |

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PIR; A01279; K0
PIR; A25276; A3
PIR; A25276; B3
PIR; B25276; B3
PIR; S02482; S0
SWISS-2DPAGE; I
                  CHAIN
                                                                            PRINTS; PRO0334; KININOGEN.

PROSITE; PS00287; CYSTATIN; 2.

PROSITE; PS00287; CYSTATIN; 2.

Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator; Bradykinin; Blood coagulation; Inflammatory response; Signal;
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HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
FACTOR XII; (3) HMW-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININOGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOPHELIUM DERIVED RELAXING FRACTOR ACTION); (5)
LMW-KININOGEN INHIBITS THE AGGREGATION OF THROMBOCYTES; (6) LMW-
KININOGEN IS IN CONTRAST TO HMM-KININOGEN NOT INVOLVED IN BLOOD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Extra the European Bioinformatics Institute. There are no restitute the companion of the companion of the control of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion of the companion 
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                                                                                                                                                                                                                                         MIM; 228960;
                                                                                                                                                                           Pfam; PF00031; cystatin;
                                                                                                                                                                                                InterPro; IPR000010; -. InterPro; IPR002395; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: SECRETED.
ALTERNATIVE PRODUCTS: 2 ISOFORMS;
PRODUCED BY ALTERNATIVE SPLICING.
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ALTERNATIVE
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M11525;
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M11521;
M11522;
M11523;
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M11437;
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A25276.
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AAB59551.1;
AAB59551.1;
AAB59551.1;
AAB59551.1;
AAB59551.1;
AAB59551.1;
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AAB59550.1;
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KININOGEN HEAVY CHAIN
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_BOVIN
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CONFLICT
SEQUENCE
SEQUENCE OF 19-376.
MEDLINE=87137530; P
Sueyoshi T., Miyata
                                                                                                                                                                                                                                                                                                                        CARBOHYD
CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                      "A single gene for bovine weight kininogens.";
Nature 305:545-549(1983).
[2]
                                                                                     Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Cetartioda Bovidae; Bovinae; Bos.
                                                                                                                  KININOGEN, HMW BRADYKININ].
                                                                                                                               21-JUL-1986 (Rel.
21-JUL-1986 (Rel.
01-OCT-2000 (Rel.
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DISULFID
                                                  Kitamura N.,
                                                       SEQUENCE FROM N.A.
MEDLINE-84014106; PubMed=6571699;
                                                                                                           Bos taurus (Bovine)
                                                                                                                                              P01045;
21-JUL-1986
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REPEAT
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DOMAIN
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Miyata T.,
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                                                                                                                                                            STANDARD;
      PubMed=3546295;
                                                                                                                              01, Created)
01, Last sequence update)
40, Last annotation updat
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                                          bovine
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593
71945
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Hashimoto N.,
                                         Furuto S., Tanaka T., high molecular weight
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                                                                                                                        annotation update)
(THIOL PROTEINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KININOGEN LIGHT CHAIN.
CYSTATIN-LIKE 1.
CYSTATIN-LIKE 2.
CYSTATIN-LIKE 3.
HIS-RICH (ASSOCIATED W
ACTIVITY).
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T -> I (IN REF. 1).
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PPKAGAEPASEREVS (IN ISOFORM L)
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                                                                                                  Craniata; Vertebrata;
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Pred. No. 1e-14;
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                                                                                            Ruminantia; Pecora;
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(GLCNAC.
(GLCNAC.
Kato H.,
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Hayashida
                                          and low molecular
                                                Nawa H., Nakanishi S.;
                                                                                                                                                                                                                                         Length
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Ξ.
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Iwanaga S.;

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Interpro; IPR000010; -.
Interpro; IPR002395; -.
Interpro; IPR002395; -.
Pfam; PF00031; cystatin; 3.
PRINTS; PR00334; KININOGEN.
PROSITE; P800287; CYSTATIN; 2.
PROSITE; P800287; CYSTATIN; 2.
Clycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; Thiol protease inhibitor; Bradykinin; Blood coagulation; Signal;
                                                                                                                                                       PIR; A01282; KGBOH2.
PIR; B29559; B29559.
HSSP; P04129; 1AFI.
                                                                                                                                                                                                                                                                             modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Studies on the primary structure of bovine high-molecular-we kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
-I- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASE:
                                                                                                                                                                                                                    EMBL; V01492; CAA24736.1; EMBL; V01492; CAA24737.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 456-496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Primary structure of bovine plasma high-molecular-weight kininogen. The amino acid sequence of a glycopeptide portion (fragment 1) following the C-terminus of the bradykinin moiety.";

"", Blochem. 79:1201-1222(1976).
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"Studies
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SUBCELLULAR LOCATION: EXTRACELLULAR.

SUBCELLULAR LOCATION: EXTRACELLULAR.

ALTERNATIVE PRODUCTS: HMW II AND LAW II KININOGEN PRECURSORS PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2) HMM-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO FACTOR XII; (3) HMM-KININOGEN INHIBITS THE THROMBIN- AND
                                                                                                                                                                                                                                                                                                                                                                                                                                       PTM: BRADYKININ IS RELEASED FROM KININGEN BY SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE BRADYKININ THAT IS RELEASED FROM HAW-KININGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS; (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4EI) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARBIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Y.N., Komiya M., Iwanaga S., Suzuki T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: PLASMA.
PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                molecular weight kininogen. The amino acid sequence, carbohydrate chains and disulfide bridges in the heavy
response
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Matches 23; Conser
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CARBOHYD
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DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
                                   Miyata T., Iwanaga S.;
"Bovine high molecular weight kininogen. The positions of carbohydrate chains and disulfic
                                                    Sueyoshi T., Miyata T., Miyata T., Iwanaqa S.:
                                                                                                                                                                                                21-JUL-1986 (Rel. 01, Last sequence update)
01-JUN-1994 (Rel. 29, Last annotation update)
KININGEN, HMW I PRECURSOR (THIOL PROTEINASE INHIBITOR) [CONTAINS:
SEQUENCE OF 378-393
MEDLINE=70180420; Pt
                                                                                            weight kininogens.";
Nature 305:545-549(1983).
                                                                                                          MEDLINE=84014106; PubMed=6571699;
Kitamura N., Takagaki Y., Furuto S., Tanaka T.,
"A single gene for bovine high molecular weight
                                                                                                                                                  Bovidae; Bovinae;
NCBI_TaxID=9913;
                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eute
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora;
                                                                                                                                                                                                         21-JUL-1986 (Rel. 01-JUN-1994 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Han Y.N., Komiya M., Iwanaga S., Suzuki T.; "Studies on the primary structure of bovine high-molecular-we kininogen. Amino acid sequence of a fragment ('histidine-rich peptide') released by plasma kallikrein.";
J. Biochem. 77:55-68(1975).
-!- FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN; 2.
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-!- PTM: BRADYKININ IS RELEASED FROM KININOGEN BY PLASMA KALLIKREIN.
-!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS.
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"Studies on the structure of bovine kininogen: cleavages of disulfide bonds and of methionyl bonds in kininogen-II.";
J., Biochem. 67:313-323(1970).
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InterPro; IPR002395; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                lycoprotein; Plasma; Duplication; Vasodilator; Alternative splicing; hiol protease inhibitor; Bradykinin; Blood coagulation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TO FACTOR XII; (3) HMW-KININGEN INHIBITS THE THOMBIN- AND PLASMIN-INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PERTIDE BRADYKININ THAT IS RELEASED FROM HMW-KININGEN SHOWS A VARIETY OF PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C)

NATRIURESIS AND DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION, INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR
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ALTERNATIVE PRODUCTS: HMW I AND LMW I KININOGEN PRECURSORS ARE PRODUCED FROM THE SAME GENE AS THE RESULT OF ALTERNATE MRNA SPLICING. THE SEQUENCES OF BOTH KININOGENS ARE IDENTICAL UP TO RESIDUE 400.
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FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (1) HAW-KININOGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXTON ENGROUP XII: (3) HWW-KININOGEN INHIBITS THE THROMEIN- AND
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CYSTATIN-LIKE 2.
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CYSTATIN-LIKE 3.
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INTERCHAIN.
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INDUCED AGGREGATION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
BRADYKININ THAT IS RELEASED FROM HMW-KININGEN SHOWS A VARIETY OF
PHYSIOLOGICAL EFFECTS: (4A) INFLUENCE IN SMOOTH MUSCLE
CONTRACTION, (4B) INDUCTION OF HYPOTENSION, (4C) NATRITRESIS AND
DIURESIS, (4D) DECREASE IN BLOOD GLUCOSE LEVEL, (4E) IT IS A
MEDIATOR OF INFLAMMATION AND CAUSES (4E1) INCREASE IN VASCULAR
PERMEABILITY, (4E2) STIMULATION OF NOCICEPTORS (4E3) RELEASE OF
OTHER MEDIATORS OF INFLAMMATION (E.G. PROSTAGLANDINS), (4F) IT HAS
A CARDIOPROTECTIVE EFFECT (DIRECTLY VIA BRADYKININ ACTION,
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION),
INDIRECTLY VIA ENDOTHELIUM-DERIVED RELAXING FACTOR ACTION,
KININGEN IS IN CONTRAST TO HMW-KININGEN NOT INVOLVED IN BLOOD
CLOTTING (BY SIMILARITY).
SUBCELLULAR LOCATION: SECRETED.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- SUBCELLULAR LOCATION: SECRETED.
-!- TISSUE SPECIFICITY: PLASMA.
-!- PTM: BRADYKININ IS RELEASED FROM KININGEN BY PLASMA KALLIKREIN.
-!- TISSUE SPECIFICITY: PLASMA.
-!- PTM: BRADYKININ IS RELEASED FROM KININGEN BY PLASMA KALLIKREIN.
-!- SIMILARITY: CONTAINS 3 CYSTATIN-LIKE DOMAINS:
             EMBL; D84435; BAA:
EMBL; D84415; BAA:
MGD; MGI:1097705;
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
                                                                                                                                       the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.

-i-FUNCTION: (1) KININGENS ARE INHIBITORS OF THIOL PROTEASES; (2)

-i-HMW-KININGEN PLAYS AN IMPORTANT ROLE IN BLOOD COAGULATION BY
HELPING TO POSITION OPTIMALLY PREKALLIKREIN AND FACTOR XI NEXT TO
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Takano M., Kondoh J., Yayama K., Ok
"Molecular cloning of cDNAs for mou
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Furuto-Kato S., Matsumoto A., Kitamura N., Nakanishi S.; "Primary structures of the mRNAs encoding the rat precursors for bradykinin and T-kinin. Structural relationship of kininogens will major acute phase protein and alpha 1-cysteine proteinase
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01-NOV-1988 (Rel. 09, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
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PRINTS; PR00334; KININOGEN;
PROSITE; PS00287; CYSTATIN; 1.
Glycoprotein; Plasma; Repeat; Thiol protease inhibitor; Vasodilator;
Bradykinin; Blood coagulation; Inflammatory response; Signal;
                                                                                                                                                                                 Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chor
Mammalia; Eutheria; Rode
                                                                                                                                                                                                                                                                                 KNG_RAT
P08934; P08933;
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InterPro;
                                                                                                                                                                     Eukaryota; Métazoa; Chordata;
Mammalia; Eutheria; Rodentia;
NCBI_TaxID=10116;
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                                                                                                          Kitagawa H., Kitamura "Differing expression
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                                                 MEDLINE=86008264;
                                                           SEQUENCE FROM N.A.
                                                                                                                                  MEDLINE=87137443; PubMed=3029068
                                                                                                                                                SEQUENCE
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                                                                                     Chem.
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661 /
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                                                                                   262:2190-2198(1987).
                                                                                                                                                                                                                                                                                            STANDARD;
                                               PubMed=2413018
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73102
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                                                                                                                       N., Hayashida H.,
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BY SIMILARITY.

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HIS-RICH.
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KININOGEN LIGHT
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                                                                                                                                                                                                                                                                                            PRT;
                                                                                                          and
                                                                                                                                                                                                                              BRADYKININ].
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                                                                                                                    Miyata T.,
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RA Kageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
RA Kageyama R., Kitamura N., Ohkubo H., Nakanishi S.;
RT "Differing utilization of homologous transcription initiation sites
RT of rat K and T kininogen genes under inflammation condition.";
RL J. Biol. Chem. 262:2345-2351(1987).
CC ... FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC ... FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC ... FUNCTION: (1) KININOGENS ARE INHIBITORS OF THIOL PROTEASES; (2)
CC ... FUNCTION: (1) HAM-KININOGEN INHIBITS THE THROMBIN-AND PLASMIN-
CC ... FUNCTION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
CC ... FUNCTION OF THROMBOCYTES; (4) THE ACTIVE PEPTIDE
CC ... FUNCTION: (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
CC ... FUNCTION: (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
CC ... FUNCTION: (4B) INDUCTION OF HYPOTENSION, (4C) NATRIURESIS AND
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CC ... FUNCTION: (4B) INDUCTION OF HYPOTENSION, (4C) RELEASE OF
CC ... FUNCTION: (4B) INDUCTION OF NOCICEPTORS (4B) RELEASE OF
CC ... FUNCTION: OF INFLAMMATION OF NOCICEPTORS (4B) RELEASE OF
CC ... FUNCTION: CONTRAST TO HAM-KININOGEN NOT INVOLVED IN BLOOD
CC ... FUNCTION: SECRETED.
CC ... ALTERNATIVE PRODUCTS: 2 ISOFORMS; HAM (SHOWN HERE) AND LAW; ARE
CC ... FUNCSUB SPECIFICITY: PLASMA.
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                                                                                                                     Pfam; PF00031; cystatin; 3. PRINTS; PR00334; KININOGEN. PROSITE; PS00287; CYSTATIN;
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                                                                                                                                                                                                                                              InterPro; IPR000010; -. InterPro; IPR002395; -.
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                                                                                                                                                                                                                                                                                                                                                                   BL; L29428; AAA41486.1; -.
M11884; AAA41487.1; -.
BL; M14369; AAA41484.1; -.
BL; M14369; AAA41485.1; ALT_SEQ.
BL; M16455; AAA41482.1; -.
R; A25486; A25486.
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                                                                                                                                                                                                                                                                                                                                     A28055; A28055.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             requires a license agreement (Se
an email to license@isb-sib.ch).
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Plasma; Repeat; Thiol protease inhibitor; Vasodilator; lood coagulation; Inflammatory response; Signal; plicing; Multigene family.
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the rat.";
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Matches 15
                                                                                             TISSUE=Intestine;

MEDLINE=98226729; PubMed=9560190;

MEDLINE=98226729; PubMed=9560190;

MCMahon R.J., Cousins R.J.;

McMahon R.J., Cousins R.J.;

"Regulation of the zinc transporter ZnT-1 by dietary zinc.";

Proc. Natl. Acad. Sci. U.S.A. 95:4841-4846(1998).

-i- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CULTURATION: MULTIMER (PROBABLE).

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.

-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
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Q62720;
30-MAY-2000
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CARBOHYD
                                                                                                                                                                                                                                                                                              Palmiter R.D., Findley S.D.; "Cloning and functional characterization of a mammalian zinc transporter that confers resistance to zinc.";
                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
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LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE). LOCALIZED ON THE BASOLATERAL SURFACE OF THE ENTEROCYTES.

TISSUE SPECIFICITY: WIDELY EXPRESSED. THE PROTEIN IS DETECTED DUODENUM AND JEJUNUM BUT NOT IN LIEUM AND COLON.
INDUCTION: SLIGHTLY BY ZINC IN THE INTESTINE, BUT NOT THE LIVE SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                σ
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Pred. No. 0.0008;
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E -> K (IN REF. 2).
: D3172DF94FF56AF5 CRC64;
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VSPSYIARVODERDPCAUGOFTHGHOMIHAKO -> RLLNS
CEYKGRLLKAGAGPAPERQAEASTVTP (IN ISOFORM
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Best Local :
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         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restruct use by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
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CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                    FSH_DROME STANDARD; PRT; 2038 AA.
P13709; P13770;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
FEMALE STERILE HOMEOTIC PROTEIN (FRAGILE-CHORION MEMBRANE PROTEIN).
FS(1)H OR FSH.
                                                                                   - I- FUNCTION: REQUIRED MATERNALLY FOR PROPER HOMEOTIC GENES INVOLVED IN PATTERN FORMATION SIMILARITY: HIGH, TO HUMAN RING3 PROTEIN.
- I- SIMILARITY: CONTAINS 2 BROMODOMAINS.
- I- SIMILARITY: CONTAINS 1 ET DOMAIN.
                                                                                                                                                       apparent membrane proteins.";
Dev. Biol. 134:246-257(1989).
                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Pterygota; Neoptera; Endopterygota; Diptera; Brachyoe Ephydroidea; Drosophilidae; Drosophila.
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                                                                                                                                                                                Haynes S.R., Mozer B.A., Bhatia-Dey N., Dawid I.B.;
"The Drosophila fsh locus, a maternal effect homeotic gene, encodes
                                                                                                                                                                                                            SEQUENCE FROM N.A. MEDLINE=89276730; PubMed=2567251;
                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                    NCBI_TaxID=7227;
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between
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15; Conservative
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10 CYTOPLASMIC
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57.7%;
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llidae; Drosophila.
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Pred. No.
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N-LINKED (GLCNAC. . .) (POTENTIAL).
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01-OCT-2000 (Rel. 40, Created)
01-OCT-2000 (Rel. 40, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update
HISTIDINE-RICH MEMBRANE PROTEIN KE4 HOMOLOG
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                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                      This
                                                                                                                                                                                                                                                         Murray B.W., Sueltmann H., Klein J.;
"Identification of a homolog of the human HKE4 gene in zebrafish.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
-i- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (PROBABLE).
                                                                                                                                                                                                                                                                                                                                                                                                                        Brachydanio rerio (Zebrafish) (Zebra danio).
Eukaryota; Metazoa; Chordata; Craniata; Petrlebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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EMBL; M23222; AAA28541.1; ALT_TERM.
EMBL; M15762; AAA70424.1; -.
EMBL; M15763; AAA70423.1; -.
EMBL; M15764; AAA70422.1; -.
Transmembrane; Glycoprotein
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                       EMBL; AF196345; AAF05821.1; -.
                                                                  or send an email to license@isb-sib.ch).
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PROSITE; PS50014; BROMODOMAIN_2; 2.
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FlyBase; FBgn0004656; fs(1)h.
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                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration sen the Swiss Institute of Bioinformatics and the EMBL outstation -
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Pfam; PF01545; Cation_efflux; 1.

21nc; Transport; Transmembrane; Multigene far
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1 1 0 CYTOPLASMIC (POT
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DOMAIN 32 35 EXTRACELLULAR (I
TRANSMEM 36 56 POTENTIAL.
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DOMAIN 79 99 POTENTIAL.
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TRANSMEM 114 134 POTENTIAL.
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Best Local Similarity
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Q60738;
30-MAY-2000 (Rel. 3
30-MAY-2000 (Rel. 3
01-OCT-2000 (Rel. 4
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-!- FUNCTION: MAY BE INVOLVED IN ZINC TRANSPORT OUT OF THE CELL.
LETHALITY OF KNOCKOUT EARLY IN GESTATION SUGGESTS A ROLE OF
PROTEIN IN FETAL ZINC ACQUISITION AND RETENTION.
                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - between Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Palmiter R.D., Findley S.D.;
"Cloning and functional characterization of transporter that confers resistance to zinc.
EMBO J. 14:639-649(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
[1]
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC TRANSPORTER 1 (ZNT-1). SLC30A1 OR ZNT1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus (Mouse)
                                                                                                                                                                                                                                                                         InterPro;
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SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN.
LOCALIZED ON THE PLASMA MEMBRANE (PROBABLE).
TISSUE SPECIFICITY: WIDELY EXPRESSED.
SIMILARITY: BELONGS TO THE SLC30A FAMILY OF TRANSPORTERS.
                                                                                                                                                                                                                                                                                             "; U17132; AAA79233.1; MGI:1345281; Slc30a1.
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Rodentia;
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HIS-RICH.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                   EXTRACELLULAR (POTENTIAL)
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.085;
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(POTENTIAL).
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Best Local
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CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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TRANSMEM
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01-OCT-2000
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                                                                                              Local Similarity
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                                     GHKHKHGHGKHKNKGKKNGKHN----GW
     GHSHSHGHSHG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Z99942; CAB17070.1;
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13; Conserv
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(Rel. 40, Last sequence update)
(Rel. 40, Last annotation update)
L KE4-LIKE PROTEIN H13N06.5 IN CHROMOSOME
                                                                           Conservative
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43.3%;
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N-LINKED (GLCNAC...
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N-LINKED (GLCNAC...
N-LINKED (GLCNAC...
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Pred. No. 0.12
1; Mismatches
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                                                                                                                                                                                                                                                                             POTENTIAL.
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POTENTIAL.

CYTOPLASMIC (POTENTIAL).

6 X 2 AA APPROXIMATE REPEATS OF H-G.

N-LINKED (GLCNAC. ..) (POTENTIAL).

; 7C4FF93FC13CDA22 CRC64;
                                                                                            Pred.
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GN CAUP.
OS Drosog
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RESULT 11
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ID_2C_DICDI
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Best Local Similarity
Matches 11; Conser
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                                                                         SEQUENCE FROM N.A.
MEDLINE=96180722; PubMed=8620542;
                                                                                                                                                                                                                                                       Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                             Gomez-Skarmeta J.-L., del
Ferres-Marco D., Modolell
                                                                                                                                                                                                                                Pterygota; Neoptera; Endopterygota; Diptera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; X16827; CAA34727.1; PIR; S08137; S08137.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as modified and this statement is not removed. U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-90205618; PubMed-2157129;
Ramji D.P., Richards A.J., Jagger P.,
"Two cyclic AMP-regulated genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Dictyostelium discoideum (Slime mold).
Eukaryota; Mycetozoa; Dictyosteliida; Dictyostelium
                                                                                                                                                                                               Ephydroidea;
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Mol. Microbiol. 4:129-135(1990)
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DOMAIN: MAY FORM AN EXTENDED COIL
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Virology 186:9-14(1992).
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InterPro; IPR001356; -.
                                                                the European Bioinformatics Institute.
                                                                                                                                                                              'Channel
                                                                                                                                                                                                         Davison A.J.
                                                                                                                                                                                                                              MEDLINE=92087490;
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TRANSCRIPTIONAL CONTROLER OF AC.5C (ACHAETE-SCUTE). MAY A
ACTIVATOR THAT INTERACTS WITH THE TRANSCRIPTIONAL COMPLEX
ASSEMBLED ON THE AC AND SC PROMOTERS AND PARTICIPATES IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SIMILARITY: BELONGS TO THE TALE/IRO FAMILY OF HOMEOBOX PROTEINS.
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                       non-profit institutions as long and this statement is not removed.
                                                                                      the Swiss
requires a license agreement (See http://www.isb-sib.ch/announce,
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(Rel. 24, Last sequence update)
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L GENE 50 PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.0%;
                                                                                                                                                                                 a new type of herpesvirus.";
                                                                                                                                                                                                                                                                                                                                                                    no RNA stage; Herpesviridae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ΜW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DNA-binding; Homeobox; Nuclear protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 69; DB
Pred. No. 0.18
2; Mismatches
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POLY-HIS.
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                                        nformatics and the EMBL outstat:

There are no restrictions on long as its content is in no
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                   Usage by
                       and for
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                                                                                          a collaboration
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                     in no way commercial
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RESULT 14
SKGR_XENLA
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                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local S
Matches 12
                                                             Berger H., Kell G.,
Berger H., Kell G.,
"The constituents of storage days. Structure of a basic laevis. Structure of 993-296(1989).
modified and this statement is not removed. entities requires a license agreement (See or send an email to license@isb-sib.ch).
                         This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was
                                                                                                                                                                                                 01-JAN-1990 (Rel.
01-APR-1990 (Rel.
01-JUN-1994 (Rel.
                                                                                                                                                                                                                            SKGR_XENLA
P13673;
                                                                                                                                                    Amphibia; Batrachia; Xenopodinae; Xenopodi
                                                                                                                                                                      Eukaryota;
                                                                                                                                                                                         SKIN GRANULE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                        REPEAT
REPEAT
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REPEAT
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                                                                                                        MEDLINE=89289999;
                                                                                                                   TISSUE=Skin;
                                                                                                                                                                               Xenopus laevis (African clawed frog).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical
REPEAT
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                            NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PIR; F36791;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M75136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REPEAT
                                                                                                                                                                                                                                                                                 642
                                                                                                                                                                                                                                                                                                  1 GHKHKHGHGHGKHKNKGKKNG
                                                                                                                                                                                                                                                                                 GHGHGHGHGHG-HGGRGPPGG
                                                                                                                                                                                                                                                                                                                   l Similarity
12; Conserv
                                                                                                                                                                      Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                (Rel. 13, Created)
(Rel. 14, Last sequence up
(Rel. 29, Last annotation
                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               F36791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; Repeat
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                                                                                                         PubMed=2737290;
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                                                                                                                                                                                                                                                                                                                             38.1%;
57.1%;
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                                                                                                                                                                                                                                                                                 661
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                                                                             granules in polypeptide
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Pred. No. 0
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                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                     213
        (See http://www.isb-sib.ch/announce,
                                                                              the dermal glands of Xenopus deduced from cloned cDNA.";
                                                                                                                                                                                                                                                                                                                             DB
. 27;
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                 Usage
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                  and
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                                            collaboration -
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                 commercial
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T2D2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Amphibian skin; (SIGNAL 1 1 CHAIN 27 DOMAIN 27 REPEAT 27 REPEAT 49 REPEAT 71
            TRANSFAC; T02120; -
FlyBase; FBgn0011836; Taf150.
Transcription regulation; Nuclear protein.
BINDS TO TBP AND TAFII-250.
Transcription regulation; Nuclear protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                024325;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
TRANSCRIPTION INITIATION FACTOR TFIID 150 KDA
                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                    binding to core promoter DNA.";
Science 264.933-941(1994).
-!- FUNCTION: TAFS ARE COMPONENTS OF THE TRANSCRIPTION FACTOR IID
-(TFIID) COMPLEX THAT ARE ESSENTIAL FOR MEDIATING REGULATION OF RNA
POLYMBRASE TRANSCRIPTION. TAFII-150 IS AN ESSENTIAL SUBUNIT WHICH
INTERACTS DIRECTLY WITH TBP AND TAFII-250 AND BINDS TO CORE
                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Embryo;
MEDLINE-9423377; PubMed-8178153;
Werrijzer C.P., Yokomori K., Chen J.-L., Tjian R.;
"Drosophila TAFIII50: similarity to yeast gene TSM-1 and specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REPEAT
SEQUENCE
                                                                                          EMBL; X79243; CAA55830.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Y07507
PIR; S04491;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TAFII150).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     r2D2_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          168 GHKMKKLGKKKHHKNRHG-GKNHHKMKKIGKHHG 200
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                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: NUCLEAR. SIMILARITY: TO YEAST TAFII-150 (TSM1).
                                                                                                                                                                                                                                                                                          PROMOTOR DNA.
SUBUNIT: TFIID IS COMPOSED OF TATA BINDING
                                                                                                                                                                                                                                                                          NUMBER OF TBP-ASSOCIATED FACTORS (TAFS).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             93
213 AA;
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23361 MW;
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47.1%;
   138533 MW;
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HIGHLY CHARGED.
W; 72A5B473E26FD064 CRC64;
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Best Local :
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        2 HKHKHGHGHGKHKNKGKKN 20
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                                        Similarity
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Pred. No.
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Search completed: July 6, 2001, 09:26:39 Job time: 970 sec

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

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Result
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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6: sp_mammal:*
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sp_bacteria:*
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       Q9M4H2
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     Q9m435 quercus rob
022671 alnus gluti
09m018 arabidopsis
Q9sm38 sporobolus
018577 caenorhabdi
Q9vu00 drosophila
09vup7 drosophila
09vk49 drosophila
09vk49 drosophila
                                                                                                          009016 rattus norv
027920 bradysia hy
09vws0 drosophila
09zrc7 alnus gluti
09ly2 arabidopsis
039115 arabidopsis
039159 arabidopsis
                                                                                          Q9w3l3 drosophila
Q9w4c1 drosophila
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|------------|------------|------------|-------------|--------------|--------------------|-------------|--------------------|------------|------------|------------|-------------|-------------|-------------|------------|-------------|--------------------|------------|-------------|-------------|------------|------------|------------|-------------|-------------|------------|
| 62         | N          | 62.5       | 63          | 63           | 63                 | 63.5        | 63.5               | 64         | 64         | 64         | 64          | 64          | 64          | 64.5       | 64.5        | 64.5               | 65         | 65          | 65          | 65.5       | 66         | 66         | 66          | 66          | 66 -       |
| 35.0       | 35.3       | 35.3       | 35.6        | 35.6         | 35.6               | 35.9        |                    |            |            | 36.2       |             |             | 36.2        | 36.4       | 36.4        | 36.4               | 36.7       | 36.7        | 36.7        | 37.0       | 37.3       | 37.3       | 37.3        | 37.3        | 37.3       |
| 180        | 472        | 366        | 735         | 213          | 208                | 226         | 110                | 1150       | 1064       | 989        | 643         | 375         | 207         | 1493       | 549         | 398                | 1219       | 194         | 102         | 218        | 1893       | 1891       | 336         | 229         | 125        |
| w          | បា         | υī         | S           | Ŋ            | 10                 | տ           | 10                 | ഗ          | ហ          | U          | σ           | 10          | 10          | ഗ          | σ           | 10                 | G          | σ           | 10          | S          | σı         | G          | N           | υ           | ω          |
| Q9HEG5     | Q9V471     | Q9VGS1     | Q9NES7      | Q9GTNO       | Q43402             | Q9XUH9      | 064396             | Q9VWN4     | Q9V5N1     | Q9W2S4     | Q9U229      | P93066      | Q43397      | Q9VEF7     | Q18009      | 081036             | Q9VT64     | 096853      | 004132      | Q9V3P9     | Q9W4J1     | 077275     | Q55451      | Q9XUI2      | 09Р6В0     |
|            |            |            |             |              |                    |             |                    |            |            |            |             |             |             |            |             |                    |            |             |             |            |            |            |             |             |            |
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| neurospora | drosophila | drosophila | caenorhabdi | drosophila ' | Q43402 brassica na | caenorhabdi | 064396 pisum sativ | drosophila | drosophila | drosophila | caenorhabdi | brassica na | brassica na | drosophila | caenorhabdi | 081036 arabidopsis | drosophila | schistosoma | glycine max | drosophila | drosophila | drosophila | synechocyst | caenorhabdi | neurospora |

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009016;
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SEQUENCE
Q27920
                                                                                                                                                                                      EMBL; AF003623; AAC09070.1; InterPro; IPR002395; -.
                                                                                                                                                                                                       "Strain-specific deletions in exon 10 of rat K-kininogen and T1-kininogen genes allow mapping of both genes to rat chromosome 11.";
Mamm. Genome 8:791-792(1997).
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MEDLINE=97468288; PubMed=9321484;
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus. NCBI_TaxID-10116;
                                                                                                                                                                           PRINTS; PR00334; KININOGEN
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nes 16; Conserv
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126 AA;
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PRELIMINARY;
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Pred. No.
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RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Dayle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Borttier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davles P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Doublos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Erleischmann W.,
RA Dolcher A., Gorrell J.H., Gu Z., Gubart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
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STRAIN-BERKELEY;
MEDLIN-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

Ephydroidea; Drosophilidae; Drosophila.
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01-MAR-2001 (TrEMBLrel.
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"Molecular characterization of an 18 kb segment of DNA puff C4 Bradysia hygida (Diptera, sciaridae).";
Chromosoma 103:715-724(1995).
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Sciaridae; Bradysia.
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TISSUE-SALIVARY GLAND;
MEDLINE-95393845; PubMed=7664619;
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; Endopterygota; Diptera; Nematocera; Sciaroidea;
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacieb J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Zheng X.H., Zhong F.N., Zhong W., Zhong W., Zhong S., Yao Q.A.,
Yang Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
"The genome sequence of Drosophila melanogaster.";
Science 287:185-2195(2000).

REMBL, AE003509; AAF48868.1:
InterPro: TPRO00164; -
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Q9ZRC7;
Q1-MAY-1999
01-MAY-1999
01-MAY-2000
                                                                                                                             Dobritsa S.V., Mullin B.C.;

Dobritsa S.V., Mullin B.C.;

"In vitro expression of actinorhizal nodulin AgNOD-GHRP and demonstration of its toxicity of Escherichia coli.";

(In) Stacey G., Mullin B.C., Gresshoff P.M. (eds.);

the Biology of Plant-Microbe Interactions:

Proceedings of the 8th International Symposium on Molecular Plant-Microbe Interactions, pp.1-1, Unknown Publisher (1996).
                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Embry Magnoliophyta; eudicotyledons; Fagales; Betulaceae; Alnus.
                                            protein from Alnus
 SEQUENCE FROM N.A.
                                                         "Isolation of a nodule-specific cDNA encoding a
                                                                                        TISSUE=ROOT NODULES;
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                                                                                                                                                                                                                                                           SEQUENCE FROM
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PRINTS; PR00334; KININOGEN.
PROSITE; PS00639; THIOL_PROTEASE_HIS; UNKNOWN_1.
SMART; SM00249; PHD; 1.
SMART; SM00249; PHD; 1.
SEQUENCE 686 AA; 70647 MW; 17C56F19B5D2B901
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Liu X., Mattei B.
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57.1%;
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dons; core eudicots; Rosidae; eurosids I;
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Rudd S., L
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Submitted (SEP-1956) to the EMBL/GenBank/DDBJ databases.
EMBL; U69156; AAD00171.1; -.
InterPro; IPR002395; -.
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01-0CT-2000 (TrEMBLrel. 15, La
01-MAR-2001 (TrEMBLrel. 16, La
HYPOTHETICAL 21.5 KDA PROTEIN.
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Eukaryota; Viridiplantae; Embryophyta; Trachec
Magnoliophyta; eudicotyledons; core eudicots;
Brassicales; Brassicaceae; Arabidopsis.
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PROSITE; PRO0190; CYTOCHROME_C; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 1:
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01-MAR-2001 (TrEMBLrel. 1:
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Miyajina N., Tabata S.;
"Structural analysis of Arabidopsis
Sequence features of the regions of
Pl and TAC clones.";
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EMBL; X84315; CAA59059.1; -.
EMBL; AB018113; BAB09163.1; -.
Mendel; 17452; Arath;2767;17452.
SEQUENCE 177 AA; 17830 MW; 3
EMBL; ALDYLLAND,
InterPro; IPR000216; -
PRINTS; PR00239; RHODOPSNTAIL.
173 AA; 18536 MW;
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EMBL; AL391151; CAC01909.1; ...
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Tabata S.,
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Nakamura Y., Kaneko T., Kato T., Asamizu E., Ko
Newes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
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f., Sato S., Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PubMed=8605310; A., Stiefel V.,
                                                                                                                                                                                                                                                                                                                                                                              (Mouse-ear
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e; eurosids II;
                                                                                                                                                                                                                            Kotani
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RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Melson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Melson D.R., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Palazzolo M., Pittnan G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
Spier E., Spradling A.C., Stapleton M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
"The genome sequence of Drosophila melanogaster.";
Science 287:2185-2195(2000).

BY THE STANDON SERVER STANDON SERVER SERVER, ARPA 46312.2;
- ENBL; AROOM SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERVER SERV
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Dodson K., Doup L.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dolohin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Dolohin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Gubar P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Ment S. M. Malford D.,
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Q1-MAR-2001 (TrEMBLrel. 16, La
FEMALE STERILE (1) HOMOEOTIC P
FS(1)H OR CG2252.
                                    Pfam; PF00439;
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InterPro; IPR000104; -
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InterPro; IPR002173; -
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Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang O., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayan A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
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Drosophilidae; Drosophila.
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A Brandon K.L., Noyle C., Baxter E.G., Helt G., Nelson C.K., MILLONGE, A Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.K., MILLONGE, C., Baldwin D., A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D., A Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Beasley E.M., RA Barkova D., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Berson K.Y., Benos P.V., Bernan B.P., Bhandari D., Bolshakov S., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I., RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P., RA Gepablos B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA de pablos B., Detcher A., Deng Z., Mays A.D., Dew I., Dietz S.M., RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P., RA Polser C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K., RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M., RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibeywam C., RA Harris N.L., Harvey D., Heiman T.J., Wein M.-H., Ibeywam C., RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., RA Liux, Mattei B., McIntosh T.C., McLeod M.P., McPherson D., RA Liux, Mattei B., McIntosh T.C., McLeod M.P., McPherson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Nelson D.L., RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shan H., Chan T., Simpson M., Skupski M.P., Smith T.,
Вþ
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Best Local S
Matches 12
          Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith Spier E., Spradling A.C., Stapleton M., Strong R., Sun E., Svirskas R., Tector C., Turner R., Venter E., Wang A.H., War Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Sibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q9W4C1;
01-MAY-2000
01-MAY-2000
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PROSITE;
PROSITE;
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Pterygota; Neoptera;
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12; · Conservative
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PS50014; BROMODOMAIN 2; 2.
PS00583; PFKB KINASES 1; UNKNOWN 1.
1937 AA; 195339 MW; 1D80AA7BB351F06B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                melanogaster (Fruit fly)
Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
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14,
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Pred. No. 0.23
3; Mismatches
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Last annotation updat
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0.23;
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                                     Yang S., Luc
G., Zhao Q., Zheng L.,
S., Zhu X., Smith H.O.,
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Best Local
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InterPro; IPR002395; -
PRINTS; PR00334; KININGEN.
SEQUENCE 554 AA.
                                                                                                                                                                                                                                                                                                                                                               SIGNAL
SEQUENCE
 and histidine-rich pactinorhizal nodule Mol. Plant Microbe I
           MEDLINE=97348585; PubMed=9204569;
Pawlowski K., Twigg P., Dobritsa S., Guan C., Mulli
"A nodule-specific gene family from Alnus glutinosa
and histidine-rich proteins expressed in the early
actinorhizal nodule development.";
                                                                                    Alnus glutinosa (Alder).
Eukaryota; Viridiplantae; Embr;
Magnoliophyta; eudicotyledons;
Fagales; Betulaceae; Alnus.
NCBI_TaxID=3517;
                                                                                                                                                              01-JAN-1998 (TrEMBLrel.
01-JAN-1998 (TrEMBLrel.
01-NOV-1998 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quercus robur (English oak).
Eukaryota; Viridiplantae; Embr.
Magnoliophyta; eudicotyledons;
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TISSUE=IN VITRO SHOOT CULTURES;
Gil B., Pastoriza E.M., Ballester
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9M435;
                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a phase-change related mRNA in oak shoot cultures derived from basal sprouts and crown branches."; submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ271778; CAB72442.1; -.
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12; Conser
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64
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05,
20,
                                                                                                          Embryophyta; Tracheophyta; Spermatophyta;
dons; core eudicots; Rosidae; eurosids I;
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Pred. No. 0.01
0; Mismatches
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Pred. No. 0.07
4; Mismatches
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Last annotation update)
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8E45CABF40F00B6F
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                               Alnus glutinosa encodes
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dicots; Rosidae;
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0.014;
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                                glycine-
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RESULT
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Q9MOL8;
Q9MOL8;
01-0CT-2000 (TrEMBLrel. 15, Cr
r 01-OCT-2000 (TrEMBLrel. 16, L;
T 01-MAR-2001 (TrEMBLrel. 16, L;
T 01-MAR-2001 (TrEMBLrel. 16, L;
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Matches 12
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Best Local
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SIGNAL
CHAIN
                                                                                                                                                                                                                           O9SM38, PRELIMINARY; PRT; 197 AA.

O9SM38; O1-MAY-2000 (TrEMBLrel. 13, Created)

O1-MAY-2000 (TrEMBLrel. 13, Last sequence update)

O1-MAR-2001 (TrEMBLrel. 16, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Benes V.,
Mayer K.F.
                                                                                                  PUTATIVE GLYCINE AND PROLINE-RICH PROTEIN.
Sporobolus stapfianus (Ressurection grass).
Sporobolus viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Chloridoideae;
Eragrostideae; Sporobolus.
NCBI_TaxID=56623;
  Neale A.D., Blc
Evans J., Gaff
"The isolation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EU Arabidopsis sequencing pusubmitted (MAR-2000) to the EMBL; AL161550; CAB78922.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Embryophyta; Tracheo Magnoliophyta; eudicotyledons; core eudicots; Brassicales; Brassicaceae; Arabidopsis.
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                                                              SEQUENCE FROM N.A.
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SEQUENCE 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; Y08436; CAA69708.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR00239; RHODOPSNTAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                        131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      51
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 GHKHKHGHGHGKHKNKGK-KNGKHNG
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12; Conser
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X;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          179 AA; 17745 MW;
Blomstedt C.K., Bronson aff D.F., Hamill J.D.; ion of lowly-transcribed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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30
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86
9188
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50
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he EMBL/GenBank/DDBJ
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Last annotation updat
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Pred. No. 0.01
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score
Pred.
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POTENTIAL.
D85B7EF888C8899A
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                                  P.,
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  genes which
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dicots; Rosidae; eurosids II;
                                      Le T.N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB
.017;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          .042;
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  are induced during
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CRC64;
                                          Guthridge
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            86;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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RESULT
Q9VU00
ID Q9
AC Q9
DT 01
DT 01
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Best Local
  Q9VU00;
Q9VU00;
01-MAY-2000
01-MAY-2000
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01-NOV-1996
                                                                                                                                                                                                                                     Waterston R.; Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases EMBL; U41991; AAA883352.1; \( \). B066535FC510F419 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                           Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.
Craxton M., Dear S., Du Z.,
Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
Lightning J., Lloyd C., Mcmurray A., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Ropora A., Saunders D., Shownkeen F.
Smaldon N., Smith A., Sonnhammer E., Staden R., Sulston J.,
Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
Watson A., Weinstock L., Wilkinson-Sproat J., Wohldman P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    dessication of the resurrection grass Sporobolus stapfianus."; submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ242804; CAB61840.1; -. InterPro; IPR000216; -. InterPro; IPR000216; -. PRINTS; PR00239; RHODOPSNTAIL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=94150718; PubMed=7906398;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q18577
                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                 Submitted
                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                      Nature 368:32-38(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Caenorhabditis elegans
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                                                                                                                                                                                        Local
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nes 16; Conser
                                                                                                                                             1 GHKHKHGHGKGKHKNKGKKNGKHNG
                                                                                                                                                                                                                                                                                                                                                                                                         teon A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
teon A., Weinstock L., Wilkinson-Sproat J., Wohldman P.;
saans ";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 GH-KHKHGHG---HGKHKNKGKKNGKHNGWK 27
                                                                                                                    GPRHGHGHGHRFHHGRRFGRNIG 190
                                                                                                                                                                                        Similarity
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(Tremblrel. 08, Last a
TO THE RAT K-KININOGEN.
    (TrEMBLrel.
                                                                                                                                                                            Conservative
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                                             PRELIMINARY;
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  13,
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01, Last sequence update)
08, Last annotation update)
                                                                                                                                                                                                                                                                                                                                 the EMBL/GenBank/DDBJ databases.
Created)
Last sequence update)
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                                                                                                                                                                                        Score 69;
Pred. No.
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Pred. No. 0.046;
1; Mismatches 10
                                             PRT;
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                                                                                                                                                                          Mismatches
                                             693 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            251
                                                                                                                                                                                                      DB 5;
                                                                                                                                                                                         .058;
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                                                                                                                                                                          8
                                                                                                                                                                                                     Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 197
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rhabditoidea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Coulson A.,
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                                                                                                                                                                         Gaps
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Golayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Galle R.F.,
RA Adams M.D., Celniker S.E., Holt R.A., Wan K.H., Galle R.F.,
RA Berondon R.C., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H.C., Blazef R.G., Champe M., Pfeiffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L.., Beasley E.M.,
RA Ballew R.M., Basu A., Baxendale J., Beyraktaroglu L.., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Burtis K.C., Busam D.A., Buller H., Cadleu E., Center A., Chandra I.,
RA Borkova D., Botchan M.R., Bouck J., Brocktein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brocktein P., Brottier P.,
RA Bortis K.C., Busam D.A., Dewler H., Cadleu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Howland T.J., Wei M.-H., Ibegwam C.,
RA Kinmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Halson P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Woshrefi A.,
RA Melson D.R., Nelson K., Nixon K., Nusskern D.R., Meshert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Wang S.H., Woy M., Murphy B., Murphy L., Murpy D.M., Nelson D.L.,
RA Randert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Wang S.H., Wei R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., A.,
RA Wang K.H., Weiss E.M., Nusskern D.R., Smith H.O.,

                                                                   Query Match
Best Local S
Matches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                              -!- SUBCELLULAR LOCATION: NUCLEAR
-!- SIMILARITY: TO OTHER HOMEOBOX
EMBL; AE003540; AAF49895.1; -.
FlyBase; FBgn0015919; caup.
InterPro; IPR001356; -.
                                                                                                                                                                                                                                                                                                                                              PROSITE; PS00027; HOMEOBOX_1; PROSITE; PS50071; HOMEOBOX_2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Drosophila melanogaster (Fruit fly).

Bukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;

Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Musc

Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                              SMART; SM00389; HOX; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00046;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ephydroidea; Dro
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CAUP PROTEIN.
CAUP OR CG10605.
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                                                                       Local Similarity
nes 12; Conser
GHKHKHGHGHGKHKNKGKKNGKHNG
                                                                                                                                                                                                                                          693 AA;
                                                                                                                                                                                                                                          Homeobox; Nuclear protein.
33 AA; 73667 MW; FBEB1616493F7EC9 CRC64.
                                                                                                39.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Last annotation update
                                                                                                   Score
Pred.
25
                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BY SIMILARITY).
DOMAINS.
                                                                                                   No.
                                                                                                   DB 5;
0.16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Brachycera; Muscomorpha;
                                                                                                                                Length 693;
                                                                   0;
                                                                   Gaps
                                                                0,
```

Search completed: July 6, 2001, 09:25:55 Job time: 991 sec

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